STIC-Biotech/ChemLib





From: Sent: To:

Whiteman, Brian Friday, April 18, 2003 10:19 AM STIC-Biotech/ChemLib

seq search Subject:

09/729,264 11/26/00 Welcher et al.

search seq id nos 1, 3, and 5 against us patent and us patent application databases. search seq id nos 2, 4, and 6 against us patent and us patent application databases.

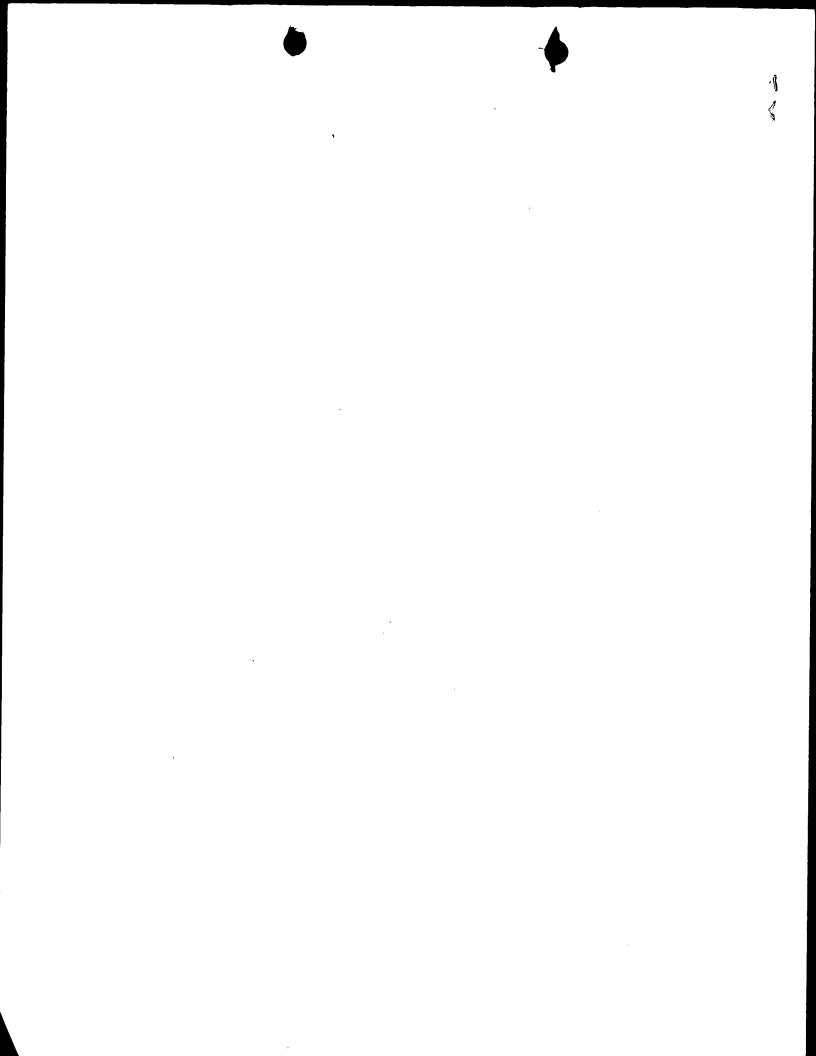
Thanks, Brian Whiteman, 11e12 Patent Examiner - Art Unit 1635 United States Patent and Trademark Office Crystal Mall 1, 11A16 (703) 305-0775

> Mary Jane Ruhl Tech. Info. Specialist, STIC TC-1600 CM-1, Room 6A-06 Phone: 605-1155

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed: 4/30/03
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (wh	ere applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:_	
Other (specify):	



OM protein - protein search, using sw model

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

April 28, 2003, 16:24:32; Search time 36.7435 Seconds (without alignments) 2142.147 Million cell updates/sec

Run on:

Title: perfect score:

US-09-729-264-2 2059

1 MGLVIFLHGSGSGNEVIEGP......HPQASFNLASPEKVSNTTVV 382

Scoring table: Sequence:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:* sp_archea:* sp_bacteria:*

sp_fungi:*

Total number of hits satisfying chosen parameters:

671580 segs, 206047115 residues

671580

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117
118
119
221
221
222
223
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227
228
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330
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331
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122.5
120.1
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120
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117.5
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344
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001761
                                                   Q9W4T9
Q9JJ09
Q9JJ09
Q9JK39
Q9H1X9
Q96RW7
Q06RW7
Q002838
Q9W4U1
Q9U1M1
Q9H3V5
Q17362
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Q9UIR0
Q9N9Y9
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                                             Q9H0T1
                                        Q9XVX3
        Q9W213
                                                                                                                                                          Q95qyl caenorhabdi
Q95qyl caenorhabdi
Q01761 caenorhabdi
Q9p121 homo
                                                                                                                                                                                  Q63155 rattus norv
Q15146 homo sapien
                                                                                                                                            Q9p121 homo sapien
Q96aa2 homo sapien
Q18238 caenorhabdi
                                                                                   Q9h1x9
Q96rw7
Q02838
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Q9w4t9 drosophila
Q9w17174 drosophila
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Q9n9y9 drosophila
                                                                Q9u1m1
Q9h3v5
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Q9hlx9 homo sapien
                                Q16861 homo sapien
Q96iq7 homo sapien
                                                         017362 caenorhabdi
                                                    Q9h0t1
        Q96sc3 homo sapien
                          Q920g3 mus musculu
                                                                7 homo sapien
8 sus scrofa
1 drosophila
1 drosophila
5 homo sapien
              drosophila
drosophila
                                              caenorhabdi
                                                     homo
                                                     sapien
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ALIGNMENTS

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RESULT 1
Q9NSI5
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.S.,
RA Toyoda A., Ishii K., Totoki Y., Choi D.K., Soeda E., Ohki M.,
RA Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Rosenthal A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Shintani A., Sasaki T., Nordsiek G., Hornischer K., Brandt P.,
RA Shintani A., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Lehrach H., Reinhardt R., Yaspo M.L.,
Lehrach H., Reinhardt R., Yaspo M.L.,
DR Lehrach H., Reinhardt R., Yaspo M.L.,
EMBL; Ali6320; CAB90447.1; -
DR InterPro; IPR00359; Ig.
DR InterPro; IPR00359; Ig.
DR InterPro; IPR03599; Ig.
DR InterPro; IPR03599; Ig.
DR Riesselmann S., Shimit R., Yaspo M.L.,
DR Riesselmann S., Shimit R., Tanki R., Shimit R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGSF5 protein (Fragment).
IGSF5.
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      NON_TER
NON_TER
SEQUENCE
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                     315 AA;
                                                 315
                                                     315
                        34599 MW; B69DCB23570FA3D1 CRC64;
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 7: 8: 9: 10: sp_invertebrate:* sp_unclassified:*
sp_rvirus:*
sp_bacteriap:* sp_phage:* sp_organelle:* sp_mhc:* sp_mammal:* sp_human:* sp_rodent:* sp_vertebrate:* sp_plant:* sp_virus:* sp_archeap:*

20 4 4 4 5 5 5 5 6 6 6 7 6 6 6 7 1 1 1 1 1 1 1 1 1 1 1 1	-	Result	
575.5 141 136.5 136.5 133 132.5 131 131 131 129.5 127.5 127.5 127.5	1694	Score	
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270 168 173 1496 1427 344 697 164 315 344 347 344 371 881	315	ngth D	
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Q9D002 Q9D04K2 Q9D626 Q915626 Q91562 Q9DF61 Q9DF61 Q9DF61 Q9DF01	Q9NSI5	ID	
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Q9d912 mus musculu Q9d4k2 mus musculu Q92626 homo sapien Q91562 xenopus lae Q91562 xenopus gall Q9dbp0 mus musculu Q92290 mus musculu Q92290 mus musculu Q92918 gallus gall Q9d915 gallus gall Q99910 mus musculu Q61987 mus musculu Q61988 mus musculu Q61988 mus musculu Q61988 mus musculu	Q9d8g2 mus musculu	Description	
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17T

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RA Kawai J., Shinagawa A., Shibata Y., Yoshino M., Itoh M., Ishii Y. RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ra Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Puruno M., Aono H., Baldarelli R., Barsh G. RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F., Ra Gustincich S., Hill D., Bojunga N., Carainci P., de Bonaldo M.F., Ra Gustincich S., Hill D., Bojunga N., Carainci P., de Bonaldo M.F., Ra Gustincich S., Hill D., Bojunga N., Lee N., Garriboldi M., Forose P., Marchioni L., Mashima J., Mazzarelli J., Mombaerts P., Ring B., Ringwald M., Forose P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Stoch K.-F., Ra Mynshaw-Boris A., Yoshida K., Wang K.H., Weitz C., Whittaker C., Wilming L., Ra Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                  Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO08060; BAB25436.1; -.
EMBL; BC004806; AAH04806.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
201003D20R1k protein (RIKEN CDNA 2010003D20 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 MILITPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEKTNKETETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 MILTPTCTLTIRCCCCRRCCGCNCCCCRCCFCCRKRGERIQFQKKSEKEKTNKETETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 CVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ENEPCEVTCLPSHWTRLPDISWELGLIVSHSSYYPVPEPSDLQSAVSILALTPQSNGTLT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 ENEPCEVTCLDSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLT 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SGSGNEVIEGPQNARVIKGSQARENCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRFT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                         annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murinae; Mus.
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RA Kawai J., Shinagawa A., Shibata Y., Konshino M., Itoh M., Ishii Y. RA Arakawa T., Hara A., Fukunishi Y., Konshino M., Itoh M., Ishii Y. RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Buno H., Kasukawa T., Saito R., RA Kadota K., Matsuda H.A., Ashburnar M., Battalov S., Yamanaka I., RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Blake J., Boffelli p., Bojunga N., Carninci P., de Bonaldo M.F., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Nordone P., Ring B., Ringwald M., Hume D.A., Kamiya M., Lee N.H., RA Sasaki H., Sato K., Schoenbach C., Seya T., Sakamoto N., Stochoka H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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85 00 08
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DR
DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4931420D14RIK.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9D9I2;
Q9D9I2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 NMRTNKADPETKLKSGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSSL--PYQELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 KEKTIK----ETETESGNENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSCGPPHQRAD 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 IILLAVAFSLLLILIIVLIIIFCCC-------CASRREKEESTYQNEIRKSA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 KVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCBRKRGFRIQFQ---KKSE 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
SMART; SM00409; IG; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 270 AA; 29604 MW; A39C273DAA950DFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 ------DSIGEEGPALPTWA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 IPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 PIITNNRFTYASYNSTDSFISELIIHDVQPSDSGSVQCSLQNSHGFGSAFLSVQ----- 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 LVILAQLTASGSSYQIIEGPQNVTVLKDSEAHFNCTVTHGWKLLMWTLNOMVVLSLTTQG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LVIF--LHGSGSGNEVIEGPONATYLKGSQARENCTVSQGWKLIMWALSDMVVLSVRPME 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73; Indels 137; Gaps
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STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE; MEDLINE-21085860; PubMed-11217851;

SEQUENCE FROM N.A. NCBI_TaxID=10090; Eukaryota; Metazoa; Mus musculus (Mouse)

SEQUENCE FROM N.A.

Nature 409:685-690(2001).

RESULT 2

Q9D8G2;

PRELIMINARY;

PRT;

270 AA.

В γ В δÃ 밁 Ş В

Ş В 밁

Matches

Loca

Similarity

82.3%;

Conservative

0; Mismatches

Score 1694; DB 4; Length 315; Pred. No. 2.6e-146;

Query Match

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SORRERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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                                                                                                                                                                                                                                                                                             RC STRAIN-C57BL/6J; TISSUB-TESTIS;
RC STRAIN-C57BL/6J; TISSUB-TESTIS;
RX MEDLINE-21085660; PubMed=11217851;
RX MADLINE-21085660; PubMed=11217851;
RX Kawai J., Shinagawa A., Shibata Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasuchi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann M., Gasaterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Feletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Feletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Feletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamjya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamjya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamjya M., Lee N.H.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).;
EMBL; AK006892; BAB24782.1;
MGD; MGI:1913992; 4931420014Rik
                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 CTLTIRCCCCRRRCCGCNC-CCRCCFCCRKRGER----IQFQKKSEKEKTNKETETESG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9D4K2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9D4K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4931420D14RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 LTRSQLELIEPE--PTMALEPSEITVAFFSHKNANVSDP----EEVPPCLDSDPFPNGDL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 NENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQASFNL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 CSLSRSCCCCRCRCC-CHCRCCRC--CCSRSRRFRSRTTLKFFQITEXGEQSLQRRIRRQ 111
                                                                                                                                                                    Functional annotation of a full-length mouse cDNA collection."; nature 409:685-690(2001).

EMBL; AK016467; BAB30253.1; -.

MGD; MGI:1913992; 4931420014Rik.

SEQUENCE 173 AA; 19581 MW; 147B6F155AC29FDF CRC64;
                                        256 CTLTIRCCCCRRRCCGCNC-CCRCCFCCRKRGFRIQFQKKSEKEKTNKETETESGNENS 314
55 CSLSRSCCCCRCRCC-CYCRCCRC--CCSRSRRFRSRTTLRVRDPKFFQ--ITEKGEQSL 109
                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 AA; 18931 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 141;
32.0%; Pred. No. 5
                                                                                                             6.6%; Score 136.5;
31.5%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 5.3e-05;
                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7A2BD279612A5E94 CRC64;
                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 168;
                                                                                                                         0.00014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Indels
                                                                                                                                              DB 11; Length 173;
                                                                                                      52;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Gaps
                                                                                                             19;
                                                                                                               Gaps
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RESULT 5
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q92626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 GYNSDEOKTTD-----TASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQ 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced analysis of cDNA clones from cell line KG-1 and brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutete
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYELOBLAST KIAA0230 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 PNGDLAS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 ASFNLAS 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97191544; PubMed=9039502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tanaka A., Kotani H., Miyajima N., Nomura N.; Prediction of the coding sequences of unidentified human genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Assignment of a human melanoma associated gene MG50 (D2S448) to chromosome 2p25.3 by fluorescence in situ hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 weiler S.R., Taylor S.M., Deans R.J., Kan-Mitchell J., Mitchell M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=MELANOMA;
MEDLINE=95048383; PubMed=7959781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 3:321-329(1996).
                                                                                                                                                                                                                                                                                                                                                           Mitchell M.S., Kan-Mitchell J., Minev B., Edman C., Deans R.J., "Identification of a novel melanoma gene (MG50) - likely the gene for IL-1 receptor antagonist - which encodes epitopes recognized by human
                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 22:243-244(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   cytolytic T lymphocytes.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                         InterPro; IPR002007; Anim_peroxidase.
InterPro; IPR002007; Anim_peroxidase.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003016; Ig_MHC.
InterPro; IPR00111; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR.Nterm.
                                                                                                                                                                                                                                                                                                                    EMBL; D86983; BAA13219.1;
                                                                                                                                                                                                                                                                                            HSSP; P05164;
                                                               PRINTS; PR00457; ANPEROXIDASE.
SMART; SM00408; IGC2; 4.
SMART; SM00082; LRRCT; 1.
                                                                                                          Pfam; PF01463; LRRCT; 1. pfam; PF00093; vwc; 1.
                                                                                                                                                                              InterPro; IPR003591;
InterPro; IPR001007;
                                                                                                                                                                  Ptam;
                                                       SMART;
               PROSITE;
Immunoglobulin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORRIRROLTRSQLELIEPEPTWALEPSEITVAFFSHKNANVSDP----EEVPPCLDSDPF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E=BONE MARROW;
                                                                                                                                                                                                                                                                                                          AF200348; AAF06354.1; -.
                                                                                                                                          PF00560;
                                                                                                                                                                     PF03098;
                            SM00013; LRRTYP; 1.
SM00369; LRR_TYP; 4.
SM00214; VWC; 1.
                                                                                                                                                                                IPR003591; LRR_typ. IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                  PS01208; VWFC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                 1CXP
                                                                                                                                            ig; 4.
LRR; 5.
                                                                                                                                                                  An_peroxidase; 1.
                                                         LRRCT; 1.
LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                           RESULT 6
Q91562
                                                                                                                         Query Match
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                                                                                                       PRINTS; PRUVULI, SMART; SM00060; FN3; 6.
SMART; SM00408; IGC2; 3.
SMART; SM00410; IG_11ke; 2.
Immunoglobulin domain; Repeat.
Immunoglobulin domain; Length
243 LORPSNVVAIEGODAVLECAVS-GYPTPTIVWMQGD-----EPVPIRTR----KYS 288
                                                                                                                                                                                                                             Pfam; PF00041; fn3; 6.
Pfam; PF00047; 1g; 4.
PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                              InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003961; FN_III.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
                                17 IEGPQNATVLKGSQARFNCTVSQGW--KLIMWALSDMVVLSVRPMEPIITNDRFTSQRYD 74
                                                                                                                                                                                                                                                                                                                                                                                EMBL; U10986; AAA70168.1; -.
                                                                                                                                                                                                                                                                                                                                                                       HSSP; P40189; 1BQU
                                                                                                                                                                                                                                                                                                                                                                                  "Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the nervous system of developing xenopus embryos.";
Dev. Biol. 166:654-665(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pierceall W.E., Reale M.A., Candia A.F., Wright C.V., Cho K.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-95113183; PubMed=7813784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91562 PRELIMINARY; PRT; 1427 AA. 991562; O1-NOV-1996 (TrEMBLrel. 01, Created) O1-NOV-1996 (TrEMBLrel. 01, Last sequence update) O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     567 GEPEPAITWINDGVQVTESGKFHISPEGFLTINDVGPADAGRYECVARNTIG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 GFSLP--TWGKVGLGL--AGTMLLTPTCTLTI-----RCCCCRRRCCG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  515 -GQYECQAV--NIIGSQKVVAHLTVQPRVTPVFASIPSDTTVEVGANVQLP-----CSSQ 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 NGTLTCVATWKSLKARKSATVNLTV------IRCPQDT----GGGINIPGVLSSLPSL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               459 RVVIEGOTVDFQC-EAKGNPPPVIAWTKGGSQLSVDRRHLVLSSGTLR--ISGVALHDQ- 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 LVVAENEPCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPOS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 -----GG-----LYIQNVVQGDSGEYACSATNNIDSVHATAFIIVQALPQFTVTPQD 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 GSPARPTEVIQPONTEVLVGESVTLECSATGHPPPRISWTRGDRTPLPVDPRVNITPS-- 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 FTSORYDOGGNETSEMITHNVEPSDSGNIRCSLONS--RLHGSAYLTVOVKGELFIPSVN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 GSGSGNEVIEGPONATVLKGSQARFNCTVS-QGWKLIMWALSDMVVLSVRPMEPIITNDR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73;
                                                                                                                                                                                                                                                                                       IPR003006;
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                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1496 AA; 167209 MW; E9B9A7069BF1ABFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 36; Mismatches 127; Indels
                                                                6.5%; Score 133; DB 13; Length 1. 25.7%; Pred. No. 0.0046; ative 33; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                   Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.6%; Score 135; DB 4; Length 1496; 25.0%; Pred. No. 0.0032;
                                                                                                    DB 13; Length 1427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56; Gaps
                                                                    Gaps
                                                                  13;
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DЬ
                                                                                                                    Qγ
                                                                                                                                                          Дb
                                                                                                                                                                                       Ωy
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                                                                                                                                                                                                                                                              γ
                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 70;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
232 GASVGQKGILQCEASAVPVAEFQ---WFKEDTRLA 263
                               217 GGGINIPGVL----SSLPSLGFSLPTWGKVGLGLA 247
                                                           177 QGFVSEDEYLE----ITGITREQSGEYECSAV-NDVAVPDVRKVKVTVNYPPYISNAKNT 231
                                                                                            162 YYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV-----IRCPQDT 216
                                                                                                                                129 H----LIVQVPPQIVNISSDITVNEGSSVTLMCLAFGRPE-----PTVTWR---HLSGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; 19; 3
SMART; SM00409; IG; 3
SMART; SM00408; IGc2; 3
SMART; SM00410; IG_11ke; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20499204; pubMed=11042360;
Lodge A.P., Howard M.R., McNamee C.J., Moss D.J.;
"Co-localisation, heterophilic interactions and regulated expression of IgLON family proteins in the chick nervous system.";
Brain Res. Mol. Brain Res. 82:84-94(2000).
EMBL; AF29294; AAGO1877.1;
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig-C2.
InterPro; IPR003598; Ig-C2.
InterPro; IPR003598; Ig-C2.
                                                                                                                                                                 106 HGSAYLTVQVMGELFTPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHSS 161
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain
                                                                                                                                                                                                  80 DKWSIDNRVVILSN---TKTQY-----SIKIHNVDVYDEGPYTCSVQTDNHPKTSRV 128
                                                                                                                                                                                                                                    55 ---SVRPMEPIITNDRFTSQRKDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRL 105
                                                                                                                                                                                                                                                                     21 LLFLVPAGVPVRSGDATFPKAMDNVTVRQGESATLRCTVDDRVRRVAW-LNRSTILYAGN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
0BCAM alpha 1 isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                     4 VIFLHGSG----SGNEVI-EGPONATVLKGSQARENCTVSQGWKLIMWALSDMVVL---- 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9DF61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9DF61
                                                                                                                                                                                                                                                                                                                                                                             тосат
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 YQCIAENEAGNIQTYAQLIIPDPAVPSSSILPSAPRDV-----VPVLVSS 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 LTCVA-----TWKSLKARKSATVNLTVI-RCPQDTGGGINIPGVLSS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 PCEVTCL----PSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 DIEFECAVSGKPS-----PTVKWTKNGEVVIPSDYFQIVDGSNLR----ILGLVKSDEGY 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 VLGG--SNLLISNVTDDDAGAYTCVATYKNENTSFSADLTVMVPPQFLNHPANLYAYESM 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 QGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENE 132
                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              344 AA; 37531 MW; 37FE6051CBF0E7B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                6.4%; Score 132.5; DB 1
25.5%; Pred. No. 0.00081;
                                                                                                                                                                                                                                                                                                                                      38; Mismatches 104; Indels 63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 AA
                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 344;
                                                                                                                                                                                                                                                                                                                                        16;
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RESULT 8
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimhl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weatz C., Whittaker C., Wilming L.,
RA Havashizaki Y.:
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Solute carrier family 34 (sodium phosphate), member 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9DBP0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=LUNG;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL, AK004832; BAB23600.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003841; Na_Pi_cotrans.
Pfam; PF02690; Na_Pi_cotrans; 1.
TIGRFAMS; TIGR01013; 2a58; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1342284; Slc34a2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                     436 FTSAMTPLIGIGVISIERAYPLTLGSNI------GTTTTAILAALASPGNT--LRSSL 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 MIVKLLGS-----VLRG-QVATVIKKTLNTDFPFPFAWLTGYLAILVGAGMTFIVQSSSV 435
                                                                                                                       567 LLVLCLRMLQFRCPR-----ILPLKLRDWNFLPLWMHSLKPWDNV-----ISLATTC
                                                                                                                                                                                                                                           151 --WELGILVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLT
                                                                                                                                                             209 VI------RCPQDTGGGINIPGVL---SSLPSLGFSLPTWGKVGLGLAGTMLLTPTC 256
                                                                                                                                                                                                    525 YRW---FAVEYLIFFFFVTP-----LTVFGLS-----LAGWPVLVGVGVPIILLL 566
                                                                                                                                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNSRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLP------DIS-- 150
                                                                                                                                                                                                                                                                                                                                                                                                           WKLIMWALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSL 100
                                                                                                                                                                                                                                                                                         QIALCH---
NENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQASFNL
                                                                                TLTIRCCCCRRRCCG-----CNC-CCRCCFCCRKRGFRIQFQKKSEKEKTNKETETESG 310
                                         -FQRRCCCCCRVCCRVCCMVCGCKCCRCSKCCR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     697 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76244 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.4%; Score 131; DB 11; 20.6%; Pred. No. 0.0028;
                                                                                                                                                                                                                                                                                           ---FFFNISGI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2A7B9384857EF16F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 123; Indels 168;
                                                                                                                                                                                                                                                                                               -----LLWYPIPFTRLPIRLAKGLGNISAK
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                                                   ---- DQG
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RESULT
Q9Z290
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Type IIb Na/phosphate-cotransporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9Z290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed in mammalian small intestine."; proc. Natl. Acad. Sci. U.S.A. 95:14564-14569(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-NMRI; TISSUE-SMALL INTESTINE; MEDLINE-99045724; PubMed-9826740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLC34A2 OR NPT2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S./
EMBL; AF081499; AAC80007.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            686 LSMKALSNTTV 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR003841; Na_Pi_cotrans. pfam; PF02690; Na_Pi_cotrans; 1. TIGR01013; 2a58; 1. TIGREAMS; 1. TIGREAMS; 697 AA; 76286 MW; 8391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tagret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hilfiker H., Hattenhauer O., Traebert M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 ASPEKVSNTTV 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1342284; Slc34a2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of a murine type II sodium-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 MIVKLLGS-----VLRG-QVATVIKKTLNTDFPFPFAWLTGYLAILVGAGMTFIVQSSSV 435
                                                                                                                                                                                                                                                                                                                                                   486
                                                                                                                                                                                                                                                                                                                                                                                  101 QNSRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLP------DIS-- 150
                                                                                                                                                                                                                                                                                                                                                                                                                    436 FTSAMTPLIGIGVISIERAYPLTLGSNI------GTTTTAILAALASPGNT--LRSSL 485
                                                                                                                                                                                                                                                                             525 YRW---FAVFYLIFFFFVTP-----LTVFGLS-----LAGWPVLVGVGVPIILLL
                                                                                                                                                                                                                                                                                                              151 --WELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLT 208
                                                                                                                                    614 -FORRCCCCCRVCCRVCCMVCGCKCCRCSKCCR-
                                                                                                                                                                                                                                            209 VI------RCPQDTGGGINIPGVL---SSLPSLGFSLPTWGKVGLGLAGTMLLTPTC
                                                                                                   311 NENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQASFNL 370
686 LSMKALSNTTV 696
                                 371 ASPEKVSNTTV 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
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                                                                                                                                                                                                                                                                                                                                               QTALCH-----FFFNISGI------LLWYPIPFTRLPIRLAKGLGNISAK 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WKLIMWALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSL 100
                                                                                                                                                                       TLTIRCCCCRRRCCG-----CNC-CCRCCFCCRKRGFRIQFQKKSEKEKTNKETETESG 310
                                                                                                                                                                                                          LLVLCLRMLQFRCPR-----ILPLKLRDWNFLPLWMHSLKPWDNV-----ISLATTC
                                                                    EE----EEEKEQD---IPVKASGAFDNAAMSKEC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.4%; Score 131; DB 1:
Similarity 20.6%; Pred. No. 0.0028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               697 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    839E5CCB0F565265 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GSQARFNCTVSQG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 168;
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                                                                                                                                                                                                                                                         256
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                                                                                                                                                                                               Q9DGI5;
Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J., "Characterisation of CEPU-Se, a secreted isoform of the IgLO protein CEPU-1.";
                                  TISSUE-BRAIN;
                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                              SEQUENCE FROM N.A.
                                                                                                                     Gallus gallus (Chicken).
                                                                                                                                     CEPU-SE
                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                 273 --NCCC-RCCFCCR 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                     102 CRTCCCTRCCTCCR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z66499; CAA91301.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q22048;
Q22048;
                                                                                                                                                                                                                                                                                                                                    213 PQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGC
                                                                                                                                                                                                                                                                                                                                                                                 153 LGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T01B7.8 protein.
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01-NOV-1996 (TremBLrel.
01-MAR-2002 (TremBLrel.
                                                                                                                                                                                                                                                                                                                   58 KRQGGCGCGCGC-----
                                                                                                                                                                                                                                                                                                                                                           6 LAILLAIGTFIAV----SQVQSAV-----LPVSSTELATVGTDVSTASTAIDTLGNSSSRV
                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00022;
PS01208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yating biology.";
282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1. PS00269; DEFENSIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001450; 4Fe4S_ferredoxin.
IPR001271; Defensin_mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 AA;
                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VWFC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          6.3%; Score 129.5; DB 5 32.1%; Pred. No. 0.00058;
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                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                      315 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                             53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 164;
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      IgLON family
                                                                                                                                                                                                                                                                                                                                                                                                             27;
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    Query Match
Best Local Similarity
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                                                                         Piam; PRO0047; 19; 3,
SMART; SM00409; IG; 3,
SMART; SM00408; IGc2; 3,
SMART; SM00410; IG_like; 2.
                                                   SEQUENCE
                                               Immunoglobulin domain.
SEQUENCE 344 AA; 37924 MW;
                                                                                                                                    InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                 nervous system.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF282980; AAK00276.1;
                                                                                                                                                                                                                                               Kim T.H., Choi S.C., Kim J
"Cloning and expression of
                                                                                                                                                                                                                                                                            STRAIN=ICR; TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                    InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                        Neurotrimin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q99PJ0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q99РJ0;
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SMART; SM00408; IGc2; 3.
SMART; SM00410; IG_like; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 GFISEDEYLE----ITGITREQSGEYECSAS-NDVAAPVVQRVKVTVNYPPYISDAKSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 VPVGQKGILMCEASAVPSADFQ---WYK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 GGINIPGVL----SSLPSLGFSLPTWGK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 YFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV-----IRCPQDTG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 VH----LIVQVSPKITEISSDISINEGGNVSLTCIA---TGRPDPTITWR----HISPKAV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPD--ISWELGLLVSHSSY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF292936; AAG01879.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin domain SEQUENCE 315 AA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 KWCLDPRVVLLANTKTQYSIQ------IHDVDVYDEGPYTCSVQTDNHPKTSR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 MVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 LLFLVPAGVPVRSGDATFPKAMDNVTVRQGESATLRCSVDNRVTRVAWLNRSSILYAGND 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VIFLHGSG----SGNEVI-EGPQNATVLKGSQARFNCTVSQ-----GW---KLIMWALSD 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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6.2%; Score 127.5; DB 25.3%; Pred. No. 0.0023
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                                                                                                                                                                                                                                                            Kim J., Jeon J.W., Kim K.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34606 MW;
                                                                                                                                                                                                                                          mouse neurotrimin gene in the developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
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                                              3ECC6D5EE6C5C17D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 AA
              DB 11; Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 315;
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Matches

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Conservative

39;

Mismatches

109;

Indels

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Gaps

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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 DLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCP-----QDTGGGINIPG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 -LIVQVSPKIVEISSDISINEGNNISLTCIATGRPE-PTVTWR----HISPKAVGFVSEDE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 YLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kimura Y., Shirabe K., Fukushima M., Takeshita M., Tanaka H.; "CEPU-1: an Immunoglobulin Superfamily Molecule, Has Cell Adhesion Activity and Shows Dynamic Expression Patterns in Chick Embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 YLQ----IQGITREQSGEYECSAS-NDVAAPVVPRVKVTVNYPPYFSEAKGTGVPVGQKG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 VL----SSLPSLGFSLPTWGK 241
                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; 19; 3.
SMART; SM00408; IGC2; 2.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB011810; BAA31514.1; .
InterPro; IPR003598; Ig_C2.
InterPro; IPR003500; Ig_11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 TLQCEASAVPSAEFQ --- WFK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 --PYAGNDKWCLDPRVVLLGNTQTQYSIEIQNVDVYDEGPYTCSVQIDNHPKTSRVH--- 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 MEPIITNDRF-TSQRYDQGGNFTSE--MIIHNVEPSDSGNIRCSLQ-----NSRLHGSA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 LLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTTDNRVTRVAWLNRSTI----- 74
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VIFLHGSG----SGNEVI-EGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRP 58
                                                                                                                                                                                                                                                                                                                                                                                                   mmunoglobulin domain
                                                                  163 YEVPEPSDLQSAVSILALTPOSNGTLTCVATWKSLKARKSATVNLTV-----IRCPQDTG 217
                                                                                                    128 VH----LIVQVSPKITEISSDISINEGGNVSLTCIA---TGRPDPTITWR---HISPKAV 177
                                                                                                                                     105 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPD--ISWELGLLVSHSSY 162
218 GGINIPGVL----SSLPSLGFSLPTWGK 241
                                                                                                                                                                      81 KWCLDPRVVLLANTKTQYSIQ-----IHDVDVYDEGPYTCSVQTDNHPKTSR 127
                                                                                                                                                                                                        51 MVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSR 104
                                                                                                                                                                                                                                                                             4 VIFLHGSG----SGNEVI-EGPQNATVLKGSQARENCTVSQ-----GW---KLIMWALSD 50
                                                                                                                                                                                                                                           LLFLVPAGVPVRSGDATFPKAMDNVTVRQGESATLRCSVDNRVTRVAWLNRSSILYAGND 80
                                   GFISEDEYLE----ITGITREQSGEYECSAS-NDVAAPVVQRVKVTVNYPPYISDAKSTG 232
                                                                                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                   344 AA; 37613 MW; 22CAA8F526A6B57E CRC64;
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                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                 6.2%; Score 127.5; DB 25.4%; Pred. No. 0.0023;
                                                                                                                                                                                                                                                                                                                       41;
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                                                                                                                                                                                                                                                                                                                           98; Indels 61; Gaps
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Q61987;
                                                                                                                                                                                                                                      Matches
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MEDIINE-95349951; PubMed-7624144;
Ganju P., Walls E., Brennan J., Reith A.D.;
Cloning and developmental expression of Nsk2, a novel receptor
"Cloning and developmental expression of Nsk2, a novel receptor
tyrosine kinase implicated in skeletal myogenesis.";
Oncogene 11:281-290(1995)
Oncogene 11:281-290(1995)
-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nsk2 protein precursor. MUSK OR NSK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR003598;
Interpro; IPR003600;
Interpro; IPR003006;
Interpro; IPR003290;
Interpro; IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 VPVGQKGILMCEASAVPSADFQ---WYK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0109; TYRKINASE.
ProDom: PD000001; Euk_Pkinase;
SMART; SM00410; IGC2; 2.
SMART; SM00410; IG_like; 1.
SMART; SM00219; TYFKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001245; Tyr_pkinase.
Pfam; PF01392; Fz; 1.
Pfam; PF00047.
                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS50038; FZ; 1.

PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.

PROSITE: PS00101; PROTEIN_KINASE_ST; 1.

PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE: PS00128; TUBULIN_B_AUTOREG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002453; Beta_tubulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pfam; pF00047; ig; 3.
pfam; pF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000024; Fz_domain.
                                                                                                                                                                                                                                                                                                                                               ATP-binding; Immunoglobulin domain; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                               Signal; Transferase.
                                                                                                                                                                     122 KITRPPINVKIIEGLKAVLPCTIMGNPKPSVSWIKGD-----NALRENSRIAALE- 171
          184 SNGTLTCVAT----WKSLKARKSATVNLTVIR------CPODTGGGINIPG-----V 225
                                                                                                       172 -----SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKLVKLEVEVLGRILRAPESHNV 223
                                          224 TFGSFVTLRCTEIGIP-----VPTISWIENGNAVSSGSIQESVKDRVIDSRLQLFITKP- 277
                                                                        129 AENEPCEVTC----LPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQ 183
                                                                                                                                                                                                    15 EVIEGPQNATVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRPMEPIITNDRFTSQRY 73
                                                                                                                                    74 DQGGNFTSEMIIHNVEPSDSGNIRCSLONSRLHGSAY----LTVQVMGELFIPSVNLVV 128
                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                        70;
871 AA; 97047 MW; F3C53DC6AFE702AB CRC64;
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                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                       6.2%; Score 127.5; DB
21.7%; Pred. No. 0.0077
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 Last annotation update)
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SMART; SM00410; IG_like; 1.
SMART; SM00219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS50038; PZ; 1.
PROSITE; PS50017; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50010; PROTEIN_KINASE_ST; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000074; Fz_domain.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003500; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003290; Ser_thr_pkinase.
InterPro; IPR003245; Tyr_pkinase.
                                                                                                                                                                       SEQUENCE 881 AA; 98435 MW; EA0D0282E9B28ED7 CRC64;
                                                                                                                                                                                                      PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.
ATP-binding; Immunoglobulin domain; Serine/threonine-protein kinase;
                                          122 KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD-----NALRENSRIAALE- 171
                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01392; Fz; 1.
Pfam; PF00047; 1g; 3.
Pfam; PF00069; Pkinase; 1.
74 DQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-----LTVQVMGELFIPSVNLVV 128
                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nsk2 protein precursor.

MUSK OR NSK2.

MUS musculus (Mouse).

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
                                                                         15 EVIEGPONATVLKGSOARENCTVSQGWK-LIMWALSDMVVLSVRPMEPIITNDRFTSQRY 73
                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ganju P., Walls E., Brennan J., Reith A.D.;
"Cloning and developmental expression of Nsk2, a novel receptor tyrosine kinase implicated in skeletal myogenesis,.";
Oncogene 11:281-290(1995).
-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                        Local Similarity
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 LVFLPTTSHRDÞEDAQELLIHTAWNEL-----KAVSÞLCRÞAAEALLCYHLFLECSÞG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 LSSLPSLGFSLP-----TWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCN-- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 --GLYTCIATNKHGEKFSTAKAAATVSTAEWSKSQKDSQGYCAQYRGEGVLMQGPGEKML 335
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                         6.2%; Score 127.5; DB 11; Length 881; 21.7%; Pred. No. 0.0078;
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                                                                                                         41; Mismatches 125; Indels 87; Gaps
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389 VVPTPMPICREYCLAVKELFCAK 411
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                                                             336 LVFLPTTSHRDPEDAQELLIHTAWNEL-----KAVSPLCRPAAEALLCYHLFLECSPG 388
                                                                                                  226 LSSLPSLGFSLP------TWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCN-- 273
                                                                                                                                      278 --GLYTCIATNKHGEKFSTAKAAATVSTAEWSKSOKDSOGYCAQYRGEGVLMQGPGEKML 335
                                                                                                                                                                             184 SNGTLTCVAT----WKSLKARKSATVNLTVIR------CPQDTGGGINIPG-----V 225
                                                                                                                                                                                                                224 TFGSFVTLRCTEIGIP-----VPTISWIENGNAVSSGSIQESVKDRVIDSRLQLFITKP- 277
                                                                                                                                                                                                                                                     129 AENEPCEVTC----LPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQ 183
                                                                                                                                                                                                                                                                                          172 -----SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKLVKLEVEVLGRILRAPESHNV 223
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Search completed: April 28, 2003, 21:07:34 Job time: 42.7435 secs

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KEYWORDS SOURCE ORGANISM

AX380398.1 GI:19575328

DNA

REFERENCE

Mammalia; Eukaryota; Homo sapiens human.

p; Metazoa; Eutheria;

Chordata; Primates;

Craniata; Vertebrata; F Catarrhini; Hominidae;

Euteleostomi;
; Homo.

AUTHORS TITLE JOURNAL

Welcher,A.A., Sarmiento,U.M., Schultz,H.J. and Chute,H.T. B7-like molecules and uses thereof Patent: WO 0200710-A 3 03-JAN-2002;

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. RESULT 1 AX380398 LOCUS DEFINITION ACCESSION VERSION 0 0 O a a a 00000 00000 O 1102.8 378.4 326.6 326.5 182.4 181.8 181.8 181.8 1122.4 1119.6 Score 100 57.4 56.6 52.8 52.8 52.8 51.8 51.4 50.6 50.6 54 1168 bp Sequence 3 from Patent W00200710. AX380398 Query Match Length DB 222922622222229292 HSU6333 AC120145 HSCAGCTIG HSCAGCTIG HSCAGCTIG AC1120346 AC11203502 AC00923502 AC009236 AC009236 AC009236 AC013439 AC013439 AC113926 AC113926 AC113926 AC113916 AC113916 AC113916 AC113916 AC113916 AC113916 AC109316 AC109316 AC109316 AC109316 AC007840 AC0093016 AC0093016 AC0093016 AC0093016 AC0093016 AC003797 AC003596 AC0153596 AC0153596 AC015396 AC015396 HS21C080 AC020851 AX380398 AX380396 AK092516 AX380400 AX380402 AX380404 AF121782 AX380406 Ħ AX380408 BC004806 SUMMARIES ALIGNMENTS linear ACQ20851 Mus muscu (16332 Human super ACQ20145 Mus muscu (16332 Homo sapi ACQ20146 Mus muscu ACQ18350 Enattus no ACQ2059 Diagnosti ACQ2059 Homo sapi ACQ2059 Homo sapi ACQ2059 Homo sapi ACQ2059 Homo sapi ACQ2058 Rattus no ACQ2058 Homo sapi ACQ2058 BC004806 Mus muscu AC120346 Mus muscu AF064857 Homo sapi AX380400 Sequence AX380402 Sequence AX380404 Sequence Description AX380408 Sequence AX380406 Sequence AF121782 Homo sapi AL163280 Homo sapi AK092516 Homo sapi AC020851 Mus muscu PAT 18-MAR-2002 Sequence Sequence Rattus no Rattus no Rattus no Drosophil Rattus no Drosophil Drosophil

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TTCATTGCCTACTTGGGGCAAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCC
                                                                                                                                                GAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGATTCGGTGTCCCCA
                                                                                                                                                                                                                                                                                                                                                                               TCTCCTGGTCAGCCATTCAAGCTATTATTTTGTTCCGGAGCCCAGCGACCTTCAAAGTGC
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                                                    AGACACTGGAGGTGGTATTAATATTCCAGGTGTATTATCAAGTTTACCGAGTTTAGGTTT
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/POOREIN_Id="CAD28217.1"
//db_xref="GI:19575329"
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/db_xref="taxon:9606"
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TITLE
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SOURCE
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    Query Match
Best Local Sim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
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Ax380396
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                         /codon_start=1
/protein_id="CAD28216:1"
/protein_id="CAD28216:1"
/bxref="Gi:19575327"
/translation="MGLVIFLHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMMALSDMYVLSVRPMEPIITNDRETSQRYDQGGNETSEMIIHNPEPSDSGNIRCSLQNSRLHGSANTYLOVMGELFIPSVNLVVARENEDECEVTCLPFHMTRLPDISWELLGLLVSHSSYYFYPEPSDLQSAVSILALTPQSNGTLTGVATWKSLKARKSATVNLTYVRCPQDTGGGINIPGVLSSLESLGSLASTWGKVGLGLAGTMLLTPTCTLTIRCCCGRRCCGCRCCCRCCCCRRCFCCFRREGERIQFQKKSEKTNKETETESGNENGGYNSDEQKTTDTASLPPKSCESSDEQRNSSCGPPHQRADQRPPRASHPQASFNLASPEKVSNTTVV"
a 307 c 286 g 287 t
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1. .1175
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/db_xref="taxon:9606"
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                 96.1%;
99.5%;
Score 1122.4; DB 6;
Pred. No. 2.2e-259;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                         202 CGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGTCCTGAAGGG 261
                                      283 GGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATC
                                                                                                                                                                                                            163 CAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTT
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                                                                                                                                                                                                                                                       CACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATGT
                                                                                                                          CACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3985) Fax:81-438-52-3986) (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) KEDO human cDNA sequencing project supported by Ministry of NEDO human cDNA sequencing project supported by Ministry of Seconomy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library Research Association: Helix Research Institute (HRI) (supported by Japan construction: Helix Research Institute of Technology RAB, Key Technology Center etc.); 5'-6 3'-end one passs sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB. RAB; annotation: HRI and RAB.
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Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE6
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HOMO Sapiens cDNA FLJ35197 fis, clone PLACE6017788, highly similar
to IGSF5.
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                                                                                                                                                                                                                                                                             TCTCCCTCCCAAATCCTGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                 AAGTGGAAATGAAAACTCCGGCTACAATTCAGATGAACAAAAGACCACAGAAACCGCTTC
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      B7-like molecules and uses thereof Patent: WO 0200710-A 5 03-JAN-2002;
                             Welcher, A.A., Sarmiento, U.M., Schultz, H.J.
                                                                                                                                            Sequence 5 from Patent WO0200710 AX380400
                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                      Primates; Catarrhini; Hominidae;
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                             and Chute, H.T
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754 ACTAGCAGGCACCATGCTTCTGACGCCGACGTGTACTCTTACAATACGCTGCTGCTG
                                                             766
                                                                                                                                                       706
                                                                                                                                                                                 634 AAATCTCACTGTGATTCGGTGTCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGT
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                                                                                                                                                                                                                                                                                                                                                                514 TCCGGAGCCCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAA 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 TGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCAT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 TGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCAT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 GTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 CCTGAAGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCAT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 AGAAGCTGTAGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 CCTGAAGGGCTCCCAGGCTCGCTTCAACTGCAGCGTCTCCCAGGGCTGGAAGCTCATCAT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 AGACCCACCCGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATGCAAGAGT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                    ATTATCAAGTTTACCGAGTTTAGGTTTTTCATTGGCTACTTGGGGCAAAGTTGGACTTGG
                                                                                                                                                                                                                                                      TGGGACTTTGACTTGCGTGGCTACCTGGAAGACCCTGAAGGCCCGCAAGTCTGCAACTGT 633
                                            ATTATCAAGTTTACCGAGTTTAGGTTTTTCATTGCCTACTTGGGGCCAAAGTTGGACTTGG
                                                                                                                                      AAATCTCACTGTGATTCGGTGTCCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGT
                                                                                                                                                                                                                              TGGGACTTTGACTTGCGTGGCTACCTGGAAGACCCTGAAGGCCCCGCAAGTCTGCAACTGT
                                                                                                                                                                                                                                                                                                                     TCCGGAGCCCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCCACAGAGCAA
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/db_xref="g1:19575331"
/translation="merhiltypeavgsgsgneviegponatvlkgsgarenctvsgg
kklimmalsdmvvlsvremæpiitndretsgrkdoggnetsemiihnvepsdsgnirg
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slonsrlægsakltyovnsilaltposngtlycomynslkarsakvnityircpg
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RCGCCCCCCRRRGGFRIOFOKKSEKERTNKETETESGNENSGYNSDEØKTTETASLp
FKSCESSDPEORNSSCGPPHQRADQRPPRPASHPQASFNLASPEKVSNTTVV"
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99.1%;
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Pred. No. 1.5e-258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCTGCTGTTGTTTCTGCTGCTGTAGAAGAAA 873
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                                                                                                                                                              Local Similarity
                       83
                                                               \vdash
                                                                                                 8 ATGGTGGCAGGAGCCATGGAAAATAGAGACCCCACCCGGTTCTGGGTCTGGTAATGAAGTC 67
ATAGAAGGCCCCCAAAATGCAAGAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACC 127
                                                             Sequence 7 from Patent W00200710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ammmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Welcher, A.A., Sarmiento, U.M., Schultz, H.J. and Chute, H.T.
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                     /protein_id="GAD28219.1"
protein_id="GAD28219.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                             ILNKETVAVALLTSGLINVHÞGQQVIHRLLLIWÞVLRRSVIQL"
300 c 283 g 266 t
                                                                                                                                                                                                                                                                                   DTGGGINIPGVLSSLESLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCCCCCCCRKRGNLKKRRQTKKLRQKVEMKTPATIQMNKRPQTPLLSLPNPVNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="unnamed protein product"
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                                                                                                                                                                   94.48;
                                                                                                                                                  0; Mismatches
                                                                                                                                                                     Score 1102.8; DB 6; Length 1139; pred. No. 1.2e-254;
                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ATAGAAGGCCCCCAAAATGCAAGAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 AGATGCAGCCTCCAGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGTTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          668 GGAGGTGTATTAATATTCCAGGTGTATTATCAAGTTTACCGAGTTTAGGTTTTTCATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1148 AGTAATACAACTGTAGTATA 1167
                                                                                                                                                                                                                                1028 AGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCTCCTCACCAGCGGGCTGATCAACGT 1087
                                      1119 AGTAATACAACTGTAGTATA 1138
                                                                                                                  1059 CCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTAATCTGGCCAGTCCTGAGAAGGTC 1118
                                                                                                                                                      1088 CCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTAATCTGGCCAGTCCTGAGAAGGTC 1147
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                                                                                                                                                                                                                                                                                                               879 GAAAAAGAGAAAGAAAGAAAGAAACTGAGACAGAAAGTGGAAATGAAAACTCCGGCTAC 938
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528 ATATTTCCTGGGAGCTTGAGGTTCCCGTAAGCCATTCGAGTTACAATTCCTTTCTGGAGC 587
                                                          468 TCACTGAGGGTGAACCCTGTAATGTGACTTGCTATGCCGTGGGCTGGACCTCACTCCCGG 527
                                                                                                                                                                                      402 TCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACCTGGCTCCCGG 461
                                                                                                                                                                                                                                                          408 CTGCCTTCCTCAGTGCAAGTCATGGGGACCCTGAACATTCCTAGCAACCATTATAG
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                                                                                                                                                                                                                                                                                                                                                                                   348 TGCAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGAT 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 TCACCTCTCAGAGGTACGACCAGGGGGGGGAACTTCACCTCGGAGATGATCATCCACAATG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 CCGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATGCAAGAGTCCTGAAGG 101
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                        Submitted (21-JAN-1999) Genome Analysis, Institute for Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
                                                                                                                                                                    Biotechnology, Beutenbergstrasse 11, Location/Qualifiers
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Taudien, S., Dagand, E., Hildmann, T., Nordsiek, G., Drescher, B., Schattevoy, R., Weber, J., Schilling, M., Menzel, U., Yaspo, M.L.
                                                                                                                                                                                                                                      Direct Submission
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HOMO Sapiens chromosome 21q22.3 PAC 206A10, complete sequence
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                                                                                             /db_xref="taxon:9/chromosome="21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44437 TCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGGGGAACTTCACCTCGGAGA 44496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44377 TCATCATGTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCA 44436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44257 AAATTGGCTACCTTCCAGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCCAAAATG 44316
                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 TGATCATCCACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 TCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGA 266
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               Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 340000)
                                                                                                                                                                                                               Homo sapiens chromosome 21 segment HS21C080.
AL163280 AP001735 BA000005
AL163280.2 GI:7717369
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                         HS21C080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(19228. .19361)
/note="MZEF, score = 92.8%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="GRAIL, score = 66.000%, comment = good"
/evidence=not_experimental
complement(18643. 24647)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="xpound exon prediction, score = 74% (0%)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="gRAIL, score = 51.000%, comment = good shadow"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(18335. .18632)
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/rpt_family="HERV17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.0%; Score 326.6; DB 9; Length 142742; 97.4%; Pred. No. 9.4e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * URL: http://genome.gbf.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tokyo 160-8582, Japan,
* e.mail: shimizu@dmb-med.keio.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * URL: http://adenine.dmb.med.keio.ac.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics (addresses see below)
The Chromosome 21 Mapping and Sequencing Consortium consists of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
Sagamihara 228-8555, Japan,
* e.mail: sakaki@ysc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * GBF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * Keio University School of Medicine, Dept. of Molecular Biology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * URL: http://genome.imb-jena.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beutenbergstrasse 11, D-07745 Jena, Germa
* e.mail: gscj-submit@genome.imb-jena.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (05-MAY-2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Kaio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular GBF, Dept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.mail: info-chr21@molgen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R., Patterson, D., Reichwald, K., Rump, A., Schillhabel, M., Schudy, A., Zimmermann, W., Rosenthal, A., Kudoh, J., Shibuya, K., Kawasaki, K., Asakawa, S., Shintani, A., Sasaki, T., Nagamine, K., Mitsuyama, S., Antonarakis, S. E., Minoshima, S., Shimizu, N., Nordsiek, G., Hornischer, K., Brandt, P., Scharfe, M., Schoen, O., Desario, A., Reichelt, J., Kauer, G., Bloecker, H., Ramser, J., Beck, A., Klages, S., Hennig, S., Riesselmann, L., Dagand, E., Wehrmeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        URL: http://chr21.rz-berlin.mpg.de/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ihnestrasse 73, D-14195 Berlin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Max-Planck Institute for Molecular Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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  /map="21q22.3"
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/clone_lib="RPCI1,3-5 PAC library"
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286628.
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PAC library"

repeat_region

1088. .1566 /note="L1M4"

'chromosome='

repeat_region

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                                                                                                                                                                                                                complement(8482. .8762)
                                                                                                                                                                                                                                                                 complement(6887. .7067)
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                                                                                                                                                                                                                                                                                                                                                                                      translation="gsekaeeggeteaQkegseDygNLpeaQekNeeegeTateetee/
/rpt_type=DISPERSED
complement(9989. .10077)
                                                                                                                                              complement(8865. .8964)
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AC020851
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                                                                                                                    Db 268677 TGATCATCCACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCGCCTCCAGAACA 268736
                                                                                                                                                                                                                                                                                                                                                                                     Matches 332; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                repeat_region
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/note="L2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(13115. .13425)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           14013. .14131
/note="(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12649. .12678
/gene="SH3BGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="SINE/MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'rpt_family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="Simple_repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_type=DISPERSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluSx"
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mRNA gene

/gene="SH3BGR"

/gene="SH3BGR" oin(<3473

'gene="SH3BGR"

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/note="AluJo"

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/note="L1MD3"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 180887 bases at least Q40
Consensus quality: 180887 bases at least Q30
Consensus quality: 180887 bases at least Q30
Estimated insert size: 147000; subsetield gel estimation
Restimated insert size: 19700; sum-of-contigs estimation
Quality coverage: 5.67 in Q20 bases; sum-of-contigs estimation
Quality coverage: 4.3 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center clone name: RPCI-21_467L12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Wainut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center Project Name: 1437240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Jul 15, 2000 this sequence version replaced gi:6686457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Sequencing of Mouse
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1641: gap of unknown
3492: contig of 1851
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                                                                                                                                                                                                                                                                                                                                                                                  Matches 237;
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Best Local Similarity 72.3%;
67739 TGGATCTGCCTTCCTCAGTGCAAGGT 67766
                                                     67679 TGATGTGCAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTT 67738
                                                                                                                   67619 CCGCTTCACCTATGCCAGTTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCA 67678
                                                                                                                                                                               67559 GACTCTTAACCAAATGGTGGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAA 67618
                                                                                                                                                                                                                                            67499 AAAGGACTCAGAGGCTCACTTCAACTGCACCGTGACTCACGGCTGGAAGCCTTCTCATGTG 67558
                                                                                                                                                                                                                                                                                                      67439 CCTTCTAGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCT 67498
                            337 TGGATCTGCTTACCTTACCGTCCAAGTT 364
                                                                                   277 CAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCA 336
                                                                                                                                                 217 CCGCTTCACCTCTCAGAGGTACGACCAGGGGGGGAACTTCACCTCGGAGATGATCATCCA 276
                                                                                                                                                                                                              157 GGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                              97 GAAGGGCTCCCAGGCTTCCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTG 156
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43823 c 44608 g 53666 t 3347 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP21-467L12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        location,
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146378: contig of 9089 bp in length
146478: gap of unknown length
161686: contig of 15208 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .61786: gap of unknown length
.76149: contig of 14363 bp in length
.76249: gap of unknown length
.76269: contig of 20651 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35688: contig of 3343 b
35788: gap of unknown l
40387: contig of 4599 b
40487: gap of unknown l
43580: contig of 3093 b
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46437: contig of 2757
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7: contig
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Pred. No. 4.8e-33;
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contig of 3647 bp in 1
gap of unknown length
contig of 4288 bp in 1
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ig of 8006 bp in length
of unknown length
ig of 9870 bp in length
of unknown length
ig of 9468 bp in length
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of 10726 bp in
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of 10468 bp in length
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 GCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 CAGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGG 167
                                                                                                                                                                                                                                                                       348 TECAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGAT 407
                                                                                                                                                                                                                                                                                                          282 TGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGAT 341
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Local Similarity 72.9%;
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                                                                                                                                                                                                                                                                                                                                                                                 TCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATG 281
                                                                                                                                                                                                                                                                                                                                                                                                                    TTAACCAAATGGTGGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACCGCT 287
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                     Sequence 11 from Patent W00200710.
                                                    AX380406.1
                                                                                                          AX380406
                   house mouse
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NCTVTHGWKLLMWTLNQMVVLSLTTQGPIITNNRFTYASYNGTDSFISELIIHDVQPS
DSGSVQCSLQNSHGFGSAFLSVQESTYQNEIRKSANMXTNKADPETKLKSGKENYGYS
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/db_xref="taxon:10090"
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/db_xref="GI:19575339"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                           1556 bp mRNA linear ROD (Mus musculus, RIKEN cDNA 2010003D20 gene, clone MGC:7960 INAGE:3584645, mRNA, complete cds. BC004806
                                      submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                   Direct Submission
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FCCCCASRREKEESTYQNEIRKSANMKTNKADPETKLKSGKENYGYSSDEAKAAQTAS
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/db_xref="GI:19575337"
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                                                                             350 TGCAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGAT 409
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Similarity 72.9%;
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Series: IRAK Plate: 10 Row: m Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
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DSGSVQCSLQNSHGFGSAFLSVQDSIGEEGPALPTWAIILLAVAFSLLLLIIIVLIII
FCCCCASRREKEESTYQNEIRKSANMRTNKADPETKLKSGKENYGYSSDEAKAAQTAS
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/protein_id="AAH04806.1"
/db_xref="GI:13435933"
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AC120346/c
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                                                                                                                                                                                                                                                                                                                                Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-roh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nuyuen, C., Nicol, R., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Topham, K., Travers, M., Travis, N., Trafamas, J., Tesfaye, S., Theodore, J., Viel, R., Voa, Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J. Zemhak, E., Zimmer, A., and Zodw, M., Young, G., Zainoun, J., Zemhak, E., Zimmer, A., and Zodw, M., Young, G., Zainoun, J., Zemhak, E., Zimmer, A., and Zodw, M., Young, G., Zainoun, J., Zemhak, E., Zimmer, A., and Zodw, M., Young, G., Zainoun, J., Zemhak, E., Zimmer, A., and Zodw, M., Young, G., Zainoun, J., Zemhak, E., Zimmer, A., and Zodw, M., Young, G., Zainoun, J., Zemhak, E., Zimmer, A., and Zodw, M., Young, G., Lander, S., Schubak, E., Zimmer, A., and Zodw, M., Young, G., Zainoun, J., Zemhak, E., Zimmer, A., and Zodw, M., Young, G., Zainoun, J., Zemhak, E., Zimmer, A., and Zodw, M., Young, G., Lander, J., Young, G., Lander, J., Zimmer, A., and Zodw, M., Zeng, G., Lander, J., Zimmer, A., and Zodw, M., Zeng, G., Lander, J., Zimmer, A., and Zodw, M., Zeng, G., Lander, J., Zimmer, A., and Zodw, M., Zeng, G., Lander, J., Zimmer, A., and Zodw, M., Zeng, G., Lander, J., Zimmer, A., and Zodw, M., Zeng, G., Lander, J., Zimmer, A., and Zodw, M., Zeng, G., Lander, J., Zimmer, A., and Zodw, M., Zeng, G., Lander, J., Zimmer, A., and Zodw, M., Zeng, G., Lander, J., Zimmer, A., and Zodw, M., Zeng, G., Lander, J., Zimmer, A., and Zodw, M., Zeng, G., Lander, J., Zimmer, A., and Zodw, M., Zeng, G., Lander, J.
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Submitted (09-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 9, 2002 this Sequence version replaced g1:20503171. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 175861)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,
                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                           Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkly,L.,
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Mus musculus, clone RP23-147E11
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http://ftp.genome.washington.edu/RM/RepeatMasker.html

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code: WIBR

Center clone name: 147_E_11 Center project name:

Sequencing vector: Plasmid;

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* NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consists of 22 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by the finished sequence as soon as it is available and the accession number will be preserved.

1 28835: contig of 28835 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 169879 bases at least 040 consensus quality: 172188 bases at least 030 consensus quality: 173133 bases at least 020 consensus quality: 173133 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 8.3 in Q20 bases; agarose-fp Quality coverage: 8.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 1/6000; agarose-1p
Insert size: 173761; sum-of-contigs
                                                                                                                       72720 81566. contig of 8847 bp in length 81567 81666; gap of 100 bp 81667 966774; contig of 15108 bp in length 96775 96874; gap of 100 bp 96875 119647; contig of 22773 bp in length 110648 110747. The first state of 27775 bp in length 110648 110747.
                                                                                                                                                                                                                                                                                                    47490 47589: gap of 100 bp
47590 50604: contig of 3015 bp in length
50605 50704: gap of 100 bp
50705 56370: contig of 5666 bp in length
56371 56470: gap of 100 bp
56471 64079: contig of 7609 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41066 41165: gap of 100 bp
41166 43203: contig of 2038 bp in length
                                                                                                                                                                                                                       72619: contig of 8440 bp in length
72620 72719: gap of 100 bp

    summary Statistics

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29562: contig of 627 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39166: contig of 1583 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yap of 100 bp 128: contig of 666 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of 100 bp
55: contig of 1799 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                             p of 100 bp contig of 4186 bp in length
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contig of 1467 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p of 100 bp
contig of 1284 bp in length
                                               ap of 100 bp
contig of 26685 bp in length
                                                                                     contig of 28025
        contig of 1204 bp in length
                                                                                                                                                                                                                                                                                      100 bp
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                                                                                                                100 bp
                                                                                            bp in length
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                                                                                                                                                                                                          Db 120535 CCTTCTAGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCT 120476
                                        Db 120415 GGACTCTTAACCAAATGGTGGTGCTGAGTCTCACCAAGGACCCATCATCATCACCAACA 120356
                                                                                                                         Db 120475 AAAGGACTCAGAGGCTCACTTCAACTGCACCGTGGGCTCACGGCTGGAAGCTTCTCATGT 120416
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                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                  Matches
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                                                                                156 GGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATG 215
216 ACCGCTTCACCTCTCAGAGGTACGACCAGGGGGGGAACTTCACCTCGGAGATGATCATCC 275
                                                                                                                                                                                                                                                     37 CCCACCCGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATGCAAGAGTCCT 96
                                                                                                                                                                    97 GAAGGGCTCCCAGGCTCGCTTCAACTGCACCGT-CTCCCAGGGCTGGAAGCTCATCATGT 155
                                                                                                                                                                                                                                                                                                                 y Match 14.7%; Score 171.4; DB Local Similarity 72.0%; Pred. No. 2.1e-30
                                                                                                                                                                                                                                                                                               237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       48903 a 39540 c 39029 g 46286 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
50705. .56370
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/clone="RP23-147E11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                           vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
174658. .175861
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72720. .81566
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119748. .147772
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147873. .174557
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)6875. .119647
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 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                  2103 others
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28836 28935:

29563 29662:

30328:

0329 30428:

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39167 39266: 37484 37583:

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47489: cont

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34513 34612: 33129 33228:

36079: cont

34512: cont

36080 36179:

FEATURES

174558 174657: gap of 174658 175861: conti 147773 147872: gap of 147873 174557: cont 119648 119747: gap of 119748 147772: cont

Location/Qualifiers

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VERSION
KEYWORDS
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AF064857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 ACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (11-MAY-1998) Genome Analysis, Institute for Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF064857 199665 bp DNA linear PRI 23 Homo sapiens BAC derived from chromosome 21q22.3, complete sequence, containing PEP19 (PCP4) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schattevoy, R. and Rosenthal, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhiní; Hominidae; Homo. 1 (bases 1 to 199665)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Taudien,S., Nordsiek,G., Korenberg,J., Drescher,B., Weber,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        cumplement(1584 . .2179)
/evidence=not_experimental
/rpt_family="LIPA2"
2174 . .3406
                                                                                                                                           /evidence=not_experimental
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complement(7057...7376)
                                                                                 complement(7387. .7491)
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6671. .6969
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                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
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747. .814
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/chromosome="21"
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                                             _family="L1ME3A"
                         .8020
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/rpt_family="MSTD"
complement(32766 . 32980)
/evidence=not_experimental
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complement(32507 32738)
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31012. .31364
                                                                                                                                                                                                                             complement(30308. .30676)
                                                                                                                                                                                                                                                                                           complement(29462. .30001)
                                                                                                                                                                                                                                                                                                                                                     complement(28932. .29335)
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/rpt_family="Alusq"
27222. .27283
                                                                                                                                                                                                                                                /evidence=not_experimental
/rpt_family="MER34"
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/rpt_family="MER58B"
25993. .26294
                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
/rpt_family="MSTA"
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/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(25434. .25767)
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/rpt_family="MSTB-internal"
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/rpt_family="MER39b"
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21213. .21500
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complement(20371, .20556)
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19378. . 19470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="homology = 81.70%, score = 28, counts = 3"
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/rpt_family="MER58A"
8650. .8823
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/rpt_family="AluJo"
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/rpt_family="L1MA"
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8.6%; Score 100; DB 9;
100.0%; Pred. No. 3.3e-13;
tive 0; Mismatches 0;
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Consensus quality: 164618 bases at least Q40
Consensus quality: 180887 bases at least Q30
Consensus quality: 18077 bases at least Q20
Estimated insert size: 147000; pulse field gel estimation
Estimated insert size: 19700; sum-of-contigs estimation
Quality coverage: 5.67 in Q20 bases; pulse field gel estimation
Quality coverage: 4.3 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 15, 2000 this sequence version replaced gi:6686457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC020851 196900 bp DNA linear HTG Mus musculus clone RP21-467L12, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center Project Name: 1437240
Center clone name: RPCI-21_467L12
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DOE Joint Genome Institute.
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Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19690)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Best Local Similarity 66.7%;
Matches 82; Conservative
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/clone_lib-"RPCI mouse PAC library
51456 a 43823 c 44608 g 53666 t 3347
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35245: gap of
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others
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0,

Search completed: April 29, 2003, 14:30:21 Job time: 4416.94 secs

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OM protein - protein search, using sw model
April 28, 2003, 16:24:30 ; Search time 10.2617 Seconds (without alignments) 1543.990 Million cell updates/sec
                                                                                                                                                                                   GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on:

Title: Perfect score: US-09-729-264-2 2059 1 MGLVIFLHGSGSGNEVIEGP......HPQASFNLASPEKVSNTTVV 382

Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10 112 13 14 14 15 16 16 17 18 19 20 20 21 22 23 24 25 25 25 27 27 28 30 31 31 31 33	14304VBVBVBQ	Result No.
119 117.5 116 117.5 113.5 113.5 113.5 110.5 110.5 110.5 110.5 100.5 100.5 100.5 100.5 100.5 100.5 100.5 100.5	147.5 131 129.5 128 128 128 127 127 124	Score
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TYO3_RAT FAS2_DROME NDHN_HUMAN KLK8_RAT CAML_MOUSE KMLS_CHICK UN52_CAEEL LAMP_HUMAN LAMP_RUMAN LAMP_ROME SREC_HUMAN TYO3_MOUSE
p55146 rattus norv p34082 drosophila o60500 homo sapien p36374 rattus norv p11627 mus musculu p11799 gallus gall 006561 caenorhabdi 013449 homo sapien 062813 rattus norv 024372 drosophila 014162 homo sapien p55144 mus musculu

ALIGNMENTS

RP RT	RA R	RP RC RX RA RA RT	RESULT RAGE_HU RAGE_HU RAG AC Q1 DT 01 DT 11: DE AC DE AC OC MC OX W
SEQUENCE FROM N.A. (ISOFORM 2). SEQUENCE FROM N.A. (ISOFORM 2). Malherbe P., Richards J., Gaillard H., Thompson A., Diener C., Schuler A., Huber G.; Schuler A., Huber G.; "CDNA cloning of a novel secreted isoform of the human Receptor for advanced Glycation End products (RAGE) and characterization of cells co-expressing cell-surface scavenger receptors and Swedish mutant amyloid precursor protein."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. [6] SEQUENCE FROM N.A. (ISOFORM 1).	JENCE FROM N.A. (IS en L., Dankers C., ta A., Spies T., He mitted (FEB-1997) ! UENCE FROM N.A. (I din M.J., Yonekura amoto H.; lecular heterogene products.";	SEQUENCE FROM N.A. (ISOFORM 1). SEQUENCE FROM N.A. (ISOFORM 1). TISSUE-Lung; MEDLINE-92340547; PubMed-1378843; Neeper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C., Elliston K., Stern D., Shaw A.; Elliston K., Stern D., Shaw A.; Elliston Ell surface receptor for advanced glycosylation end products of proteins."; J. Biol. Chem. 267:14998-15004(1992). [2] SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE-95137587; PubMed-7835890; SIGNAR K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A., SIGNAR K., Fukagawa T., Isoforok G., Mita K., Takahashi E., Ando A., TINOKO H., Ikemura T.; INOKO H., Ikemura T.; INOKO H., Ikemura T.; INOKO H., Ikemura T.; TOOKO H., Ikemura H., Ikemura H.,	Tr 1 HUMAN STANDARD; PRT; 404 AA. RACE_HUMAN STANDARD; PRT; 404 AA. Q15109; Q15279; Q9Y3R3; Q9H2X7; Q15109; Q15279; Q9Y3R3; Q9H2X7; Q15109; Q15279; Rel. 35, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Advanced glycosylation end product-specific receptor precursor Advanced glycosylation end products). RACER OR RAGE. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo. MCBI_TaxID=9606;

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THE PRESENTATION OF THE PROPERTY OF THE PROPER
         CONFLICT
                                                   VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00410; IG_like; 1.
SMART; SM00408; IGC2; 1.
PROSITE; PS00290; IG_MHC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_C2.
InterPro; IPR003600; Ig_11ke.
Pfam; PF00047; Ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted (isoform 2).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB036432; BAA89369 1;
AJ133822; CAB43108.1; -
BC020669; AAH20669.1; -
AF200289; AAG35728.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:320; AGER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG_MHC; 1
                                              100
                                                                                                                                                                                   404
106
215
308
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208
301
25
81
384
67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Transmembrane; Repeat; Signal;
/FTId=VAR_011338
M -> G (IN REF. )
                                                                                                                                                                                                                                                                                                                                         IG-LIKE V-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 1.
TG-LIKE C2-TYPE DOMAIN 2.
                                                           GACRTESVGGT (IN ISOFORM 2).
                                                                            PGPGDPGRPGDSRPAHWGHLVAKAATPRRGEEGPRKPGGRG
                                                                                                    LIGVILWQRRQRRGEERKAPENQEEEEERAELNQSEEPEAG
ESSTGGP -> VSDLERGAGRTRRGGANCRLCGRIRAGNSS
                                                                                                                                              GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRA
VSISIIEPGEEGPTAGSVGGSGLGTLALALGILGGLGTAAL
                                                                                                                                                                                               MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL). IG-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR.
                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHOWN HERE) AND 2/RAGESEC;
                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                              (POTENTIAL).
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AMEDILINE=99157768; PubMed=9004047;

RA Wilson D.J.A., Kim D.-S., Clarke G.A., Marshall-Clarke S., Moss D.J.;

RT "A family of glycoproteins (GP55), which inhibit neurite outgrowth,

RT are members of the Ig superfamily and are related to OBCAM,

RT neurotrimin, LAMP and CEBU-1.",

RI J. Cell Sci. 109:3129-3138(1996).

C -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -!- TISSUE SPECIFICITY: RESTRICTED TO THE NERVOUS SYSTEM.

CC -!- TISSUE SPECIFICITY: RESTRICTED TO THE NERVOUS SYSTEM.

CC -!- DEVELOPMENTAL STAGE: INCREASES DURING DEVELOPMENT FROM VERY LOW

CC -- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERPAMILY. IGLON
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-!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS
                                                                                                                                                                                                                                                                                                            Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                            "Lodge A.P., Kim D. S., Howard M.R., McNamee C.J., Smith "Cloning of CEPU-S, a secreted isoform of CEPU-1, and Of chick: structural diversity of IgLON family proteins.";
                                                                                                                                                                                                                                                                        SEQUENCE OF 64-337 FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurite inhibitor GP55-A precursor (OBCAM protein gamma isoform).
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G55A_CHICK
Q98892;
                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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22.6%; Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 AA
                                                                                                                                                                                            Marshall-Clarke S., Moss D.J.; ch inhibit neurite outgrowth,
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SOLUTION OF THE STREET 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                                   Neurotrimin precursor (GP65).
                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                         062718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 AENEPCEVTCL----PSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQS 184
                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 ---WFKEDTRLA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 NATYLKGSOARFNCTVSQGWKLIMWALSDMVVL-----SVRPMEPIITNDRFTSQRYD 74
STRAIN-Sprague-Dawley MEDLINE-95198094; Publ
                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 NYTYROGESATLROTYDDRYRRYAW-LNRSTILYAGNDKWSIDNRVVILSN---TKTQY- 91
                                              SEQUENCE FROM N.A., AND SEQUENCE OF 217-229
                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SIKIHNVDVYDEGPYTCSVQTDNHPKTSRVH----LIVQVPPQIVNISSDITV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRLHGSAYLTVQVMGELFIPSVNLVV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEGSSVTLMCLAFGRPE----PTVTWR---HLSGKGQGFVSEDEYLE----ITGITREQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00410; ĬG_like; 1.
SM00408; IGC2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGEYECSAV-NDVAVPDVRKVKVTVNYPPYISNAKNTGASVGQKGILQCEASAVPVAEFQ 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGTLTCVATWKSLKARKSATVNLTV-----IRCPQDTGGGINIPGVL----SSLPSLGFS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPTWGKVGLGLA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43
143
229
50
150
133
133
277
285
                                                                                                                              ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                       STANDARD;
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        PubMed=7891157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36887 MW;
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REMOVED IN MATURE FORM (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 131; DB 1
pred. No. 0.002;
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(GLCNAC. .) (POTENTIAL).
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(GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                     344 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
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J. Neurosci. 15:2141-2156(1995).

J. Neurosci. Neural Molecule.

J. FUNCTION: Attached to the membrane by a GPI-anchor.

J. SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

J. TISSUE SPECIFICITY: CENTRAL HERVOLS SYSTEM.

J. TISSUE SPECIFICITY: CENTRAL HEVELS IN SEVERAL.

J. DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN SEVERAL.

J. DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN SEVERAL.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning of neurotrimin defines a new subfamily of differentially
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SMART; SM00410; IG_like; 1.
SMART; SM00408; IGC2; 2.
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                                                                                                                                                                                           107 GSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PONTINE NUCLEUS, CEREBELLAR GRANULE CELLS, AND PURKINUE CELLS
182 EDEYLE----IQGITREQSGEYECSAS-NDVAAPVVRRVNVTVNYPPYISEAKGTGVPVG 236
                                                           167 EPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCP-----QDTGGGIN 221
                                                                                                                                                                                                                                                                                                                         56 ---VRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRLH 106
                                                                                                                                                                                                                                                                                                                                                                                       21 LLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGND 80
                                                                                                                                                                                                                                                          81 KWCLDPRVVLLSN---TQTQY-----SIEIQNVDVYDEGPYTCSVQTDNHPKTSRVH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VIFLHGSG----SGNEVI-EGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLS--- 55
                                                                                                                                ----LIVQVSPKIVEISSDISINEGNNISLTCIATGRPE-PTVTWR----HISPKAVGFVS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΑA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell adhesion; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.3%; Score 129.5; DB
34.2%; Pred. No. 0.0028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REMOVED IN MATURE FORM IG-LIKE C2-TYPE DOMAIN IG-LIKE C2-TYPE DOMAIN IG-LIKE C2-TYPE DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CBB39BE53B33B224 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conmercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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222 IPGVL----SSLPSLGFSLPTWGK 241

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                                                                                                                DISULFID DISULFID
                                   CARBOHYD
                                                          CARBOHYD
                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                 Pfam; Pr00047; ig; 3. 3. SMART; SM00410; IG_like; 1. SMART; SM00408; IGc2; 2. Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor; Repeat; Signal; Alternative splicing.
                                                                                                                                                                        DISULFID
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 272497; CAA96578.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A MAJOR FORM AND A MINOR FORM
-1- TISSUE SPECIFICITY: FOUND ON THE DENDRITES, SOMATA AND AXONS OF
-1- DEVELOPING PURKINJE CELLS. UNDETECTABLE ON OTHER NEURONS LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "CEPU-1, a novel immunoglobulin superfamily molecule, is expressed developing cerebellar Purkinje cells.";
J. Neurosci. 16:1770-1779(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEPO-1 protein precursor.

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spaltmann F., Bruemmendorf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96370549; PubMed=8774445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 QKGTLQCEASAVPSAEFQ---WFK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOLGI OR GRANULE CELLS.

GOVERNMENTAL STAGE: EXPRESSED BY DEVELOPING CEREBELLAR PURKINJE CELLS. EXPRESSION COINCIDES WITH THE GROWTH OF THE DENDRITIC TREJECTER PURKINJE CELLS HAVE FINISHED THEIR MIGRATION FROM THE CELLS HAVE EINISHED THEIR MIGRATION FROM THE CHAPTER PURKINJE CELLS HAVE FUNTIL E21). EXPRESSED IN THE ADULT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: IT MAY BE A CELLULAR ADDRESS MOLECULE SPECIFIC TO PURKINUE CELLS. IT MAY REPRESENT A RECEPTOR OR A SUBUNIT OF A RECEPTOR COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                    206
300
113
199
293
     N-LINKED (GLCNAC. . N-LINKED (GLCNAC. . N-LINKED (GLCNAC. .
                                                                                                                                                IG-LIKE C2-TYPE DOMAIN IG-LIKE C2-TYPE DOMAIN POTENTIAL.
                                                                                                 POTENTIAL.
                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                             REMOVED IN MATURE FORM IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                        CEPU-1 PROTEIN.
                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
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DCC_HUMAN
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GENE STRUCTURE, AND VARIANTS CARCINOMA HIS-1375.
MEDLINE-94245241; PubMed-8188295;
Cho K.R., Oliner J.D., Simons J.W., Hedrick L., Fearon E.R.,
                                                                               Nigro J.M., Cho K.R., Fear
Oliner J.D., Kinzler K.W.,
"Scrambled exons.";
                                                                   Cell 64:607-613(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P43T46;
01-NOV-1995 (Rel. 32, C
01-NOV-1995 (Rel. 32, L
15-JUN-2002 (Rel. 41, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                     SEQUENCE OF 107-472 FROM N.A. (SCRAMBELD EXONS).
MEDLINE=91121517; PubMed=1991322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                  colorectal cancers.";
Science 247:49-56(1990).
                                                                                                                                                                            "Identification of a chromosome 18q gene that is altered in
                                                                                                                                                                                                               Vogelstein B.;
                                                                                                                                                                                                                  Fearon E.R., Cho K.R., Nigro J.M., Kern S.E., Ruppert J.M., Hamilton S.R., Preisinger A.C.,
                                                                                                                                                                                                                                                MEDLINE=90100559; PubMed=2294591;
                                                                                                                                                                                                                                                                                                "The DCC gene product in cellular differentiation and colorectal tumorigenesis.";
                                                                                                                                                                                                                                                                                                                                       Hedrick L., C
Vogelstein B.
                                                                                                                                                                                                                                                                  SEQUENCE OF 1-750 FROM N.A.
                                                                                                                                                                                                                                                                                                                                             MEDLINE=95011532; PubMed=7926722; Hedrick L., Cho K.R., Fearon E.R.,
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor suppressor protein DCC precursor (Colorectal cancer suppressor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DCC_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 --WYK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 PTWGK 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 INEGGNVSLTCIA----TGRPDPTITWR---HISPKAVGFISEDEYLE----ITGITREQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 VAENEPCEVTCLPSHWTRLPD--ISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 -----IHDVDVYDEGPYTCSVQTDNHPKTSRVH----LIVQVSPKITETSSDIS 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 DQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRLHGSAYLTVQVMGELFIPSVNLV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 NYTYROGESATLRCSYDNRYTRYAWLNRSSILYAGNDKWCLDPRYYLLANTKTQYSIQ-- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 NATYLKGSQARFNCTVSQ-----GW---KLIMWALSDMVVLSVRPMEPIITNDRFTSQRY 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTLTCVATWKSLKARKSATVNLTV-----IRCPQDTGGGINIPGVL----SSLPSLGFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                            8:1174-1183(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                Fearon E.R., Kern S.E., Ruppert J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38736 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.2%; Score 128; DB 1;
25.7%; Pred. No. 0.0038;
                                                                                        Vogelstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
GPI-ANCHOR (POTENTIAL).
MISSING (IN MAJOR ISOFORM).
; 2550C48591EBBBA6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1447 AA
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                                                                                                                                                                                                             Simons J.W.,
Thomas G., Kinzler K.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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CANCET Res. 54:3007-3010(1994).

CANCET Res. 54:3007-3010(1994).

-i- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.

-i- SUBCELLULAR LOCATION: Type I membrane protein.

-i- SUBCELLULAR LOCATION: Type I membrane protein.

-i- TISSUE SPECIFICITY: FOUND IN AXONS OF THE CENTRAL AND PERIPHERAL

-i- TISSUE SPECIFICITY: FOUND IN AXONS OF THE CENTRAL AND PERIPHERAL

-i- SUBCELLULAR LOCATION OF THAT LOST THEIR CAPACITY TO

-I- DISEASE: COLORECTAL TUMORS THAT LOST THEIR CAPACITY TO

-I- DISEASE: COLORECTAL TUMORS PRODUCING CELLS UNIFORMLY LACK DCC

DIFFERENTIATE INTO MUCUS PRODUCING CELLS UNIFORMLY LACK DCC

DIFFERENTIATE INTO MUCUS PRODUCING CELLS UNIFORMLY LACK DCC

DIFFERENTIATE INTO MUCUS PRODUCING CALL CARCINOMAS.

METASTASIS OF OESOPHAGEAL SQUAMOUS CELL CARCINOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human esophageal squamous cell carcinomas and their relation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miyake S., Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y.; Point mutations and allelic deletion of tumor suppressor gene DCC in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preisinger A.C., Hedge P., Silverman G.A., Vogelstei "The DCC gene: structural analysis and mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT CARCINOMA THR-168, AND VA
MEDLINE-94243823; PubMed-8187090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 19:525-531(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A40098; A40098.
PIR; A38442; A38442.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                              Pfam; PF00041; fn3; 6. Pfam; PF00047; 19; 4. PRINTS; PR00014; FNTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                          SMART; SM00410; IG_like; 2.
SMART; SM00408; IGC2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 120470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew;
                                                                                                                                                                                                                                                                                                                            SMART; SM00060; FN3; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003961; FN_III
                                                                                            DOMAIN
DOMAIN
                                                                                                                                                               DOMAIN
                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                            Repeat; Anti-oncogene;
SIGNAL 1 25
                                                                                                                                                                                                                                                         Glycoprotein;
                                            DOMAIN
                                                                     DOMAIN
                                                                                                                                           TRANSMEM
    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation een the Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is not the long as its content is 
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M32286;
M32288;
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M63700;
M63702;
M63718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGNC:2701; DCC
                                                                                                                                                                                                                                                                                                                                                                                                              IPR003006; Ig_MHC.
IPR003598; Ig_c2.
IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             equires a license agreement (See http://www.lsb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003962;
IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; CAA53735.1; -.

2; AAA53751.1; -.

3; AAA53751.1; -.

3; AAA52175.1; ALT_SEQ.

3; AAA52176.1; -.

5; AAA52177.1; -.

6; AAA52179.1; -.

2; AAA52179.1; -.

8; AAA52180.1; -.

8; AAA52180.1; -.
       1098
1123
54
154
254
254
345
                                                                                                                                                                                                                                                           Immunoglobulin domain; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLK.
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                                                                                                                                                                    1447
1097
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                                                                                                                                                                                                                                          Disease mutation; Polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _repeat.
                             CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
                                                                                                                                                POTENTIAL
                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                  TUMOR SUPPRESSOR PROTEIN DCC
                                                                                                                                                                                                                        POTENTIAL
         FIBRONECTIN TYPE-III
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RESULT 6
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Best Local
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CONFLICT
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                                                                                                                                                                                                    KMLS_HUMAN STANDARD; PF
Q15746; Q14844; Q16794; O95796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 SRTGNEAEVRILSDPGLHRQLYFLQRPSNVVAIEGKDAVLECCVS-GYPPPSFTWLRGEE 278
                                                                                                                                          15-UUI-1970 (Rel. 40, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Myosin light chain kinase, smooth muscle and non-muscle isozymes
Myosin light chain kinase, smooth muscle and rotein)
                                                                                                                                                                                                                                                                                                                                                             324 ELTYLVPPWFLNHPSNLYAYESMDIEFECTVS-GKPVPTVNWMKNGDVVIPSDYFQIVGG
                                                                                                                                                                                                                                                                                                                                                                                  110 YLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEP 168
                                                                                                                                                                                                                                                                                                                   383
                                                                                                                                                                                                                                                                                                                                        169
                                                                                                                                                                                                                                                                                                                                                                                                          279 VI----
         TISSUE-Umbilical vein endothelial cells;
MEDLINE-97304466; PubMed-9160829;
Garcia J.G.N., Lazar V.L., Gilbert-Mcclain L.I., Gallagher P.J.,
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                             09UIT9;
                                                                                                                                                                                                                                                                       431 AP 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                              229 LP 230
                                                                                                                                                                                                                                                                                                                                                                                                                             52 VVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSA 109
  Verin A.D.;
                                                                  NCBI_TaxID=9606;
                                                                                                                           KRP)
                                                                                                                                                                                                                                                                                                                  SNLR----ILGVVKSDEGFYQCVAENEAGNAQTSAQLIVPKPAIPSSS-----VLPS
                                                                                                                                                                                                                                                                                                                                       SDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSS
                                                                                                                                    2.7.1.117) (MLCK) [Contains:
                                                                                                                OR MLCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1447 AA;
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261
352
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FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 128;
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MISSING (IN REF. 3).
MISSING (IN REF. 3).
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P -> H (IN A COLORECTAL CARCINOMA).
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                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4A8612766ED0471F CRC64;
                                                                                                                                                                                                             RT; 1914 AA.
O95797; O95798; O95799; Q9UBG5;
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(GLCNAC...)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                               430
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restrictions on EMBL outstation

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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC), AN EVENT THAT DETERMINARY IN THE DEVELOPMENT OF VASCULAR PERMEABILITY AND TISSUE CONTROL THE GROWTH INITIATION OF VASCULAR PERMEABILITY AND TO SECOND OF THE NERVOUS SYSTEM IT HAS BEEN SHOWN TO AND TO PARTICIPATE IN TRANSMITTER RELEASE AT SYMAPSES FORMED IN SIGNALING SEQUENCES THAT RESULT IN FIEROBLAST APOPTOSIS.

-i- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin light-chain] = ADP + [myosin light-chain]
                                                                          -i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES -i- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shrinsky v.P., Van Eldik L.J., Haiech J.;
"Analysis of the kinase-related protein gene found at human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watterson D.M., Schavocky J.P., Guo L., Weiss C., Chlenski A.,
Shrinsky V.P., Van Eldik L.J., Haiech J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Lung, and Placenta; MEDLINE-20007838; PubMed-10536370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The human myosin light chain kinase (MLCK) from hippocampus: cloning, sequencing, expression, and localization to 3qcen-q2 Genomics 29:562-570(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1456-1914 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3921 in a multi-gene cluster: organization, expression, alternative splicing and polymorphic marker.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1614-1914 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potier M.-C., Chelot E.,
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MEDLINE-96121365; PubMed-8575746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 923-1914 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99216419; PubMed-10198165;
Lazar V.L., Garcia J.G.N.;
"A single human myosin light chain kinase gene (MLCK; MYLK).";
Genomics 57:256-267(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           furnell W.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS (ISOFORM 2).
                                                                                                                                        ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; 1 (SHOWN HERE), 2, 3A, 3B, 4 AND DEL-1790; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES ARE EXPRESSED IN A WIDE VARIETY OF ADULT AND FETAL TISSUES AND IN CULTURED ENDOTHELLIM WITH QUALITATIVE EXPRESSION APPEARING TO BE THE DOMINANT SPLICE VARIANT EXPRESSED IN VARIOUS TISSUES. TELOKIN HAS BEEN FOUND IN A WIDE VARIETY OF ADULT AND FETAL TISSUES.

PTM: MLCK IS PROBABLY DOMN-REGULATED BY PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 2; 3A; 3B AND 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birukov K.G., Garcia J.G.N.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Am. J. Respir. Cell Mol. Biol. 16:489-494(1997).
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                                                                                                                                                                                                                                                                                                                                                                                  light-chain] phosphate.
SUBUNIT: TELOKIN BINDS CALMODULIN.
ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; A NON-MUSCLE FORM (THE LONGEST FORM), A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH NO CATALYTIC ACTIVITY); ARE PRODUCED BY ALTERNATIVE
                       SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pekarsky Y., Gardiner K., Rossier J.,
                    REPEAT
REPEAT
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BINDING

ACT_SITE

DOMAIN
                    REPEAT
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SMART; SM00410; IG_like; 1.

SMART; SM004408; IGC2; 8.

SMART; SM00020; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Serine/threonine-protein kinase; Calmodulin-bin
ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00014; FNTYPEIII.
ProDom; PD000001; Euk_pkinase;
SMART; SM00060; FN3; 1
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   INIT_MET
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Pfam; PF00069; pkinase; 1
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InterPro; [PR003962; FNIII_repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the Elthe European Bioinformatics Institute. There are no rest: use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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L; AF096771; AAD51380.1; JOINED. AF096766; AAD51380.1; JOINED. AF096767; AAD51380.1; JOINED.
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II-1 (INCOMPLETE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; AAD15922/AAD15923/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD15922/AAD15923).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD15922/AAD15923)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD15922/AAD15923/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD15922/AAD15923).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
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RESULT 7

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DCC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor suppressor protein DCC precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cooper H.M., Armes P., Britto J., Gad J., Wilks A.F.; "Cloning of the mouse homologue of the deleted in colorectal cancer gene (mDCC) and its expression in the developing mouse embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases - I FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96112625; PubMed=8570174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cooper H.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/c; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene 11:2243-2254(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION AND REMAIN AT THIS LEVEL IN THE ADULT.
AND REMAIN AT THIS LEVEL IN THE ADULT.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                              CHAIN
INIT_MET
DOMAIN
TRANSMEM
DOMAIN
                                                                                                 Repeat;
                                                                                                                                                SMART;
                                                                                                                                                                                              Pfam; PF00041; fn3; 6.
Pfam; PF00047; 1g; 4.
PRINTS; PR00014; FNTYPEIII
                                                                                                                                                                                                                                                                                                                                                                EMBL; x85788; CAA59786.1; -.
                                                                                                                                Glycoprotein; Immunoglobulin domain; Transmembrane;
                                                                                                                                                                                  SMART; SM00060; FN3; 6
                                                                                                                                                                                                                                                                               InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                   InterPro; IPR003598; InterPro; IPR003600;
                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are produced by alternative initiation. A third isoform: C is produced by alternative splicing.

TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGHLY EXPRESSED IN DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN DEVELOPING BRAIN AND LEVELS FOUND IN TESTIS, HEART AND THYMUS.

BRAIN WITH VERY LOW LEVELS FOUND IN THE EMBRYO.

ISOFORM C IS EXPRESSED ONLY IN THE EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                    MGI:94869;
                                                                                                                                                  SM00410;
SM00408;
                                                                                                                  Anti-oncogene;
                                                                                                                                                                                                                                                                                                    IPR003962; FnIII_repeat.
                                                                                                                                                                                                                                                                                                                      IPR003961; FN_III.
   1098
1123
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                                                                                                                                                                                                                                                                                                                                                      1TLK
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                                                                                                                                                    IGc2;
                                                                                                                                                                    IG_like; 2.
                                                                   25
1447
1447
   85
1097
1122
1122
                                                                                                                                                                                                                                                   Ig_c2.
Ig_like.
                                                                                                                                                                                                                                                                                   Ig_MHC.
                                                                                                                    obulin domain; Transmembrane; Signal; Alternative initiation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                    TUMOR SUPPRESSOR PROTEIN
TUMOR SUPPRESSOR PROTEIN
FOR ISOFORM B.
       CYTOPLASMIC (POTENTIAL)
                     POTENTIAL
                                      EXTRACELLULAR (POTENTIAL).
                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1447 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                           DCC,
                                                                               ISOFORM
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Matches
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                                                                                                                                   MEDLINE=96074849; PubMed=7478540;
Mossie K., Jallal B., Alves F., Sures I.
"Colon carcinoma kinase-4 defines a new
tyrosine kinase family.";
                              MEDLINE-97037064; PubMed=8882711; Park S.-K., Lee H.-S., Lee S.-T.;
                                                                                                                      Oncogene 11:2179-2184(1995).
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                   PTK7 OR CCK4.
Homo sapiens (Human).
   Park S.-K., Lee H.-S., Lee S.-T.;
Characterization of the human full-length PTK7 cDNA encoding a
                                                                    TISSUE-Fibroblast;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase-like 7 precursor (Col.
                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               Q13308; Q13417;
30-MAY-2000 (Re
                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTK7_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 AENEAGNAQSSA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 ATWKSLKARKSA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 LLGG--SNLLISNVTDDDSGTYTCVVTYKNENISASAELTVLVPPWFLNHPSNLYAYESM 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIEFECAVS-GKPVPTVNWMKNGDVVIPSDYFQIVGGSNLR----ILGVVKSDEGFYQCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQRPSNVIAIEGKDAVLECCVS-GYPPPSFTWLRGEEVI------QLRSKKYS 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    819
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑĄ,
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219
317
407
522
518
618
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940
1042
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                                                                                                                                                                                                            and Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 6
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW.
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IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
                                                                                                                                     , Sures I., Pion...
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Pred. No. 0.026;
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MISSING (IN ISOFORM C).
MW; OD1F1097C22D5B9F CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1070 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                  (Colon carcinoma kinase-4)
                                                                                                                                                                      Plowman
                                                                                                                                                                                                                                                                                Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86;
                                                                                                                                                 of.
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the
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                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
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                                                                                                                                                                      Ullrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                  A.;
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 THE TERM OF THE PROPERTY OF TH
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EMBL; U40271; AAC50484.2; -...
EMBL; AF447176; AAL39062.1; -...
EMBL; AF447157; AAL39062.1; JC
EMBL; AF447158; AAL39062.1; JC
EMBL; AF447162; AAL39062.1; JC
EMBL; AF447163; AAL39062.1; JC
EMBL; AF447170; AAL39062.1; JC
EMBL; AF447170; AAL39062.1; JC
EMBL; AF447171; AAL39062.1; JC
EMBL; AF447171; AAL39062.1; JC
EMBL; AF447172; AAL39062.1; JC
EMBL; AF447173; AAL39062.1; JC
EMBL; AF447174; AAL39062.1; JC
EMBL; AF447174; AAL39062.1; JC
EMBL; AF447174; AAL39062.1; JC
EMBL; AF447174; AAL39062.1; JC
                                DOMAIN
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DOMAIN
DOMAIN
                                                                                                                                                              CHAIN
                                                                                                                                                                             SIGNAL
                                                                      DOMAIN
                                                                                                                          TRANSMEM
                                                                                                                                         DOMAIN
                                                                                                                                                                                                              Receptor;
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 7. Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew;
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biochem. 119:235-239(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROGRESSION MARKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC:9618; PTK7
                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003006; Ig_MHC.
IPR003598; Ig_c2.
IPR003600; Ig_like.
IPR002011; RTKinaseII.
                                                                                                                                                                                                                                                                                                                                                                                                            IPR001245;
                                                                                                                                                                                              domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAD5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, PANCREAS, KIDNEY, PLACENTA AND MELANOCYTES. WEAKLY EXPRESSED IN THYROID GLAND, OVARY, BRAIN, HEART AND SKELETAL MUSCLE. ALSO EXPRESSED IN ERYTHROLEUKEMIA CELLS. BUT NOT EXPRESSED IN COLON.
-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND REVISION TO 834.

Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABI

THE CATALYTIC ACTIVITY OF TYROSINE KINASE. MAY BE CONNECTED TO THE

PATHOPHYSIOLOGY OF COLON CARCINOMAS AND/OR MAY REPRESENT A TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor protein tyrosine kinase-like molecule closely related chick KLG.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LACKS PROBABLY
                                                                                                                                                                                                                                                                                      ons on its
in no way
commercial
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PRINTS; PRO0109; TYRKINASE.

PRODOM; PD000001; Euk_pkinase; 1.

SMART; SM00410; IG like; 2.

SMART; SM00408; IGC2; 5.

SMART; SM00219; TYRKC; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; FALSE_NEG. Transmembrane; Signal; Glycoprotein; IPR000719; Euk_pkinase. 7 AAL39062.1 JOINED
2 AAL39062.1 JOINED Tyr_pkinase. POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 4.

IG-LIKE C2-TYPE DOMAIN 6. EXTRACELLULAR TYROSINE-PROTEIN KINASE-LIKE POTENTIAL (POTENTIAL). Cell adhesion;

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                                                                                                                                                                                                                                                RESULT 9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                             014982:
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
0pioid binding protein/cell adhesion molecule precursor (OBCAM)
(Opioid-binding cell adhesion molecule) (OPCML).
                                                                                                                                                                                                                                                                                                                                                                                                                        227
                                                                                                                                                                                                                              OPCM_HUMAN
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                  388 VYTCHAA--NLAGQRRQDVNITVATVPSWLKKPQDSQLEEGKPGYLDCL 434
                                                                                                                                                                                                                                                                                                                               338 EE---RVTCLPPKGLPEPSVWWEHAGVRLPTHGRVY-----QKGHELVLANIAESDAG
                                                                                                                                                                                                                                                                                                                                                    130 ENEPCEVTCLPSHWTRLPDISWE-LGL-LVSHSSYYFVPEPSDLQSAVSILALTPQSN-G 186
                                                                                                                                                                                                                                                                                                                                                                           283 ----NGSLLLTQVRPRNAGIYRCIGQGQRGPPIILEATLHLAEIEDMPLFEPRVFTAGS
         encoding a human opioid-binding cell adhesion molecule (OBCAM)."; Gene 155:213-217(1995).
                                          Shark K.B., Lee N.M.;
                                                     TISSUE=Occipital cortex;
MEDLINE=95237612; PubMed=7721093;
                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                         187 TLTCVATWKSLKARKSATVNLTV-----IRCPQDTGGGINIPGVLSSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                            16 VIEGPQNATVLKGSQARFNCTVS-QGWKLIMWALSDMVVLSVRPMEPIITNDRFTSQRYD 74
                                                                               SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=9606;
                              "Cloning, sequencing and localization to chromosome 11 of a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                  75
                                                                                                                                                                                                                                                                                                                                                                                                                       VVLAPQDVVVARYEEAMFHCQFSAQPPPSLQWLFEDETPITNRSRPPHLRRATVFA---- 282
                                                                                                                                                                                                                                                                                                                                                                                                 QGGNFTSEMIIHNVEPSDSGNIRCSLQNSR-----LHGSAYLTVQVMGELFIPSVNLVVA 129
FUNCTION: BINDS OPIOIDS IN THE PRESENCE OF ACIDIC LIPIDS; PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                              STANDARD;
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481
570
664
116
175
184
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268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32; Mismatches
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PROTEIN KINASE; I
BY SIMILARITY.
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N-LINKED (GLCNAC.
P-> R (IN REF. 2 F
K-> T (IN REF. 2 F
S-> G (IN REF. 2 F
VL -> RV (IN REF.
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E -> G (IN REF. 2
A -> P (IN REF. 2
S -> F (IN REF. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 124; DB 1; Length 1070; pred. No. 0.031;
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                                                                                                                                                                                                                                  PRT;
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(GLCNAC...)
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                                                                                                                                                                                                                                    345 AA.
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(POTENTIAL).
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
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              RESULT 10
OPCM_BOVIN .
ID OPCM BO
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OPCM_BOVIN

STANDARD;

PRT;

345 AA

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-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity)

-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use different the statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - i - SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00408; IGC2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003006; I9_MHC.
InterPro; IPR003598; I9_c2.
InterPro; IPR003600; I9_11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 600632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L34774; AAA36387.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; Signal
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                                                                                                                                                                                                                                                                 106
                                                                                                                                                                                                           129 H----LIVQVPPQIMNISSDITVNEGSSVTLLCLAIGRPE-----PTVTWR------HLS 173
                                                213 PODTGGGINIPGVL----SSLPSLGFSLPTWGK----VGLGLAG 248
                                                                                                    174 VKEGQGEVSEDEYLE----ISDIKRDQSGEYECSAL-NDVAAPDVRKVKITVNYPPYISK 228
  229
                                                                                                                                                          162
                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                     55 ---SVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRL 105
                                                                                                                                                                                                                                                                                                                                                                                                                            21 LLFLVPTGVPVRSGDATFPKAMDNVTVROGESATLRCTIDDRVTRVAW-LNRSTILYAGN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VIELHGSG----SGNEVI-EGPQNATVLKGSQARENCTVSQGWKLIMWALSDMVVL---- 54
                                                                                                                                                                                                                                                              HGSAYLTYQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHSS 161
                                                                                                                                                                                                                                                                                                                     DKWSIDPRVIILVN---TPTQY-----SIMIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
                                                                                                                                                       YY----FVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV-----IRC 212
AKNTGVSVGQKGILSCEASAVPMAEFQ----WFKEETRLATGLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:8143; OPCML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
OPIOID BINDING PROTEIN/CELL ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 120; DB 1;
pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPI-ANCHOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 345;
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) (POTENTIAL).
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                                           δÃ
                                                                                                                         Matches
                                                                                              Query Match
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CARBOHYD
                                                                                                                                                                                                                   DISULFID
DISULFID
CARBOHYD
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                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003500; Ig_like.
InterPro; IPR003600; Ig_like.
InterPro; IPR003600; Ig_like.
InterPro; IPR003600; Ig_like.
InterPro; IPR003600; Ig_like.
IMART; SM00410; IG_like; 1.
Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                        Repeat; Signal.
SIGNAL 1
21 LLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAW-LNRSTILYAGN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schoffeld P.R., McFarland K.C., Hayflick J.S., Wilcox J.N., Cho T.M., Roy S., Lee N.M., Loh H.H., Seeburg P.H.;

"Molecular characterization of a new immunoglobulin superfamily protein with potential roles in opioid binding and cell contact.";

EMBO J. 8:489-495(1989).

"Introvers The Presence OF ACIDIC LIPIDS; PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INVOLVED IN CELL CONTACT.

-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                          4 VIFLHGSG----SGNEVI-EGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVL---- 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89251576; PubMed=2721489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P11834;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
0p1o1d binding protein/cell adhesion molecule precursor (OBCOML)
0p1o1d-binding cell adhesion molecule) (OPCML).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                  loca1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S03199; S03199.
                                                                    70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X12672; CAA31192.1; -.
                                                                              Similarity
                                                                                                                     345 AA;
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                        28
                                                                           5.8%;
25.1%;
                                                                                                                   37914 MW;
                                                               36;
                                                                        Pred.
                                                                      Score 119; DB : Pred. No. 0.02;
                                                                                                                                                         N-LINKED
                                                                                                                            GPI-ANCHOR (POTENTIAL)
                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
                                                                                                                                            N-LINKED
                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                N-LINKED
                                                                                                                                                                                                                N-LINKED
                                                                                                                                                                                                                                                             REMOVED IN MATURE FORM IG-LIKE C2-TYPE DOMAIN IG-LIKE C2-TYPE DOMAIN IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                          OPIOID BINDING PROTEIN/CELL ADHESION
                                                                                                                                                                                                                                                                                                                     MOLECULE.
                                                                                                            D1ECC8D9E7D8CB19 CRC64;
                                                           Mismatches
                                                                                                                                         GLCNAC...)
GLCNAC...)
GLCNAC...)
GLCNAC...)
GLCNAC...)
GLCNAC...)
GLCNAC...)
                                                                                 DB 1; Length 345;
                                                           103;
                                                                                                                                                                                          .) (PROBABLE)..) (POTENTIAL).
                                                                                                                                      ·) (POTENTIAL)
                                                         Indels
                                                                                                                                                               (POTENTIAL).
                                                                                                                                                     (POTENTIAL)
                                                       70;
                                                       Gaps
                                                       17;
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OPCM_RAT
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                                                                              EMBL;
InterPro;
Pfam; PF0
                     InterPro; IPR003598; Ig_c2.
                                                        PIR; JC1239; JC1239.
                                                                                                         EMBL; M88710; AAA40859.1; -.
                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                  "Cloning of neurotrimin defines a new subfamily of differentially expressed neural cell adhesion molecules.";
J. Neurosci. 15:2141-2156(1995).
i. FUNCTION: BINDS OPIOISE IN THE PRESENCE OF ACIDIC LIPIDS; PROBABLY
                                                                                                                                                                                                                                                                     -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS
                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY, IGLON
                                                                                                                                                                                                                                                                                                                 INVOLVED IN CELL CONTACT.

-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

-!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2

MAY BE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Struyk A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Eustachio P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 195-214, AND GPI-ANCHOR. MEDLINE=95198094; PubMed=7891157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92347701; PubMed=1339369;
Lippman D.A., Lee N.M., Loh H.H.;
"Opioid-binding cell adhesion molecule (OBCAM)-related clones from a
rat brain cDNA library.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P32736; Q01654; P32735; Q01653;
01-JUL-1993 (Rel. 26, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Opioid binding protein/cell adhesion molecule precursor (OBCAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPCML OR OBCAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPCM_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Opioid-binding cell adhesion molecule) (OPCML).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AKNTGVSVGQKGILSCEASAVPMAEFQ---WFKEDTRLA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 PQDTGGGINIPGVL----SSLPSLGFSLPTWGKVGLGLA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 VKEGQGFVSEDEYLE----ISDIKRDQSGEYECSAL-NDVAAPDVRKVKITVNYPPYISK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 HGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHSS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 DKWSIDPRVIILVN---TPTQY-----SIMIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 ---SVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRL 105
                                                                      M88709; AAA40858.1; -.
                                                                                            M88711; AAA40860.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YY----FVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV-----IRC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H----LIVQVPPQIMNISSDVTVNEGSSVTLLCLAIGRPE-----PTVTWR------HLS 173
     IPR003600; Ig_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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PF00047; ig;

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SMART; SM00410; IG_like; 1.
SMART; SM00408; IGc2; 2.
Immunoglobulin domain; Cell

Signal; Alternative

CARBOHYD

DISULFID DISULFID DISULFID DOMAIN DOMAIN

CARBOHYD

CARBOHYD CARBOHYD PROPEP

DOMAIN

Repeat;

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090610;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vielmetter J., Roman J.M., Dreyer W.J.;

"Neogenin, an avian cell surface protein expressed during
neuronal differentiation, is closely related to the human
suppressor molecule deleted in colorectal cancer.";

J. Cell Biol. 127:2009-2020(1994)
J. Cell Biol. 127:2009-2020(1994)
J. FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 HGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHSS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 H----LIVQVPPQIMNISSDITVNEISSVTLLCLAIGRPE-----PTVTWR------HLS
                                                                                  STRAIN-White leghorn; TISSUE-Embryonic brain; MEDLINE-95105243; PubMed-7806578;
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                   229 AKNTGVSVGQKGILSCEASAVPMAEFQ---WFKEDTRLATGLDGVRI 272
                                                                                                                                                                                                                                                                                                                                                                              213 PQDTGGGINIPGVL----SSLPSLGFSLPTWGK----VGLGLAGTML
                                                                                                                                                                                                                                                                                                                                                                                                         174 VKEGQGFVSEDEYLE----ISDIKRDQSGEYECSAL-NDVAAPDVRKVKITVNYPPYISK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                   162 YY----FVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV-----IRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 DKWSIDPRVIILVN---TPTQY-----SIMIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VIFLHGSG----SGNEVI-EGPQNATVLKGSQARENCTVSQGWKLIMWALSDMVVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLFLYPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAW-LNRSTILYAGN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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N-LINKED (GLCNAC...)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Mismatches
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IG-LIKE C2-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGYCGYLFLPWKCLVVVSLRLLFLVPT ->
SATTALLFIP (IN ISOFORM 2).
; A3181B0753F9658E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 118;
Pred. No. 0
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                                                                                                                                                                                                                                                                                     PRT; 1443 AA.
                                                                                                                                                                          Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) (POTENTIAL).
) (POTENTIAL).
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              IN THE
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                                   В
                                                                                                                                                              Best
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                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00041; fn3; 6.
Pfam; PF00047; 19; 4.
PRINTS; PR00014; ENTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U07644; AAC59662.1; -. HSSP; P11276; 2MFN.
                                                                                                                                                                                                                                                                                                                                             DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR003006; Ig_MHC. Interpro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003961; FN_III.
InterPro; IPR003962; FnIII_r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003600;
                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                            218
                                   265 LRAGGS----LLISDVTEEDVGTYTCIADNENETIEAQAELAVQVPPEFLKRPANIYAHE
                                                                                                                       17
                                                                                                                                                               Local
                                                              -DQGGNETSEMIIHNVEPSDSGNIRC--SLQNSRLHGSAYLTVQVMGELFIPSVNLVVAE 130
                                                                                         VRQPSSLTKVTGQNAVFPC-VAGGFPTPYVRWTKNG
                                                                                                                      IEGPQNATVLKGSQARFNCTVSQGW--KLIMWALSDMVVLSVRPMEPIITNDRFTSQRY- 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00410; IG_like; 2.
SM00408; IGC2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00060; FN3;
                                                                                                                                                   49;
                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1091
                                                                                                                                                                                                         1443 AA;
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin domain; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1090
1111
1443
                                                                                                                                                                                                                                                                                                                                                                                           1037
                                                                                                                                                                                                                        894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig_like
                                                                                                                                                                    26.2%;
                                                                                                                                                                                                           158050 MW;
                                                                                                                                                                                5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                  IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                   FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                  Score 117.5; D
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                               FIBRONECTIN TYPE-III
BY SIMILARITY.
                                                                                                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                             N-LINKED
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                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                           N-LINKED
                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
                                                                                                                                                        Mismatches
                                                                                                                                                                                                              INKED (GLCNAC. . . 558C6795579C0E26
                                                                                                                                                                                                                                                                    (GLCNAC. .
                                                                                                                                                                                                                                                        (GLCNAC. .
                                                                                                                                                                                    DB 1;
                                                                                                                                                           73;
                                                                                                                                                            Indels
                                                                                                                                                                                      Length 1443;
                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                    (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                 (POTENTIAL)
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                                                                                                                                                               Gaps
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21

Query Match Best Local : Matches

71; Conservative Similarity SEQUENCE VARSPLIC CARBOHYD CARBOHYD

345 AA;

38067 MW; 5.7%;

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RESULT 12

CHICK

NEO1_CHICK

STANDARD;

SEQUENCE FROM N.A.

NCBI_TaxID=9031;

11;

Gallus gallus (Chicken). Neogenin (Fragment)

밁 δõ В

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RESULT 13
PGBM_HUMAN
                                                                                        SEQUENCE OF 1-21 FROM N.A.
MEDLINE-94052171; PubMed-8234307;
Cohen I.R., Graessel S., Murdoch A.D., Tozzo R.V.;
"Structural characterization of the complete human perlecan gene
                                                                                Proc
                                                                                                                                                                                                    "Cloning of human heparan sulfate proteoglycan core protein, assignment of the gene (HSPG2) to 1p36.1-->p35 and identific
                                                                                                                                                                                                                                                                                                                                          "Heparan sulfate proteoglycan of human colon: cloning, cellular expression, and mapping of t short arm of human chromosome 1.";
                                                                                                                                                                                 Genomics 11:389-396(1991).
                                                                                                                                                                                                                                               Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
                                                                                                                                                                                                                                                                                         TISSUE-Fibrosarcoma;
                                                                                                                                                                                                                                                                                                 SEQUENCE OF 892-1398 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91365376; PubMed-1679749;
Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;
"Primary Structure of the human heparan sulfate proteoglycan from basement membrane (HSPG2/perlecan). A Chimeric molecule with multiple domains homologous to the low density lipoprotein receptor, laminin, neural cell adhesion molecules, and epidermal growth factor.";
J., Biol. Chem. 267:8544-8557(1992).
                                                                                                                                                                                                                                                                      MEDLINE=92120660; PubMed=1685141;
                                                                                                                                                                                                                                                                                                                                  Genomics 10:673-680(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rallunki P. Trygyvason K.;

"Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD protein containing multiple domains resembling elements of the molecules, and epidermal growth factor.";

J. Cell Biol. 116:559-571(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1018-1472 FROM N.A.
                                                                                                                                                                                               BamHI restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P99160; Q16287;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Basement membrane specific heparan sulfate proteoglycan core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92235084; PubMed=1569102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Skin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=92112994; PubMed=1730768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein precursor (HSPG) (Perlecan) (PLC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGBM_HUMAN
                  FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 GFYQCIA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186
                                                                   Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMDIVFECEVTGKPT-----PTVKWVKNGDVVIPSDYFKIVKEHNLQ-----VLGLVKSDE 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NE----PCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTLTCVA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Colon;
               It serves as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                           fragment length
                                                                                                                                                                                                                                                                                                                                                     and mapping of the gene (HSPG2)
    attachment substrate for cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                         polymorphism.
                                                                                                                                                                                                                                                                                                                                                                     partial molecular
                                                                                                                                                                                                 and identification
                                                                                                                                                                                                                                                                                                                                                   to the
 DOMAIN
                                                                      Heparan
                                                                                                                                                                                                                                                                                                                                             Pfam;
Pfam;
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Pfam;
                                                                                                                                                                                                                                                                                                                 ProDom;
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PROSITE; PS00022; EGF_1; 9.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01248; LAMININ_TYPE_EGF; 11

PROSITE; PS50025; LAM_DOMAIN; 3.

PROSITE; PS50068; LDLRA_1; 4.

PROSITE; PS50068; LDLRA_2; 4.

PROSITE; PS50024; SEA; 1.
                                                                                                                                                                                                                                                                      SMART; SM00192; LDLa, 4.
SMART; SM00281; LamB, 3.
SMART; SM00282; LamG, 3.
SMART; SM00200; SEA, 1.
                                                                        Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                     ProDom; PD003031; Laminin_B; 3.
SMART; SM00180; EGF_Lam; 6.
SMART; SM00001; EGF_like; 8.
SMART; SM00408; IGc2; 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L22078; -; NC
HSSP; P00740; 1EDM.
Siena-2DPAGE; P9816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X62515; CAA44373.1; --
EMBL; M85289; AAA52700.1; --
EMBL; M64283; AAA52699.1; --
EMBL; S76436; AAB21121.2; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane components such as laminin, prolargin and collagen type
                                                                               Basement membrane; Proteoglycan; Repeat; Glycoprotein; sulfate; Laminin EGF-like domain; Immunoglobulin domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:5273; HSPG2
                                                                                                                                                                                                                                                                                                                                                                                                                  PD003031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ), IPR000742; EGF_2.
), IPR001438; EGF_II.
), IPR003006; Ig_MHC.
), IPR003598; Ig_c2.
), IPR002172; LDL_recept_A.
), IPR0002174; Laminin_EGF.
), IPR001791; Laminin_EGF.
), IPR001791; Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000561;
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80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF; 4.
ig; 22.
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ldl_recept_a; 4.
SEA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laminin_EGF;
                                     4393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .aminin_B; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOT_ANNOTATED_CDS
194
                                                                    EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig_c2.
LDL_recept_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEA_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , 7.
SULFATE PROTEOGLYCAN CORE PROTEIN
                    BASEMENT MEMBRANE-SPECIFIC HEPARAN
                                                    POTENTIAL.
                                                                               domain;
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                                                                                                                                                                                                                                                                                                                                     DOMAIN
3030 PPSSTVQQGQDASFKCLIHDGAAPISLEWKTRNQELEDNVHIS--PNGSIIT-----
                 20 PQNATVLKGSQARFNCTVSQG-----WKLIMWALSDMVVLSVRPMEPIITNDRFTSQR 72
                                               Similarity
                                                                                                                                                                                                                                           3886
                                                                                                                                                           4301
                                                                         199
206
219
285
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332
                                     Conservative
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1160
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3401
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3883
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IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 5.
IG-LIKE C2-TYPE DOMAIN 7.
IG-LIKE C2-TYPE DOMAIN 7.
IG-LIKE C2-TYPE DOMAIN 10.
IG-LIKE C2-TYPE DOMAIN 11.
IG-LIKE C2-TYPE DOMAIN 11.
IG-LIKE C2-TYPE DOMAIN 13.
IG-LIKE C2-TYPE DOMAIN 13.
IG-LIKE C2-TYPE DOMAIN 14.
IG-LIKE C2-TYPE DOMAIN 15.
IG-LIKE C2-TYPE DOMAIN 16.
IG-LIKE C2-TYPE DOMAIN 16.
IG-LIKE C2-TYPE DOMAIN 17.
IG-LIKE C2-TYPE DOMAIN 19.
IG-LIKE C2-TYPE DOMAIN 20.
IG-LIKE C2-TYPE DOMAIN 20.
IG-LIKE C2-TYPE DOMAIN 20.
IG-LIKE C2-TYPE DOMAIN 21.
                                       25;
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LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
                                                                                                                                                                   HEPARAN SULI
MEDIATES MO'
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAMININ
                                               Score 116; DB Pred. No. 0.77;
                                                                           MEDIATES MOTOR NEURON ATTACHMENT
                                                                                                                                                                                                                                           LAMININ G-LIKE 2
                                                                                                                                                 (POTENTIAL)
                                                                        SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
                                                                                                                                          SIMILARITY.
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VALUE EGF-LIKE 9 (N-TERMINAL).
VIN DOMAIN IV 3 (DOWAIN III C).
VIN EGF-LIKE 9 (C-TERMINAL).
VIN EGF-LIKE 10.
VIN EGF-LIKE 11.
VIN EGF-LIKE 11.
                                             No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-LIKE 1 (N-TERMINAL).
DOMAIN IV.1 (DOMAIN III A).
EGF-LIKE 1 (C-TERMINAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-LIKE 4 (INCOMPLETE).
EGF-LIKE 5 (N-TERMINAL).
DOMAIN IV 2 (DOMAIN III B).
EGF-LIKE 5 (C-TERMINAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C2-TYPE DOMAIN 1
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                                                                                                                                                                                     SULFATE (POTENTIAL).
SULFATE (POTENTIAL).
SULFATE (POTENTIAL).
                                                                                                                                                                                                                                                                        G-LIKE
                                                                                                                                                                                                                  G-LIKE 3
                                                                                                                                                                              MOTOR NEURON ATTACHMENT
                                                         1;
                                        72;
                                                         Length 4393;
                                        Indels
                                         72;
                                         Gaps
     3079
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RESULT 14
NEO1_HUMAN
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEO1_HUMAN STANDARD;
092859; 000340;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequal)
15-JUN-2002 (Rel. 41, Last annumber)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3171 VLQISSAKPSDAGTYVCLAQNALGTAQKQVEVIV------DTG 3207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                             Vielmetter J., Chen X.-N., Miskevich F., Lane R.P., Yamakawa Korenberg J.R., Dreyer W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 AVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTG
                                                                                            the European Bioinformatics Institute. There are no rest
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entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fetal brain;
MEDLINE=97312699; PubMed=9169140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97236653; PubMed=9121761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neogenin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 14:1129-1136(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meyerhardt J.A., Look A.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissum=Fetal brain;
                          EMBL; U61262; AAB17263.1;
EMBL; U72391; AAC51287.1;
HSSP; P02751; lTTF.
Genew; HGNC:7754; NEO1.
                                                                                                                                                    between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular characterization of human neogenin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 YDQGGNFTSEMIIHNVEPSDSGNIRC-----SLQNSRLHGSAYLTVQVMGELFI- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGKAVTLECVSAGEPRS----SARWTRISSTPAKLEQRTYGLMDSH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --PSVNL-VVAENEPCEVTCLPSHWTRLPDISWEL----GLLVSHSSYYFVPEPSDLQS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----IVGTRPSNHGTYRCVASNAYGVAQSVVNLSVHGPPTVSVLPEGPVWVK 3127
                                                                                                                                                                                                                                                                  LINES.
                                                                                                                                                                                                             SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                                                                                                                                                                                                                                                                                                       the mapping of its gene (NEO1) to chromosomal position
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Last annotation updat
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erization of neogenin,
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mal position 15q22.3-
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MIM; 601907; InterPro;

IPR003961; FN_III

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RAGE_BOVIN
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Best Local
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RAGE_BOVIN
Q28173;
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                                                          422 GAQL-IILEHAPATTGPLPSAPRDYVASLVSTRFIKLTW 459
                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                              202 SATVNLTVIRCPODTGGGINIP-GVLSSLPSLGFSLPTW 239
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                                                                                                                                            311 TEDDAGTYFCIADNGNETIEAQAELTVQAQPEFLKQPTNIYAHESMDIVFECEVTGKPT- 369
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Alternative splicing.
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Pfam; PF00047; ig; 4.
PRINTS; PR00014; FNTYPE
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SMART; SM00408; IGC2; 3.
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                                                                                                                                                               89 EPSDSGNIRCSLQNSR--LHGSAYLTVQVMGELFIPSVNLVVAENE----PCEVTCLPSH 142
                                                                                                                                                                                                                   66 -----
                                                                                                                                                                                                                                                    12 SGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                           Local
                                                                                                 ----PTVKWVKNGDMVIPSDYFKIVKEHNLQ----VLGLVKSDEGFYQCIAENDVGNAQA 421
                                                                                                                      WTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARK 20:
                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                          1248
168
1461
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IPR003006; Ig_MHC.
IPR003598; Ig_c2.
IPR003500; Ig_like.
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                                                                                                                                                                                                                                                                                                                          AA;
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24.4%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                         159958 MW;
                                                                                                                                                                                                            31; Mismatches
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IG-LIKE C2-TYPE DOMAIN 2
IG-LIKE C2-TYPE DOMAIN 3
IG-LIKE C2-TYPE DOMAIN 3
IG-LIKE C2-TYPE DOMAIN 4
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 2
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 5
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N-LINKED
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BY SIMILARITY.
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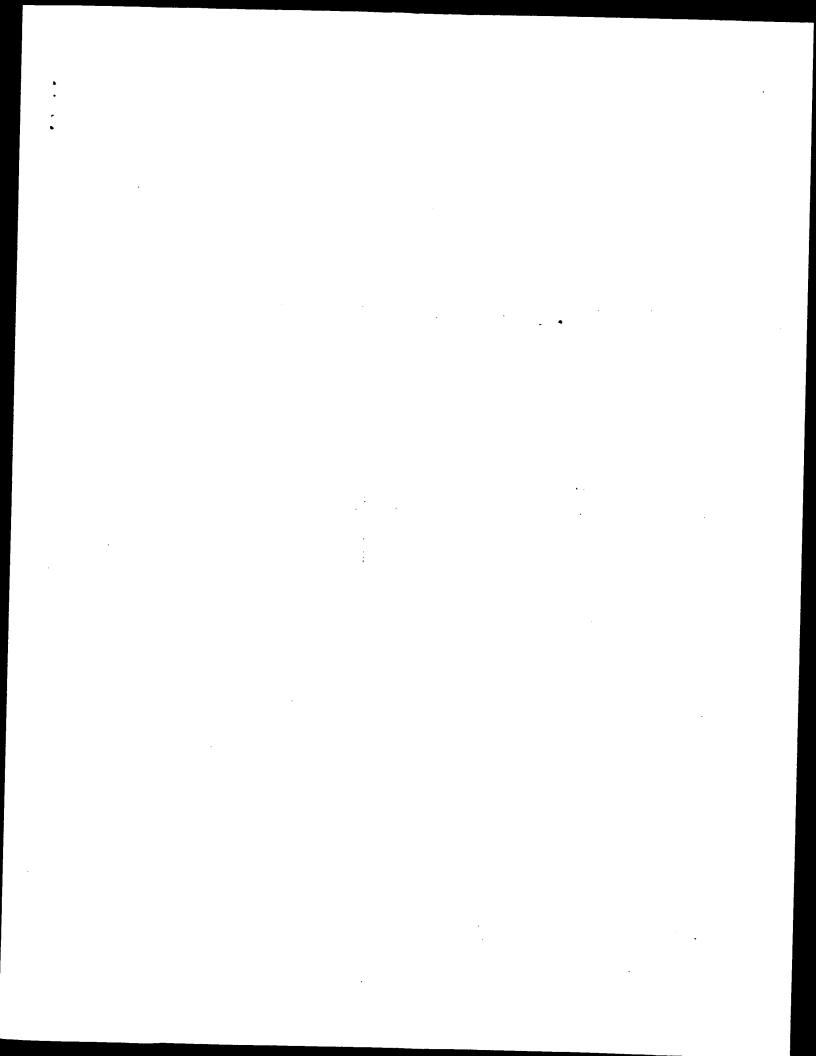
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Q
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                           176 TKRHPKTGLFTLHSELM----VTPARGGALHPTFSCSFTPGLPRRRALHTAPIQLRVWSEH 232
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SIGNAL ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neeper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
Elliston K., Stern D., Shaw A.;
"Cloning and expression of a cell surface receptor for advanced
glycosylation end products of proteins.",
J. Biol. Chem. 267:14998-15004(1992).
1. Biol. Chem. 267:14998-15004(1992).
1. FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
PRODUCTS (AGE), THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006; Ig_MHC
InterPro; IPR003598; Ig_c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M91212; AAA03575.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003600; Ig_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Advanced glycosylation end product-specific receptor precursor (Receptor for advanced glycosylation end products).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Type I membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92340547; PubMed=1378843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                         70 SQRYDQGGNFT--SEMIIHNVEPSDSGNIR----CS----LQNSRLHGSAYLTVQVMGE- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: ENDOTHELIAL CELLS.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
   RATE IN DIABETES.
                                                                                                                                                                                                                                                                                                                                                                                                                          SM00410; IG____.
SM00408; IGC2; 1.
SM00408; IG_MHC; 1.
                                                                                                                                                                416 AA;
                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                domain; Glycoprotein; Transmembrane; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig; 2.
IG_like; 1.
                                                                                                                                                              44182 MW;
                                                                                                             23.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig_MHC.
                                                                                                                                5.5%;
                                                                                                  35;
                                                                                                            Score 113.5; DB
Pred. No. 0.069;
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                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                      ADVANCED GLYCOSYLATION END PRODUCT-
SPECIFIC RECEPTOR.
                                                                                                                                                         B703815573E767AE CRC64;
                                                                                                Mismatches
------CEVTCLPS---HWTR----LP 147
                                                                                                                           DB 1;
                                                                                              87;
                                                                                            Indels 127;
                                                                                                                           Length 416;
                                                                                           Gaps
                                                                                           18;
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Sea1 Job	В	Qy	밁	Qy	망	Qy	Дb	Qy	Ър
Search completed: April 28, 2003, 18:09:37 Job time : 18.2617 secs	405EPEAAESSTGGP 416	326 TASLPPKSCESSDPEQRNSSCGPP 349	1	266 RRRCCGCNCCCRCCFCCRKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKTTD 325	329 TITETGEEGTTAGSVEGPGLETLALTLGILGGLGTVALLLGVIVW 3/3	208 TVIRCPQDTGGGINIPGVLSSLPSLGESLPTWGKVGLGLAGTMLLTPTCTLTIRCCCC 265	290LPPGPMLLLPEVGPEDQGTYSCVATHPSHGPQESKAVSV 328	148 DISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNL 207	233 RGGEGPNVDAVPLKEVQLVVEPEGGAVAPGGTVTLTCEAPAQPPPQIHWIKDGRPLP 289



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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model
Run on:

April 28, 2003, 18:09:54; Search time 18.8683 Seconds
(without alignments)
1946.300 Million cell updates/sec
1946.300 Million cell updates/sec
1946.300 Million cell updates/sec
Sequence:

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5
Searched:
283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters:
283224
Minimum DB seq length: 200000000
Maximum DB seq length: 200000000
Post-processing:
Maximum Match 100%
Listing first 45 summaries

Database:

PIR_73:*
3: pir3:*
3: pir4:*
4: pir4:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No)
Score 147.5 129.5 129.5 129.5 127.5 127.5 125.5 126.5 126.5 126.5 116.5 116.5 116.5 116.5 116.5 116.5 116.5 116.5 116.5 116.5	
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1	protein-tyrosine k	CD22 homolog/B Lym	nypotherical Proce		coverckie- and ade	mannose 6-phosphat	hypothetical proce	sax-3 protein ca	110000000000000000000000000000000000000	hypothetical prote	hypothetical proce	dillaryour process for	amalgam protein pr	protein-tyrosine K	polyprotein - Lava	U.S. 7 (1) figure	edk protein - frui	differentiation an	Hedrar Cert design	roman colladhesi	ror-related recept

ALIGNMENTS

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Query Match 7.2%; Score 14/.3; DE 1, Eury	./1; 274/; n, a DNA-l receptor receptor ed <sig> roducts r ed <ext> ed <tmm> ted <tmm> ted <tmm <tmm="" <tmm<="" td="" ted=""><td>A; Accession: B428/9 A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 'G', 2-99, 'R', 101-404 <nee> A; Residues: 'G', 2-99, 'R', 101-404 <nee> A; Residues: 'G', 2-99, 'R', 101-404 <nee> A; Rosidues: 'G', 2-99, 'R', 101-404 <nee> A; Rosidues: 'G', 2-99, 'R', 101-404 <nee> A; Experimental source: Lung A; Experimental source: Lung A; Note: sequence extracted from NCBI backbone (NCBIP:109438) A; Note: sequence extracted from NCBI backbone (NCBIP:109438) A; Note: sequence extracted from NCBI backbone (NCBIP:109438) C; Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly C; Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly C; Comment: This receptor appears also to mediate the effects of amyloid beta peptide C; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment</nee></nee></nee></nee></nee></td><td>cid sequence not shown; Eransiacion not shown; Eransiacion not shown; Eransiacion not shown; Eransiacion not specifical and specifical not shown; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Ellis dt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Ellis not not specifical not not specifical not specifical not specifical not specifical not not specifical not specif</td><td>RESULT 1 161596 advanced glycosylation end-products receptor precursor - human advanced glycosylation end-products receptor precursor - human Advanced glycosylation end product-binding protein, 35K; glycoprot N; Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprot N; Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprot N; Species: Homo saplens (man) C; Species: Homo saplens (man) R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, M.; Mita, K.; Mita, K.; Takahashi, E.; Ando, A.; Mita, M.; Mita, M.;</td></tmm></tmm></tmm></ext></sig>	A; Accession: B428/9 A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 'G', 2-99, 'R', 101-404 <nee> A; Residues: 'G', 2-99, 'R', 101-404 <nee> A; Residues: 'G', 2-99, 'R', 101-404 <nee> A; Rosidues: 'G', 2-99, 'R', 101-404 <nee> A; Rosidues: 'G', 2-99, 'R', 101-404 <nee> A; Experimental source: Lung A; Experimental source: Lung A; Note: sequence extracted from NCBI backbone (NCBIP:109438) A; Note: sequence extracted from NCBI backbone (NCBIP:109438) A; Note: sequence extracted from NCBI backbone (NCBIP:109438) C; Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly C; Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly C; Comment: This receptor appears also to mediate the effects of amyloid beta peptide C; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment: This receptor appears also to mediate the effects of amyloid beta peptide c; Comment</nee></nee></nee></nee></nee>	cid sequence not shown; Eransiacion not shown; Eransiacion not shown; Eransiacion not shown; Eransiacion not specifical and specifical not shown; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Ellis dt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Ellis not not specifical not not specifical not specifical not specifical not specifical not not specifical not specif	RESULT 1 161596 advanced glycosylation end-products receptor precursor - human advanced glycosylation end-products receptor precursor - human Advanced glycosylation end product-binding protein, 35K; glycoprot N; Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprot N; Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprot N; Species: Homo saplens (man) C; Species: Homo saplens (man) R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R; Sugaya, K.; Fukagawa, T.; Matsumoto, M.; Mita, K.; Mita, K.; Takahashi, E.; Ando, A.; Mita, M.;

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-1427 <PIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dev. Biol. 166, 654-665, 1994
A;Title: Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the A;Reference number: I51668; MUID:95113183; PMID:7813784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor suppressor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                         398 YQCIAENEAGNIQTYAQLIIPDPAVPSSSILPSAPRDV-----VPVLVSS 442
                                                                                              188 LTCVA-----TWKSLKARKSATVNLTVI-RCPQDTGGGINIPGVLSS 228
                                                                                                                                      347 DIEFECAVSGKPS-----PTVKWTKNGEVVIPSDYFQIVDGSNLR----ILGLVKSDEGY 397
                                                                                                                                                                            133 PCEVTCL----PSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGT 187
                                                                                                                                                                                                                      289 VLGG--SNLLISNVTDDDAGAYTCVATYKNENTSFSADLTVMVPPQFLNHPANLYAYESM 346
                                                                                                                                                                                                                                                                                                       243 LQRPSNVVAIEGQDAVLECAVS-GYPTPTIVWMQGD-----EPVPIRTR----KYS 288
                                                                                                                                                                                                                                                             75 QGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENE 132
                                                                                                                                                                                                                                                                                                                                             17 IEGPQNATVLKGSQARENCTVSQGW--KLIMWALSDMVVLSVRPMEPIITNDRFTSQRYD 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 -QSEEPEAGESSTGGP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 CESSDPEQRNSSCGPP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 ------ QRRGEERKAPENQEEEEERAELN------ 389
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 -----PTAGSVGGSGLGTLALALGILGGLGTAALLIGVILWQRR----- 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 CRCCFCCRRKRGFRIQFQKKSEKEKT--NKETETESGNENSGYNSDEQKTTDTASLPPKS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 PGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT-----PTCTLTIRCCCCRRRCCGCNCC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 -GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISIIE-PGEEG----- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 YFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 EPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS----PQIHWMKD----- 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 IP----SWNILVVAENEP-------CEVTCLPSHWTRLPDISWELGILVSHSSY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 KEQTRRHPETGLFTLQSELM----VTPARGGDPRPTFSCSFSPGLPRHRALRTAPTQPRVW 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 EIVDSASELTA--GVPNKVGTCVSEGSYPAGTLSWHLDG-----KPLVPNEKGVSV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 ----QRYDOGGNFT---SEMIIHNVEPSDSGNIR----CSLQNSRLHGSAYLTVQVMGELF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1, W.E.; Reale, M.A.; Candia, A.F.; Wright, C.V.; Cho, K.R.; Fearon, E.R. 166, 654-665, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVIEGPQNATVLKGSQARFNCTVSQG---WKLIMWALSDMVVLSVRPMEPIITNDRFTS- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                             6.5%; Score 133; DB 2
25.7%; Pred. No. 0.088;
ative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.6%; pred. No. 0.0019;
httve 40; Mismatches 114; Indels 137; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB_2; Length 1427;
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A;Title: Cloning of neurotrimin defines a new subfamily of differentially expressed na;Reference number: 156551; MUID:95198094; PMID:7891157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross_references: EMBL:U16845; NID:g755184; PIDN:AAA67445.1; PID:g755185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-344 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: I56551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP:T01B7.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A: Experimental source: clone T01B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL;Z66499;_PIDN:CAA91301.1; GSPDB:GN00020; CESP:T01B7.8
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A;Residues: 1-164 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T01B7.8 - Caenorhabditis elegans c;Species: Caenorhabditis elegans c;Species: Caenorhabditis elegans c;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: Z19867
A;Accession: T24272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics
                                182 EDEYLE----IQGITREQSGEYECSAS-NDVAAPVVRRVNVTVNYPPYISEAKGTGVPVG 236
222 IPGVL----SSLPSLGFSLPTWGK 241
                                                                          167 EPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCP-----QDTGGGIN 221
                                                                                                                       130 ----LIVQVSPKIVEISSDISINEGNNISLTCIATGRPE-PTVTWR----HISPKAVGFVS 181
                                                                                                                                                                      107 GSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVP 166
                                                                                                                                                                                                                  81 KWCLDPRVVLLSN---TQTQY-----SIEIQNVDVYDEGPYTCSVQTDNHPKTSRVH 129
                                                                                                                                                                                                                                                                 56 ---VRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRLH 106
                                                                                                                                                                                                                                                                                                                 21 LLELVPTGVPVRSGDATFPKAMDNVTVROGESATLRCTIDNRVTRVAWLNRSTILYAGND 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 CRICCCTRCCTCCR 115
                                                                                                                                                                                                                                                                                                                                                           4 VIFLHGSG----SGNEVI-EGPQNATVLKGSQARENCTVSQGWKLIMWALSDMVVLS--- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 --NCCC-RCCFCCR 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 PODTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 LGLLVSHSSYYFVÞEÞSDLOSAVSILALTÞOSNGTLTCVATWKSLKARKSATVNLTVIRC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 KRQGGCGCCGCGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LAILLAIGTFIAV----SQVQSAV-----LPVSSTELATVGTDVSTASTAIDTLGNSSSRV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        6.3%; Score 129.5; DB 24.2%; Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.3%; Score 129.5; DB 2; Length 164;
32.1%; Pred. No. 0.015;
1tive 11; Mismatches 53; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       43; Mismatches 104; Indels 53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --GCCGCGGGGG--CGCCCCRPRCCCCRRCCTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                            14;
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C;Accession: A54100; A40098
R;Hedrick, L.; Cho, K.R.; Fearon, E.R.; Wu, T.C.; Kinzler, K.W.; Vogelstein, B. Genes Dev. 8, 1174-1183, 1994
A;Title: The DCC gene product in cellular differentiation and colorectal tumorigenesis. A;Reference number: A54100; MUID:95011532; PMID:7926722
A;Accession: A54100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             멍
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
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A;Residues: 1-750 <FEA>
A;Cross-references: GB:M32292; NID:g181492; PIDN:AAA35751.1; PID:g181493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-1447 < HEDD A; Cross-references: EMBL: X76132; NID: 9453209; PIDN: CAA53735.1; PID: 9453210 A; Cross-references: EMBL: X150, X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Keywords: transmembrane protein; tumor suppressor F;1-25/Domain: signal sequence #status predicted <SIG> F;26-1447/Product: tumor suppressor protein DCC #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type:
A; Residues: 1-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:119838; OMIM:120470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB: DCC
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R;Ganju, P.; Walls, E.; Brennan, J.; Reith, A.D. Oncogene 11, 281-290, 1995
A;Title: Cloning and developmental expression of Nsk2, a novel receptor tyrosine kinase A;Reference number: I48696; MUID:95349951; PMID:7624144
A;Accession: I48696
                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
C;Accession: 148696; S60738
                                                                                                                                                                                                                                                                                                                                                         protein-tyrosine kinase (BC 2.7.1.112) nsk2 precursor, splice form 2 - mouse N;Alternate names: receptor-type tyrosine kinase N;Contains: protein-tyrosine kinase nsk2 precursor, splice form 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 ELTVLVPPWFLNHPSNLYAYESMDIEFECTVS-GKPVPTVNWMKNGDVVIPSDYFQIVGG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 YLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 SNLR----ILGVVKSDEGFYQCVAENEAGNAQTSAQLIVPKPAIPSSS------VLPS 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 SDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 VVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 SGSGNEV-----IEGPQNATVLKGSQARFNCTVSQGW--KLIMWALSDM 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431 AP 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 LP 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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24.8%; Pred.
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C;Keywords: ATP; glycoprotein; phosphotransferase; receptor; transmembrane protein; t F;1-21/Domain: signal sequence #status predicted <SIG> F;2-871/Product: protein-tyrosine kinase nsk2, splice form 2 #status predicted <MAT2 F;22-871/Product: protein-tyrosine kinase nsk2, splice form 4 #status pre F;22-456, A, 466-871/Product: protein-tyrosine kinase nsk2, splice form 4 #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: splice form 4 C; Comment: For alternate splice forms see PIR:I48697. C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-456, 'A', 466-871 <GAN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: splice form 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X86444; NID:g929723; PIDN:CAA60165.1; PID:g929724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-871 <GAN1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: MGI:103308
C;Superfamily: mouse ror-related receptor; immunoglobulin homology; protein:kinase ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: X86444; NID: 9929723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;575-865/Domain: protein kinase homology <KIN>
F;583-591/Region: protein kinase ATP-binding motif
F;222,462/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;498-518/Domain: transmembrane #status predicted <TRM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;236-284/Domain: immunoglobulin homology <IMM2>F;226-284/Domain: immunoglobulin homology <IMM3>
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                                                                                                                                                                                                                                                                                                                                                                                                         172 -----SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKLVKLEVEVLGRILRAPESHNV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 KITRPPINVKIIEGLKÄVLPCTTMGNPKPSVSWIKGD-----NALRENSRIAALE- 171
                                                                                                                                                                                                                                                                                                                                                       129 AENEPCEVTC----LPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQ 183
                                                                                                                                                                                                                                                        184 SNGTLTCVAT----WKSLKARKSATVNLTVIR-----CPQDTGGGINIPG-----V 225
  389 VVPTPMPICREYCLAVKELFCAK 411
                                                 274 ------CCCRCC-----FCCR 283
                                                                                                  336 LYFLPTTSHRDPEDAQELLIHTAWNEL-----KAVSPLCRPAAEALLCYHLFLECSPG 388
                                                                                                                                                   226 LSSLPSLGESLP-----TWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCN-- 273
                                                                                                                                                                                                       278 --GLYTCIATNKHGEKESTAKAAATVSIAEWSKSQKDSQGYCAQYRGEGVLMQGPGEKML 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 DQGGNFTSEMITHNVEPSDSGNIRCSLQNSRLHGSAY----LTVQVMGELFIPSVNLVV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 EVIEGPQNATVLKGSQARENCTVSQGWK-LIMWALSDMVVLSVRPMEPIITNDRFTSQRY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocal Similarity
                                                                                                                                                                                                                                                                                                         TFGSFVTLRCTEIGIP-----VPTISWIENGNAVSSGSIQESVKDRVIDSRLQLFITKP- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; Score 127.5; D. 21.7%; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87; Gaps
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RESULT 7

148697

N;Alternate names: receptor-type tyrosine kinase
N;Contains: protein-tyrosine kinase nsk2 precursor, splice form 1 - mouse
N;Contains: protein-tyrosine kinase nsk2 precursor, splice form 3

N;Contains: protein-tyrosine kinase nsk2 precursor, splice form 3

C;Species: Mus musculus (house mouse)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
C;Accession: 148697, S60740
C;Accession: 148697, S60740
R;Ganju, P; Walls, E.; Brennan, J.; Reith, A.D.
Oncogene 11, 281-290, 1995
Oncogene 11, 281-290, 1995
A;Title: Cloning and developmental expression of Nsk2, a novel receptor tyrosine kina A;Title: Cloning and developmental expression of Nsk2, a novel receptor tyrosine kina A;Reference number: 148696; MUID:95349951; PMID:7624144
A;Reference number: 148697
A;Accession: 148697
A;Residues: 1-881 <GAN1>
A;Residues: 1-881 <GAN1>
A;Residues: 1-881 <GAN1>
A;Cross-references: EMBL:X86445; NID:g929725; PIDN:CAA60166.1; PID:g929726
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A;Map position: 1
A;Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1;
/3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1
                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6642 <DUZ>
A;Cross-references: EMBL:AF003131; PIDN:AAB54132.1; GSPDB:GN00019; CESP:unc-89
                                                                                                       A; Gene: CESP:unc-89
                                                                                                                                A; Experimental source: strain Bristol N2; clone C09D1
                                                                                                                                                                                                                                                                                        R;Du, Z.; Le, T.T.; Wilson, R. submitted to the EMBL Data Library, May 1997 A;Description: The sequence of C. elegans cosmid C09D1.
                                                                                                                                                                                                                                                                                                                                                                                 protein UNC-89 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                 A; Reference number: Z20679
A; Accession: T29757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;575-865/Domain: protein kinase homology <KIN>F;583-591/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;498-518/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;22-4861/Product: protein-tyrosine kinase nsk2, splice form 1 *status predicted <MATI>F;22-456, A',466-881/Product: protein-tyrosine kinase nsk2, splice form 3 *status predicF;42-101/Domain: immunoglobulin homology <IMMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: MGI:103308
C;Superfamily: mouse ror-related receptor; immunoglobulin homology; protein kinase homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X86445; NID:g929725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A: Residues: 1-456, 'A', 466-881 <GAN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: splice form 1 A; Accession: S60740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comment: For alternate splice forms see PIR:I48696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 VVPTPMPICREYCLAVKELFCAK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 ------CCCRCC-----FCCR 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 LVFLPTTSHRDPEDAQELLIHTAWNEL------KAVSPLCRPAAEALLCYHLFLECSPG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 LSSLPSLGFSLP------TWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCN-- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 --GLYTCIATNKHGEKFSTAKAAATVSIAEWSKSOKDSQGYCAQYRGEGVLMQGPGEKML 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 SNGTLTCVAT----WKSLKARKSATVNLTVIR-----CPQDTGGGGINIPG-----V 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 AENEPCEVTC----LPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 TFGSFVTLRCTEIGIP-----VPTISWIENGNAVSSGSIQESVKDRVIDSRLQLFITKP- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 -----SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKLVKLEVEVLGRILRAPESHNV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD------NALRENSRIAALE- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 DQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY----LTVQVMGELFIPSVNLVV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 EVIEGPQNATVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRPMEPIITNDRFTSQRY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ords: ATP, glycoprotein; phosphotransferase; receptomain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.2%; Score 127.5;
21.7%; Pred. No. 0.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 881;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C;Keywords: cell adhesion; extracellular protein; glycoprotein; phosphotransferase; t
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A;Molecule type: mrNA
A;Residues: 1-1070 cpan>
A;Cross-references: GB:U40271; NID:g1322231; PIDN:AAC50484.1; PID:g1322232
C;Comment: This protein is a member of receptor protein tyrosine kinase family, but_p
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A;Map position: 6p21.1-6p12.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: receptor protein tyrosine kinase-like protein (RPTK) C;Species: Homo sapiens (man) C;Date: 16-Apr_1996 #sequence_revision 24-May-1996 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine kinase related receptor PTK7 precursor - human
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Biochem. 119, 235-239, 1996
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388 VYTCHAA--NLAGQRRQDVNITVATVPSWLKKPQDSQLEEGKPGYLDCL 434
                                                                                   187 TLTCVATWKSLKARKSATVNLTV-----IRCPQDTGGGINIPGVLSSL 229
                                                                                                                                                                                                                                        130 ENEPCEVTCLPSHWTRLPDISWE-LGL-LVSHSSYYFVPEPSDLQSAVSILALTPQSN-G 186
                                                                                                                                                                                                                                                                                                                       283 -----NGSLLLTQVRPRNAGIYRCIGQGQRGPPIILEATLHLAEIEDMPLFEPRVFTAGS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 VVLAPODVVVARYEEAMFHCQFSAQPPPSLQWLFEDETPITNRSRPPHLRRATVFA---- 282
                                                                                                                                                                                                                                                                                                                                                                                                      75 QGGNFTSEMIIHNVEPSDSGNIRCSLQNSR-----LHGSAYLTVQVMGELFIPSVNLVVA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 VIEGPQNATVLKGSQARFNCTVS-QGWKLIMWALSDMVVLSVRPMEPIITNDRFTSQRYD 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2240 SGTLTAKAKNAAGECETSAKVTVNGGNKKPEFVQAPQN 2277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2183 DEGEPLRWNLELDGPSPGT---EVSWLLNGQPLTKSDTVQVVDHGDGTYHVTIAEAKPEM 2239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2077 VVDGPKSVTIKETETAEFKATIS-GFPAPTVKWTINEKIVEESKTITTIKTEDVYT---- 2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 NGTLTCVATWKSLKARKSATVNLT-----VIRCPQD 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 AENEPCEVTCL---PSHWTRLPDISWEL-GLLVSHSSYYFVPEPSDLQSAVSILALTPQS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDB: PTK7
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                                                                                                                                                              EE---RVTCLPPKGLPEPSVWWEHAGVRLPTHGRVY-----QKGHELVLANIAESDAG
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23.9%; Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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RESULT 10
T15651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: JC4025
R;Shark, K.B.; Lee, N.M.
Gene 155, 213-317, 1995
A;Title: Cloning, sequencing and localization to chromosome A;Reference number: JC4025; MUID:95237612; PMID:7721093
A;Accession: JC4025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U58760; NID:g1330384; PID:g1330389; PIDN:AAB00710.1; GSPDB:GN0CA;Experimental source: strain Bristol N2; clone C27A2 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-188 <NHA>
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A; Introns: 19/3; 91/2
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C; Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:L34774; NID:g514373; PIDN:AAA36387.1; PID:g514374
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-345 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:251677; OMIM:600632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB:OPCML; OBCAM; OPCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Comment: This protein binds opioid alkaloids in the presence of acidic lipids, exhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Homo sapiens (man)
Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 CTLTIRCCCCRRRCCGC--NCCC-RCCFCCR 283
                                        174 VKEGQGFVSEDEYLE----ISDIKRDQSGEYECSAL-NDVAAPDVRKVKITVNYPPYISK 228
                                                                                                                          129 H----LIVQVPPQIMNISSDITVNEGSSVTLLCLAIGRPE-----PTVTWR------HLS 173
                                                                                                                                                                 106 HGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHSS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
  213 PQDTGGGINIPGVL----SSLPSLGFSLPTWGK-----VGLGLAG
                                                                               162 YY----FVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV-----IRC 212
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                                                                                                                                                                                                                                                                                       21 LLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAW-LNRSTILYAGN 79
                                                                                                                                                                                                                                                                                                                                4 VIFLHGSG----SGNEVI-EGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVL----
                                                                                                                                                                                                                                                                                                                                                                                             ocal Similarity
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                                                                                                                                                                                                          DKWSIDPRVIILVN---TPTQY-----SIMIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
                                                                                                                                                                                                                                                 ---SVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
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                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                          5.8%;
25.0%;
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                                                                                                                                                                                                                                                                                                                                                                           37; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ب.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 122.5; DB Pred. No. 0.059;
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 188;
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A; Residues: 1-345 <SCH>
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                                                                                                                                                                                                 C; Keywords:
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A; Residues: 1-345 <LIP>
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                              21 LLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAW-LNRSTILYAGN 79
                                                                                                                                       Local
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                                                                                                                                     Similarity
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                                                                                                                    Conservative
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C;Accession: S03199
R;Schofield, P.R; McFarland, K.C.; Hayflick, J.S.; Wilcox, J.N.; Cho, T.M.; Roy, S.; EMBO J. 8, 489-495, 1989
A;Title: Molecular characterization of a new immunoglobulin superfamily protein with A;Reference number: S03199; MUID:89251576; PMID:2721489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              opioid-binding protein OPCAM precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1-27/Domain: signal sequence *status predicted <SIG> F;28-345/Product: opioid-binding protein OPCAM *status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: carcinoembryonic antigen;
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X12672; NID:g585; PIDN:CAA31192.1; PID:g586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           opioid-binding protein (clones SG8 and SG13) - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 03-May-1994 #sequence_revision 03-May-1994 C;Accession: JC1239
                                                                                                                                                                                                                                                             A;Cross-references: GB:M88710; NID:g203247; PIDN:AAA40859.1; PID:g203248; GB:M88711;
                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Opioid-binding cell adhesion molecule (OBCAM)-related clones A; Reference number: JC1238; MUID:92347701; PMID:1339369
                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Lippman, D.A.; Lee, N.M.; Loh, H.H. Gene 117, 249-254, 1992
                                                                                                                                                                                               Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-ter; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 AKNTGVSVGQKGILSCEASAVPMAEFQ---WFKEETRLATGLDG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 VKEGQGFVSEDEYLE----ISDIKRDQSGEYECSAL-NDVAAPDVRKVKITVNYPPYISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 YY----FVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV-----IRC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 HGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHSS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 AKNTGVSVGQKGILSCEASAVPMAEFQ---WFKEDTRLA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 DKWSIDPRVIILVN---TPTQY-----SIMIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 LLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAW-LNRSTILYAGN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VIFLHGSG----SGNEVI-EGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVL----
4 VIFLHGSG----SGNEVI-EGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVL---- 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H----LIVQVPPQIMNISSDVTVNEGSSVTLLCLAIGRPE-----PTVTWR------HLS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQDTGGGINIPGVL----SSLPSLGFSLPTWGKVGLGLA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%;
Similarity 25.1%;
                                                                                                          5.7%;
24.7%;
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                                                                                                          Score 118; DB 2; Pred. No. 0.24;
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                                                                           Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-May-1994 #text_change 19-May-2000
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s:;

from a rat

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A;Molecule type: mRNA
A;Residues: 1-338 <LIP>
A;Residues: 1-338 <LIP>
A;Cross-references: GB:M88709; NID:g203245; PIDN:AAA40858.1; PID:g203246
A;Experimental source: brain
C;Genetics:
C; Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
                                                                                                                                                                                                A;Title: Opioid-binding cell adhesion molecule (OBCAM)-related clones from a rat brain A:Reference number: JC1238; MUID:92347701; PMID:1339369
A;Accession: JC1238
                                                                                                                                                                                                                                                                                                                                                           opioid-binding protein (clone DUZ1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                      C;Accession: JC1238
R;Lippman, D.A.; Lee, N.M.; Loh, H.H.
Gene 117, 249-254, 1992
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I50600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Vielmetter, J.; Kayyem, J.F.; Roman, J.M.; Dreyer, W.J.
J. Cell Biol. 127, 2009-2020, 1994
A;Tittle: Neogenin, an avian cell surface protein expressed during terminal neuronal diff
A;Reference number: A55193; MUID:95105243; PMID:7806578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neogenin - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep_1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U07644; NID:g641965; PIDN:AAC59662.1; PID:g641966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: I50600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372 GFYQCIA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 GTLTCVA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 NE----PCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 LRAGGS----LLISDVTEEDVGTYTCIADNENETIEAQAELAVQVPPEFLKRPANIYAHE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 VRQPSSLTKVTGQNAVFPC-VAGGFPTPYVRWTKNG-----EELITED---SERFA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 PQDTGGGINIPGVL----SSLPSLGFSLPTWGK----VGLGLAGTML 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 VKEGQGFVSEDEYLE----ISDIKRDQSGEYECSAL-NDVAAPDVRKVKITVNYPPYISK 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 -DOGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSAYLTVQVMGELFIPSVNLVVAE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 AKNTGVSVGQKGILSCEASAVPMAEFQ---WFKEDTRLATGLDGVRI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 IEGPQNATVLKGSQARFNCTVSQGW--KLIMWALSDMVVLSVRPMEPIITNDRFTSQRY- 73
                                                   OBCAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKWSIDPRVIILVN---TPTQY-----SIMIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SVRPMEPIITNDRFTSQRYDQGGNFTSEMTIHNVEPSDSGNIRCSLQ-----NSRL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 117.5; DB 2; 26.2%; Pred. No. 1.2;
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Best Local :
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                                                                 245 AEFQ---WFKEDTRLATGLDGVRI 265
                                                                                                                                                    186 KRDQSGEYECSAL-NDVAAPDVRKVKITVNYPPYISKAKNTGVSVGQKGILSCEASAVPM 244
                                                                                                                                                                                              181 TPQSNGTLTCVATWKSLKARKSATVNLTV-----IRCPQDTGGGINIPGVL----SSLPS 231
                                                                                                              232 LGFSLPTWGK----VGLGLAGTML 251
                                                                                                                                                                                                                                         141 NEISSVILLCLAIGRPE-----PIVTWR-----HLSVKEGQGEVSEDEYLE----ISDI 185
                                                                                                                                                                                                                                                                                     129 AENEPCEVTCL----PSHWTRLPDISWELGLLVSHSSYY----FVPEPSDLQSAVSILAL 180
                                                                                                                                                                                                                                                                                                                             92 -----SIMIQNVDVYDEGPYTCSVQTDNHPKTSRVH----LIVQVPPQIMNISSDITV 140
                                                                                                                                                                                                                                                                                                                                                                          75 QGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRLHGSAYLTVQVMGELFIPSVNLVV 128
                                                                                                                                                                                                                                                                                                                                                                                                                       37 NVTVRQGESATLRCTIDDRVTRVAW-LNRSTILYAGNDKWSIDPRVIILVN---TPTQY- 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 NATVLKGSQARENCTVSQGWKLIMWALSDMVVL-----SVRPMEPIITNDRFTSQRYD 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%; Score 116.5; DI 25.0%; Pred. No. 0.31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 338;
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time : 26.8683 secs

OM protein - protein search, using sw model

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:

Title: Perfect score:

US-09-729-264-2 2059 1 MGLVIFLHGSGSGNEVIEGP......HPQASFNLASPEKVSNTTVV 382

April 29, 2003, 11:05:56; Search time 18.8683 Seconds (without alignments) 1622.277 Million cell updates/sec

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

ALIGNMENTS

Database

published_Applications_AA:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

301932 seqs, 80129803 residues

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US-10-175-739-584
US-10-175-740-584
US-10-176-488-584
US-10-176-492-584
US-10-176-747-584
US-10-176-798-584
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US-10-176-993-584
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CCRRECCGCNC 274 IE-PGEEG----MKD---- 274 ELGLLVSHSSY 162 LRTAPIOPRVW 230 YLTVOVMGELF 120 PLVPNEKGVSV 173 PIITNDRFTS. ls 138; RCPQDTGGGIN 221

Gaps

19;

Qy	Qy Db	Qy	Qу	Ωу	Quer Best Matc	RESULT US-08-7 ; Seque ; Publi ; GENER ; APPI ; APPI ; APII ; TITI ; CURI ; CUR
222 IPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT	163 YFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKAKKS-AXVXXXXXIII	121 IPSVNLYVAENBP	71QRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY 71QRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY 11:	15 EVIEGPQNATVLKGSQARPNCTVSQGWKLIMWALSDMVVLSVKPRUE 15	6.9%; Score 142; DB 1; Query Match Best Local Similarity 22.8%; Pred. No. 0.0048; Best Local Similarity 40; Mismatches 113;	US-08-755-235-4 US-08-755-235-4 US-08-755-235-4 Sequence 4, Application US/08755235 Sequence 4, Application VS20030059423A1 Publication No. US20030059423A1 GENERAL INFORMATION: APPLICANT: Stern, David M. APPLICANT: Stern, David M. APPLICANT: Stern, David M. APPLICANT: Stern, David M. APPLICANT: Wu, Jun TITLE OF INVENTION. METHOD FOR TREATING SYM TITLE REFERENCE: 0575/50159 FILE REFERENCE: 0575/50159 FILE REFERENCE: 01575/50159 FILE REFERENCE: 0157/50159 FILE REFERENCE: 0
	HGPQESRAVVSISII	TCLPSHWTRLPDISW	CSLQNSRLHGSA	ALSDMVVLSVKFMDE	DB 1; Length .0048; .es 113; Indel	O f

Result ŏ

Score

Query Match

Length DB

Description

US-08-755-235-4
US-10-184-644-559
US-10-174-590-584
US-10-175-737-584
US-10-175-737-584
US-10-175-732-584
US-10-176-752-584
US-10-176-913-584
US-10-176-952-584
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US-10-176-957-584
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US-10-174-572-584
US-10-174-572-584
US-10-174-582-584
US-10-174-582-584
US-10-174-582-584

Sequence 4, Appli Sequence 559, App Sequence 584, App

score Pred. No.

5: 6: 7: 8: 9: 10: 11: 12: 13: 14:

ruullsheu_hpiloata/2/pubpaa/USO8_NEW_PUB.pep:*
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[/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

SUMMARIES

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US-10-184-634-559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-184-644-559
                                                                                                                                                                                                                                   Sequence 559, Application US/10 Publication No. US20030068684A1 GENERAL INFORMATION:
                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                              APPLICANT:
CURRENT APPLICATION NUMBER: US/10/184,634
        APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-10-184-644-559
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                                                                                       APPLICANT:
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CURRENT FILING DATE: 2002-06-28
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RIC227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Publication No.
                                                                                                                                                                                                                                                                                                                                  2308 -----ATTCCTCATCGCCCACCCCACCCCGGCCCCACCACC 2344
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                                                                                                                                                                                                                                                                                                                                                                                               2274 AATTGAAGTTTCAATTAAAATTTAATATGTTTCC---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                       239 WGKVGLGLAGTMLLTPTCTLTIRCCCCR-RRCCGCNCCCRCCFCC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2473
                                                                                                                                                                                                                                                                                                                                                                                                                        179 ALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 6.7%; Score 138.5; DB Local Similarity 29.5%; Pred. No. 0.071; les 31; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 -- OSEEPEAGESSTGGP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 SCESSDPEQRNSSCGPP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 ----- QRRGEERKAPENQEEEEERAELN----- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 CCRCCFCCRKRGFRIQFQKKSEKEKT---NKETETESGNENSGYNSDEQKTTDTASLPPK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 ------PTAGSVGGSGLGTLALALGILGGLGTAALLIGVILWQRR----- 367
                                                                              Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                         Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                             Desnoyers, Luc
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Gurney, Austin L.
Pan, James
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o. US20030044930A1
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RESULT 5
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                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                               Prior application removed - See File Wrapper or Palm SEQ ID NO 584
LENGTH: 708
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 584, Application US/10174590 Publication No. US20030008352A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C42
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SEQ ID NO 559
LENGTH: 2473
                         180 GTPGSVESTLTLTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                          168 -- PSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                        125 APOVLGG----PSVSLVA--GVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHOTLLKE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                       114 --QVMGELFIPSVNI,VVAENEPCEVTCLPSHWTR-LPDISW-ELGLLVSHSSYY--FVPE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE:
                                                                                                                                                        68 ---DLPGWSRYWISGNAANGOHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVLVPPE 124
                                                                                                                                                                                       63 ITNDRFTSORYDQGGNFTS---EMIIHNVEPSDSGNIRCSLQNSRLHG-SAYLTV----- 113
                                                                                                                                                                                                                          13 LFCFRGRAGDSPHFLQQPEDLVVLLGEEARLPCALGAYWGLVQWTKSGLALGGQR----- 67
                                                                                                                                                                                                                                                                                              y Match
Local Similarity 23.8%; Pred. No. 0.026;
hes 55; Conservative 40; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2308 -----ATTCCTCATCGCCCACCCCACCCCGGCCCCACCACC 2344
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                 3 LVIFLHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2274 AATTGAAGTTTCAATTAAAATTTAATATGTTTCC-------
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US-10-176-758-584
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US-10-175-737-584
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CURRENT FILING DATE: 2002-06-21
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Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 584
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APPLICANT:
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C50
                                                      CURRENT APPLICATION NUMBER: US/10/175,737 CURRENT FILING DATE: 2002-06-19
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o. US20030013153A1
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; TYPE: PRT; ORGANISM: Homo Sapien US-10-175-737-584
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LENGTH: 708
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 612
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   168 --PSDLOSAVSILALTPOSNGTLTCVATWKSLKARKSATVNLTVIRCPODT 215
                                         125 APOVIGG---PSVSLVA--GVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHCTLIKE 179
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CURRENT APPLICATION NUMBER: US/10/175,752
                 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C60
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LENGTH: 708
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FILE REFERENCE: P3430R1C45
CURRENT APPLICATION NUMBER: US/10/175,738
CURRENT FILING DATE: 2002-06-19
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6.6%; Score 136; DB 9; Length 708;
Local Similarity 23.8%; Pred. No. 0.026;
hes 55; Conservative 40; Mismatches 106; Indels
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                                                                                                                                                  Godowski, Paul J.
Gurney, Austin L.
                                                                                  Watanabe, Colin K. Wood, William I.
                                                                                                                    Smith, Victoria
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    See File Wrapper or Palm

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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddward, Audrey
APPLICANT: Goddwski, Paul
APPLICANT: Gurney, Austin I
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LENGTH: 708
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                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/176,482
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo Sapien
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LENGTH: 708
114 --QVMGELFIDSVNLVVAENEPCEVTCLPSHWTR-LPDISW-ELGLLVSHSSYY--FVPE 167
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Prior Application removed - See File Wrapper or Palm
NUMBER OF SEO ID NOS: 612
                                                      68 ---DLPGWSRYWISGNAANGOHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVLVPPE 124
                                                                                         63 ITNDRFTSORYDQGGNFTS---EMIIHNVEPSDSGNIRCSLQNSRLHG-SAYLTV----- 113
                                                                                                                              13 LFCFRGRAGPSPHFLQQPEDLVVLLGEEARLPCALGAYWGLVQWTKSGLALGGQR----- 67
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23.8%; Pred. No. 0.026;
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CURRENT FILING DATE: 2002-06-20

Prior Application removed - See File Wrapper or Palm
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                                                                                                                                                                                                                                    Publication No.
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  Zhang, Zemin
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                                                                                               Gurney, Austin L.
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63 ITNDRFTSQRYDQGGNFTS---EMIIHNVEPSDSGNIRCSLQNSRLHG-SAYLTV----- 113
                                          13
                                                                                                                     Match 6.6%; Score 136; DB 9; Length 708; Local Similarity 23.8%; Pred. No. 0.026; es 55; Conservative 40; Mismatches 106; Indels
                                                                                 3 LVIFLHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPI 62
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                                        LECFRGRAGPSPHFLQQPEDLVVLLGEEARLPCALGAYWGLVQWTKSGLALGGQOR----- 67
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Godowski, Paul
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                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                       Sequence 584, Application US/10173700 Publication No. US20030027262A1
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LENGTH: 708
TYPE: PRT
ORGANISM: Homo Sapien
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GENERAL INFORMATION:
    APPLICANT:
                                                                                                                                                                                                       APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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Publication No. US20030022301A1
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CURRENT APPLICATION NUMBER: US/10/180,557
CURRENT FILING DATE: 2002-06-25
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                              Godowski, Paul J. Gurney, Austin L.
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Pan, James
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; ORGANISM: Homo Sapien
US-10-173-700-584
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LENGTH: 708
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Best Local :
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APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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180 GTPGSVESTLTLTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVT 230
                                                                                                    125 APQVLGG---PSVSLVA--GVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKE 179
                                                     168 --PSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDT 216
                                                                                                                                                    114 -- QVMGELFIPSVNLVVAENEPCEVTCLPSHWTR-LPDISW-ELGLLVSHSSYY--FVPE 167
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Search completed: April 29, 2003, 20:16:58 Job time: 28.8683 secs

Scoring table: Sequence: Title: Perfect score:

BLOSUM62

Searched:

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OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/:
2: /cgn2_6/ptodata/
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Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Dackfiles1.pep:*
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                                US-08-977-767-3
US-09-041-886-25
PCT-US94-05277-2
US-08-374-834-16
US-08-644-271-29
US-09-651-200-2
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US-09-651-200-24
US-09-651-200-24
US-09-651-200-20
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PCT-US95-08493-13
US-08-597-495B-22
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                                               Sequence 15, Appl
Sequence 19, Appl
Sequence 21, Appl
Sequence 6, Appli
Sequence 3, Appli
Sequence 2, Appli
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; Patent No. 5972684
                                                         CLONE:
US-08-977-767-3
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                     Query Match
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APPLICANT: Yue, Henry
APPLICANT: Greenwald, Sara
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: CARBONIC ANHYDRASE VIII
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 31.
CITY: Palo Alto
CTATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FASTSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1345 amino acids
                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                               LIBRARY: GenBank CLONE: 1532042
                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                  TELEFAX: 650-845-4166
                                                                                                                                           TOPOLOGY:
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                                                                                                                                             linear
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There: 36,749
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US-09-540-245A-17

US-09-540-245A-16

US-08-554-612C-1

US-08-659-984A-1

US-08-660-531-1

US-08-660-531-1

US-08-660-531-5

US-08-660-531-5

US-08-640-2

US-08-145-640-2

US-08-170-588-2

US-08-445-614-2

US-08-445-6135A-1

US-08-286-305A-1

US-08-441-104A-1
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US-09-336-536-67
US-09-254-465A-6
US-07-906-349A-6
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                                Score 128.5;
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                                      DB 2;
                                      Length 1345;
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Result NO.

Score 128

Match

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Query

109.5 109.5 109.5 107.5 107 107 106.5

Qγ В

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; MOLECULE TYPE: protein US-09-041-886-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09041886 Patent No. 6235872
             383 SNLR----ILGVVKSDEGFYQCVAENEAGNAQTSAQLIVPKPAIPSSS-----VLPS 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 37; Conserv
                                                               169 SDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                  110 YLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEP 168
                                                                                                                   324 ELTVLVPPWFLNHPSNLYAYESMDIEFECTVS-GKPVPTVNWNKNGDVVIPSDYFQIVGG 382
                                                                                                                                                                                                                    279 VI-----QLRSKKYSLLGG--SNLLISNVTDDDSGMYTCVVTYKNENISASA 323
                                                                                                                                                                                                                                                                                                                       220 SRTGNEAEVRILSDPGLHRQLYFLQRPSNVVAIEGKDAVLECCVS-GYPPPSFTWLRGEE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                      52 VVLSVRPMEPIITNDRFTSQRVDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSA 109
                                                                                                                                                                                                                                                                                                                                                                            10 SGSGNEV------IEGPQNATVLKGSQARENCTVSQGW--KLIMWALSDM 51
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STREET
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456 CGTGAAGAGGGTCCTCTATGACCCCTTCCTGCCCCCTCTGAGACTCAGCACC 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 VGLGLAGTMLLT-PTCTLTIRCCCCRRRCCGCNCCCRC-----CFCC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 GTCTCTGT------GC-CGTGGGAAGCGTCAGAGCCCCGTGGATGTGGA 455
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States
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Rabizadeh, Sharroz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.2%; Score 128; DB 4; Length 1447; 24.8%; Pred. No. 0.012;
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""smatches 41; Indels 33; Gaps
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GENERAL INFORMATION:
431 AP 432
                                                                          383 SNLR----ILGVVKSDEGFYQCVAENEAGNAQTSAQLIVPKPAIPSSS-----VLPS
                                                    229 LP 230
                                                                                                                         169 SDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSS 228
                                                                                                                                                                             324 ELTVLVPPWFLNHPSNLYAYESMDIEFECTVS-GKPVPTVNWMKNGDVVIPSDYFQIVGG 382
                                                                                                                                                                                                                            110 YLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEP 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                              279 VI------QLRSKKYSLLGG--SNLLISNVTDDDSGMYTCVVTYKNENISASA 323
                                                                                                                                                                                                                                                                                                                                                                                    220 SRTGNEAEVRILSDÞGLHRQLYFLQRPSNVVAIEGKDAVLECCVS-GYPPPSFTWLRGEE 278
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                               52 VVLSVRPMEPIITNDRFTSQRKDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                      10 SGSGNEV------IEGPQNATVLKGSQARFNCTVSQGW--KLIMWALSDM 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Vogelstein, Bert
APPLICANT: Zabrecky, James R.
TITLE OF INVENTION: Antibodies Specific for DCC Gene Product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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STREET: 1001 G Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Kinzler, Kenneth W.
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Jarosz, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202.508.9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.2%; Score 128; DB 5; Length 1447; 24.8%; Pred. No. 0.012; Indels 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Release #1.0, Version #1.25
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Matches Query Match

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US-08-374-834-16
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STREET: //.
CITY: Tarrytown
CITY: New York
TGA
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TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTOR
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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LENGTH: 869 amino acid
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    122 KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD-----SPLRENSRIAVLE- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cobert, Robert J. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/095,658 FILING DATE: 21-JUL-1993
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                                                                                                                                                                                                                                                                                                                              172 -----SGSLRIHNVOKEDAGOYRCVAKNSL--GTAYSKVVKLEVEVFARILRAPESHNV 223
                                                                                                                                                                                                                     184 SNGTLTCVAT----WKSLKARKSATVNLTVIRCPQDTGGG-----INIPGVLSSLP 230
                                                                                                                                                                                                                                                        224 TFGSFVTLHCTATGIP----VPTITWIENGNAVSSGSIQESVKDRVIDSRLQLFITKP- 277
                                                                                                                                                                                                                                                                                           133 P-----CEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQ 183
                                                                                                          336 FLNTSYADPEEAQELLVHTAWNEL-----KVVSPVCRPAAEALLCNHIFQECSPGVVP 388
                                                                                                                                             231 SLGFSL-------PTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCN----
                                                                                                                                                                                278 --GLYTCIATNKHGEKFSTAKAAATISIAEWSKPQKDNKGYCAQYRGEVCNAVLAKDALV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                       15 EVIEGPQNATVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRPMEPIITNDRFTSQRY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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324 TDTASLPPKSCESSDPEQRNSSCGPPHQRADQRP----PRPASHPQASFNLA 371
                                  389 TPIPICREYCLAVKELFCAKE----WLVMEEKTHRGLYRSEMHLLSVPECSKLPSMHWDP 444
                                                                   274 ----CCCRCC-----FCCRRKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKT 323
                                                                                                                                                                                                                                                                                                                                                                 74 DQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMGELFIPSVNLVVAENE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           869 amino acids
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(914) 345-7721
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.1%; Score 126.5; DB 1; Length 869; 20.9%; Pred. No. 0.0078;
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US-08-644-271-29
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TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
TITLE OF INVENTION: AND LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 60/008,657
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TELEPHONE: 914-345-7400
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                               122 KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD------Splrensriavle- 171
                                                                                                                                                                                  133 P-----CEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVS1LALTPQ 183
                                                                                                                                                                                                                     172 -----SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKVVKLEVEVFARILRAPESHNV 223
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TELEFAX: 914-345-7721
336 FLNTSYADPEEAQELLVHTAWNEL------KVVSPVCRPAAEALLCNHIFQECSPGVVP 388
                                 231 SLGFSL-------PTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCN----- 273
                                                                      278 --GLYTCIATNKHGEKFSTAKAAATISIAEWSKPQKDNKGYCAQYRGEVCNAVLAKDALV 335
                                                                                                         184 SNGTLTCVAT----WKSLKARKSATVNLTVIRCPQDTGGG-----INIPGVLSSLP 230
                                                                                                                                              224 TFGSFYTLHCTATGIP-----VPTITWIENGNAVSSGSIQESVKDRVIDSRLQLFITKP- 277
                                                                                                                                                                                                                                                      74 DQGGNFTSEMIIHNVEPSDSGNIRCSLONSRLHGSAY-LTVQVMGELFIPSVNLVVAENE 132
                                                                                                                                                                                                                                                                                                                                 15 EVIEGPQNATVLKGSQARENCTVSQGWK-LIMWALSDMVVLSVRPMEPITINDRFTSQRY 73
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US-09-062-365-1
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                                          GENERAL INFORMATION:
                                                                  Sequence 1, Application US/09062365
Patent No. 6465422
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: Sequence 33, Application US/09077955A

: Patent No. 6413740
APPLICANT: Stern, David
                   APPLICANT: Schmidt, Ann Marie
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EARLIER FILING DATE: 1995-12-15
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TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
FILE REFERENCE: REG195-B-PCT-US
                                                                                                                                                                                         445 TACARLP-----HLDYNKENLKTFPP--MTSSKPSVDIPNLPSSSSSSFSVS 489
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                                                                                                                                                                                                                                        324 TDTASLPPKSCESSDPEQRNSSCGPPHQRADQRP----PRPASHPQASENLA 371
                                                                                                                                                                                                                                                                                389 TPIPICREYCLAVKELFCAKE----WLVMEEKTHRGLYRSEMHLLSVPECSKLPSMHWDP 444
                                                                                                                                                                                                                                                                                                                                                                           336 FLNTSYADPEBAQELLVHTAWNEL-----KVVSPVCRPAAEALLCNHIFQECSPGVVP 388
                                                                                                                                                                                                                                                                                                                            274 ----CCCRCC-----FCCRRKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKT 323
                                                                                                                                                                                                                                                                                                                                                                                                                     231 SLGFSL------PTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCN----- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 --GLYTCIATNKHGEKFSTAKAAATISTAEWSKPOKDNKGYCAQYRGEVCNAVLAKDALV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 SNGTLTCVAT----WKSLKARKSATVNLTVIRCPQDTGGG-----INIPGVLSSLP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 TFGSFVTLHCTATGIP-----VPTITWIENGNAVSSGSIQESVKDRVIDSRLQLFITKP- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 P-----CEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQ 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 DQGGNFTSEMIIHNVEPSDSGNIRCSLONSRLHGSAY-LTVQVMGELFIPSVNLVVAENE 132
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US-09-651-200-2
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SEQ ID NO 2
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CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 332
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ORGANISM: Human
63 ITNDRFTSQRYDQGGNF------TSEMIIHNVEPSDSGNIRCSLQNSRLHGS 108
                                                                         10 SGSGNEVIEGPQNATV-LKGSQARENCTVS--QGWKL----IMWALSDMVVLSVRPMEPI 62
                                    48 SPTGAVEVQVPEDPVVALVGTDATLHCSFSPEPGFSLTQLNLIWQLTDTKQLV------ 100
                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 --------PTAGSVGGSGLGTLAL 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 EPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS----PQIHWMKD----- 252
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                                                                                                                 5.9%; Score 122.5; DB 4; Length 340; Conservative 50; Mismatches 128; Indels 109;
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Patent No. 6429303
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/
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TYPE: PRT
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                                                                                315 VTTSQMANEQGLFDVHSVLRVVLGANGTYSC------LVRNPVLQQDA 356
                                                                                                                                                                                                           109 AYLTVQVMGELFIPSVNLV----VAENEPCEVTCLPSHWTRLP--DISWELGL---LVSH 159
                                                                                                                                                                                                                                                       202 ---HSFTEGR-DQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV-SIRDFGS 256
357 HGSVTITGQPMTFPPEAL----WVTVGLSVCLIALLV---
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                                         GGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCC 276
                                                                                                                         SSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCP---QDT 216
                                                                                                                                                                    AAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITC--SSYRGYPEAEVFWQDGQGVPLTGN 314
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; sequence 24, Application US/09651200 ; Patent No. 6429303
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 ---HSFTEGR-DQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV-SIRDFGS 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 5.9%; Score 121.5; DB Local Similarity 21.2%; Pred. No. 0.011; nes 77; Conservative 49; Mismatches 1
                                                                                                                                                                                                                              483 ALAFYCWRK-----IKOSCEEENAGAEDODG------EGEGSKTALQPLKHSDS 525
                                                                                                                                                                                                                                                                                                                     450 HGSVTITGQPMTFPPEAL----WVTVGLSVCLIALLV----
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                                                                                                                                         526 KEDD 529
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APPLICATION UNUMBER: 60/172909
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
NUMBER: 60/183578
NUMBER: 60 PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
NUMBER: 60 PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
NUMBER: 60 PRIOR FILING DATE: 2000-02-18
SOOTWARE: Patentin Ver: 2.0
LENGTH: 534
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Patent No. 5864018
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                                                                                   APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO.
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Green e
                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Unknown Organism: Sequence OTHER INFORMATION: mz5020.protein from Figure 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                526 KEDD 529
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ADDRESSEE: TOWNSEND & LUNDOUS STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 RCCFCCRKKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKTTDTASLPPKSCES 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 ITNDRFTSQRYDQGGNF-----TSEMITHNVEPSDSGNIRCSLQNSRLHGS 108
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US-08-633-148-2
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                                                                                                                                                                                                                                                                                          Sequence 2, Application Patent No. 5864018
GENERAL INFORMATION:
APPLICANT: MORSER,
                                                                                         APPLICANT: HOLLANDER, DOKLS A.

APPLICANT: HOLLANDER, DOKLS A.

APPLICANT: HOLLANDER, DOKLS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP

ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                     STATE: CALL.
COUNTRY: U.S.A.
7IP: 94111
7IP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 326-242
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
1415) 326-2400
                                                                                                                                                                                                                APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 YFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINI 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 EIVDSASELTA--GVPNKVGTCVSEGSYPAGTLSWHLDG------KPLVPNEKGVSV 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 ---- QRYDQGGNFT--SEMIIHNVEPSDSGNIR----CSLQNSRLHGSAYLTVQVMGELF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 EVIEGPQNATVLKGSQARENCTVSQG---WKLIMWALSDMVVLSVRPMEDIITNDRETS- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 5.8%; Score 118.5; DB 2; Length 318; Local Similarity 24.0%; Pred. No. 0.01;
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OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 16-AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CALIFORNIA
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                                                                                      CALIFORNIA
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                                                                                                                                                                                                                                                                                          MORSER, MICHAEL J.
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CURRENT APPLICATION DATA:

FILING DATE: APPLICATION NUMBER:

16-APR-1996

US/08/633,148

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

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; ORGANISM: sus sp. US-09-651-200-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/09651200 Patent No. 6429303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: 2:
                                                                        SEQ ID NO 20
LENGTH: 325
                                                                                                                                                                                                            APPLICANT: Green et al
APPLICANT: Green et al
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 15966-562 (CURA-62)
CURRENT PPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
                                                                                                                  PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
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NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 EIVDSASELTA--GVPNKVGTCVSEGSYPAGTLSWHLDG-----KPLVPNEKGVSV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 IP----SVNLVVAENEP-------CEVTCLPSHWTRLPDISWELGLLVSHSSY 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 -GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISIIE-PGEEG---- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 YFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 EPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIHWMKD-----
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REFERENCE/DOCKET NUMBER: 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 ---- ORYDOGGNET---SEMIIHNVEPSDSGNIR---- CSLQNSRLHGSAYLTVQVMGELF 120
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SEQ ID NO 15
LENGTH: 1395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 15, Application US/09540245A Patent No. 6270984
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                                                                                                                                                                                                                                                      Query Match
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tessier-Lavigne, Marc TITLE OF INVENTION: Modulating Robo: Ligand Interactions FILE REFERENCE: B98-031-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/540,245A CURRENT FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                       ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 GGGINIPGVLSSLPS--LGFSLP------TWGKVGLGLAGTMLLTPTCT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 SSTQGYPEPQ-----RMYMLLNTKNSTTEHDADMKKSQNNITELYNVSIRVSLPIPPET 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 GLVPIHQMSSDLSLLANFSQPEINLLTNHTENSVINLTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 GSAYL-----TVQVMGELFIPSVNLVV--AENEPCEVTCLPSHWTRLPDISWELGLLVSH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 HERSDDAQCDVNILKTASDDNSTTD 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 LTIRCCCCRRRCCGCNCCCRCCFCCRRKR------GFRIQFQKK-SEKEKTNKET 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 ETESGNENSGYN----SDEQKTTD 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 MVVL--SVRPME-PIITNDRFTSQ-RYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLH 106
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130 ENEP----CEVTCLPSHWTRLPDISW---ELGLLVSHSSYYFVPEPSDLQSAVSILALTP 182
                                                                                                                             161 PKDTRVAKGETALLECGPPKGIPEPTLIWIKDGVPLDDLKAMSFGASSRV------R 211
                                            212 IVDGGN----LLISNVEPIDEGNYKCIAQNLVGTRESSYAKLIVQVKPYFMKEPKDQVML 267
                                                                                     73 YDQGGNFTSEMIIHNVEPSDSGNIRCSLQN---SRLHGSAYLTVQVMGELFIPSVNLVVA 129
                                                                                                                                                                       20 PQNATVLKGSQARFNCTVSQG--WKLIMW-----ALSDMVVLSVRPMEPIITNDRFTSQR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --NVSIVCVLQLEPSKTLLFSLPCNIDAKPPVQPPVPDHILW-----IAALLVTVVVV 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Conservative
                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brose, Katja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kid, Thomas
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                                                                                                                                                                                                                  5.5%; Score 114; DB 4; Length 1395; 25.8%; Pred. No. 0.2; ative 29; Mismatches 102; Indels 56; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --CGMVSFVTLRKRKKKOPGPSNECGETIKMNRKASEQTKNRAEV 299
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                                                                                                                                                                                          A_Geneseq_101002:*
1: /SIDS2/gcgdata/ge
2: /SIDS2/gcgdata/ge
3: /SIDS2/gcgdata/ge
4: /SIDS2/gcgdata/ge
6: /SIDS2/gcgdata/ge
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2059
1 MGLVIFLHGSGSGNEVIEGP......HPQASENLASPEKVSNTTVV 382
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
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1337.141 Million cell updates/sec
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and is derived by analysis of the total score distribution score greater than or equal is the number of results predicted by chance to have a ater than or equal to the score of the result being printed,

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
2059 2014 2014 2004 1514 1326 924.5 583.5 575.5 494 147.5	Score
100.0 97.8 97.3 73.5 64.4 44.9 28.3 28.3 7.2	Query Match Length DB
382 386 386 377 463 370 631 631 270 223	ength [
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		Himan transmembran	Prostate cancer-as	color	Amino acid sequenc	Protein of muscle	Mutant protein min			7 4 6	1000	Nak' (a	receptor	rnatively	receptor	Mouse receptor tyr	Nsk2 receptor. Mu	- (0	Inditact	NSKA CACLACCELATE	artcrimering ar	Alternatively spli	protein MYLK diffe	Deleted in Colorec		Human DCC protein.	m	perc	w	oma associat	qp35	_		_	Human RAGE protein	Human receptor ror		•

ALIGNMENTS

AAU75540

AAU75540;

AAU75540 standard; Protein; 382 AA.

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Human; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; approductive disorder; graft versus host disease; autoimmune disease; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                    Human B7-like protein, B7-L_h1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2002
                                                                                                               28-JUN-2001; 2001WO-US20719
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Welcher AA, Sarmiento UM,
                                                                28-JUN-2000;
28-NOV-2000;
                                (AMGE-) AMGEN INC.
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2000US-0729264.
       Schultz HJ,
          Chute HT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                        241 KVGLGLAGTMLLTPFCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEK 300
                                                                                                                   181 TPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWG 240
                                                                                                                                                                                    121 IPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSTLAL 180
                                                                                                                                                                                                                                121 IPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLOSAVSILAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphoproliferative disorders such as multiple myeloma. The psequence represents the amino acid sequence of human B7-L_h1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for enhancing the immune response to tumours. (I) plays a role in growth and maintenance of cancer cells based on the observation of seminal vesicle hyperplasia in transgenic mice overexpressing B7-L cancer including seminal vesicle cancer, lung, brain, breast, ovarian, pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell molecules are useful for alleviating the symptoms associated with autoimmune diseases involving chronic immune cell dysfunction or to treat diseases involving chronic immune cell dysfunction or to treat the symptoms associated with autoimmune diseases and account or treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polypucleotide encoding it and antibody against (I) as useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are incentive for anhancing the immuner regulators of B7-L polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombocytopenias, Guillain-Barre syndrome and myasthenia
                                                                                                                                                                                                                                                                                                       61 PIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Fig 1; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                        1 MGLVIFLHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPME 60
                                                                                                                                                                                                                                                                                                                                                                                                   1 MGLVIFLHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPME 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New B7-like polypeptides, polynucleotides and their modulators, useful
KVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRKRGFRIQFQKKSEKEK 300
                                                                                           TPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWG
                                                                                                                                                                                                                                                                               PIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2059; DB 23;
Pred. No. 5.5e-162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gravis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present
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The invention relates to an isolated B7-like (B7-L) polypeptide (I).

CC useful for treating B7-like polypufeder related disease, disorders (C) conditions including reproductive disorders (e.g. infertility, C) are conditions including reproductive disorders (e.g. infertility, C) miscarriage, preterm labour and delivery and endometricsis) and comparison of comparis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR
DR
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AAU75542
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purpura and psoriasis, chronic inflammatory disease such as
                      autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Fig 3; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New B7-like polypeptides, polynucleotides and their modulators, for diagnosing, preventing and treating reproductive, immune an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABK13030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-130881/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; B7-like protein; B7-L; antiinfertility; gynaecological; antiinferminity; cytostatic; immunosuppressive; antiarthritic; antirher antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; canc reproductive disorder; graft versus host disease; autoimmune toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-2000; 2000US-214512P.
28-NOV-2000; 2000US-0729264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUN-2001; 2001WO-US20719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human B7-like protein, B7-L_h3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU75542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 ASHPQASFNLASPEKVSNTTVV 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preventing and treating reproductive, immune and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schultz HJ, Chute HT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of allergy, asthma and hypersensitivity reactions, treatment of allergy, asthma and hypersensitivity reactions, the stream of allergy, asthma and hypersensitivity reactions, the stream of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU75541 standard; Protein; 386 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 TCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 AENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTL 188
                                                                                                                                                                                                                                                                                        Human; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirherantiinflammatory; dermatological; antipsoriatic; neuroprotective; antidabetic; haemostatic; antithyroid; antiulcer; antiallergic; antidabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 TSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVV 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human B7-like protein, B7-L_h2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253
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                                                                                                                                        antiasthmatic; nephrotropic; antibacterial; virucide; tunour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                373 NLASPEKVSNTTVV 386
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                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGNENSGYNSDEOKTTETASLPPKSCESSDPEORNSSCGPPHORADORPPRPASHPOASF 372
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99.7%;

    Mismatches

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Pred. No. 2.9e-158;
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mascarrage, precent about an vertical movements of professions of professions are comprising and other regulators of B7-L polypeptides are consistent for enhancing the immune response to tumours. (I) plays a role in constitution of the immune response to tumours. (I) plays a role in constitution of the profession of the treatment of the profession of t
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                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated B7-like (B7-L) polypeptide (I) are the polypeptide, polynucleotide encoding it and antibody against (I) are useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and miscarriage, preterm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Welcher AA, Sarmiento UM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic arthritis, multiple sclerosis inflammatory disease such as purpura and psoriasis, chronic inflammatory disease such as purpura and psoriasis, cronic solitis, inflammatory bowel disease (Crohn's disease and ulcerative colitis), inflammatory bowel disease (Crohn's disease and diabetes mellitus. They grave's disease, Hashimoto's thyroiditis and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for shock syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions, the periodic periodic properties (grave's disease), various pneumopathies pemphigoid), endocrinopathies (grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present lymphoproliferative disorders such as multiple myeloma B7-Lh2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also refer for Advanced to the prolong graft survival.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
129 AENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-130881/17.
                                                          73 TSQRYDQGGNFTSEMITHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVV 132
                                                                                                                     69 TSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVV 128
                                                                                                                                                                                       13 GSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMMALSDMVVLSVRPMEPIITNDRF 72
                                                                                                                                                                                                                                                     9 GSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLINWALSDMVVLSVRPMEPIITNDRF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK13029
                                                                                                                                                                                                                                                                                                                           372;
                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 AA;
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                 97.3%; Score 2004; DB 2
99.5%; Pred. No. 2e-157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schultz HJ, Chute HT;
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                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              DB 23; Length 386;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plays a role in
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The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) are useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are growth and maintenance of cancer cells based on the observation of seminal vesicle hyperplasia in transgenic mice overexpressing B7-L
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                                                                                                                                                                                                                                                                                                                                                                                                         proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                         New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABK13031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Welcher AA, Sarmiento UM, Schultz HJ, Chute HT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-2000; 2000US-214512P.
28-NOV-2000; 2000US-0729264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; B7-11ke protein; B7-1; antiinfertility; gynaecological; antilumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antityroid; antilicer; antilargic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W0200200710-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endocrinopathy; lymphoproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human B7-like protein, B7-L_h4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249
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310 T---PATIQMNKRPQTPLLSLP 328
                                       309 SGNENSGYNSDEQKTTDTASLP 330
                                                                                        249 TMLLIPTCILTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEKTNKETETE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of alleryy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and hymphoproliferative disorders such as multiple myeloma. The present sequence represents the amino acid sequence of human B7-L_hd.
                                                                                                                                                     193 TCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAG
                                                                                                                                                                                                                                  189
                                                                                                                                                                                                                                                                          133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell
                                                                                                                                                                                                                                                                                                                             73 TSÓRYDÓGGNLTSEMITHNVEPSDSGNIRCSLÓNSRLHGSÁYLTVQVMGELFIPSVNLVV 132
                                                                                                                                                                                                                                                                                                                                                     69 TSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVV 128
                                                                                                                                                                                                                                                                                                                                                                                                               13 GSGSGNEVIEGPONARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRF 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dependent B-cell mediated diseases and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                         9 GSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                 TMLLTPTCTLTTRCCCCRRCCGCNCCCRCCECCRRRG---NLKKRRQTKKLRQKVEMK 309
                                                                                                                                                                                             TCVATWKSLKARKSATVNLTVIRCPODTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAG
                                                                                                                                                                                                                                         AENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTL
                                                                                                                                                                                                                                                                 AENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.5%; Score 1514; DB 23; 88.2%; Pred. No. 6.5e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 377;
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ABG28169
ID ABG28169;
XX ABG28169;
AC ABG28169;
XY
DT 18-FEB-2002 (first entry)
XX
XX
ED NOVel human diagnostic protein #28160.
XX
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ED NOVEL human diagnostic protein #28160.
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ED NOVEL human diagnostic protein #28160.
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Human: chromosome mapping; gene mapping; gene therapy; forensic XX
Homo sapiens.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, ollipomers, and for chromosome polymerase chain reaction (PCR) primers, ollipomers, and for chromosome polymucleotides are also used in diagnostics as expressed sequence tags polynucleotides are also used in diagnostics as expressed sequence tags polymucleotides are also used in diagnostics as expressed sequence tags polymucleotides are also used in diagnostics as expressed sequence tags polymucleotides are also used in diagnostics as expressed sequence tags polymucleotides are also useful in gene therapy techniques for itesting expression antibodies against it, detecting or (II), (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and a quantitating a polypeptide in tissue, as molecular weight markers and a quantitating of sites expressing (II). (I) and (II) are useful for treating imaging of sites expressing (II). (I) and (II) are useful for treating imaging of sites expressing (II). (I) and (II) are useful for treating imaging of sites expressing (II). (II) are useful for treating imaging of sites expressing (II).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess responsible for genetic disorders or other traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 58528; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                              105 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYF 164
                                                                                                                                                                                                            165 VPEPSDLOSAVSILALTPOSNGTLTCVATWKSLKARKSATVNLTVIRCPODTGGGINIPG 224
                                                                                                     225 VLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCGCCCRC 284
                                                                                                                                                                    121 VPEPSDLQSAVSILALTPQSNCTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPG
                                                                                                                                                                                                                                                                                                                                                                                     45 MWALSDMYVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSR 104
                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOCGT
                                          285 KRG 287
                                                                                                                                                                                                                                                           61
241 KRG 243
                                                                                                                                                                                                                                                                                                                                             1 MWALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRGSLQNSR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-639362/73
                                                                                                                                                                                                                                                         LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYF 120
                                                                                    VLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCCCCCCCCCCCCRC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS92356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1326; DB 2;
pred. No. 3e-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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RESULT 6

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AAU75544
               cc dependent B-cell mediated diseases and autoimmune diseases. B7-L CC diseases involving chronic immune cell dysfunction or to treat cd diseases involving chronic immune cell dysfunction or to treat color diseases involving chronic immune cell dysfunction or to treat color diseases involving chronic immune cell dysfunction or to treat color diseases involving chronic immune cell dysfunction or to treat color diseases. Also cleared is cleared in flammatory diseases such as systemic lupus crythematosus, rheumatoid cell dysfunction or to provide inflammatory disease such as first and disease involving abnormal cell crytical solution or to prolong graft survival. B7-L molecules are also cransplantation or to prolong graft survival. B7-L molecules are also cransplantation, including arteriosclerosis and vascular restenosis. CC proliferation, including arteriosclerosis and vascular restenosis. CC proliferation including arteriosclerosis and vascular restenosis. CC antagonists of B7-L polypeptides are useful for alleviation of toxic cross syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU75544 standard; Protein; 370 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse B7-like protein, B7-L_m1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-2001; 2001WO-US20719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUN-2000; 2000US-214512P.
28-NOV-2000; 2000US-0729264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) a useful for treating B7-like polypeptide-related disease, disorders or useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometricsis) and miscarriage, preterm labour and delivery and endometricsis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a rol growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Fig 5; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABK13032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  welcher AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seminal vesicle hyperplasia in transgenic mice overexpressing B7-L seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (1) are useful for the treatment of polypeptide seminal vesicle cancer, lung, brain, breast, ovarian, cancer including seminal vesicle cancer, lung, brain, breast, ovarian, teaticular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be manipulated to regulate cytotoxic T-lymphocyte response pathway can be respons
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                                 28-JUN-2000; 2000US-214512P.
28-NOV-2000; 2000US-0729264,
     (AMGE-) AMGEN INC.
                                                                                                                                                                                                                          Rat; B7-like protein; B7-L; antiinfertility; gynaecological; antiinflammatory; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease;
                                                                                  28-JUN-2001; 2001WO-US20719
                                                                                                                       03-JAN-2002.
                                                                                                                                                                                       Ratus rattus.
                                                                                                                                                                                                                    endocrinopathy;
                                                                                                                                                                                                                                                                                                                                                            Rat B7-like protein, B7-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                            23-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU75547 standard; Protein; 631 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 KHQPGPATHPRVSFDIASPQKVRNVTLV 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 QRPPRPASHPQASFNLASPEKVSNTTVV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 NMRTNKADPETKLKSGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSSL--PYQELN 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 KEKTUK---ETETESGNENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSCGPPHQRAD 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 IILLAVAFSLLLILIIVLIIIFCCC-------CASRREKEESTYONEIRKSA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the amino acid sequence of mouse B7-L_m1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 KVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRKKRGFRIQFQ---KKSE 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 TPLGNGTLTCVAELKDLQASKSLTVNLTVVQPPPD-----SIGEEGPALPTWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TPQSNGTLTCVATWKSLKARKSATVNLTVIRCPODTGGGINIPGVLSSLPSLGFSLPTWG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 IPSVNLVVAENEDCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 PIITNNRPTYASYNSTDSFISELIIHDVQPSDSGSVQCSLQNSHGFGSAFLSVQVMGTLN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LVIF--LHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPME 60
                                                                                                                                                                                                      shock syndrome; allergy; nephropathy; skin disorder;
rinopathy; lymphoproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPŚNNLIVTEGEPCNVTCYAVGWTSLPDISWELEVPVSHSSYNSFLEPGNFWRVLSVLDL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVILAQLTASGSSYQIIEGPQNVTVLKDSEAHFNCTVTHGWKLLMWTLNQMVVLSLTTQG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 AA;
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Pred. No. 3.6e-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 104; Indels 37;
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PI Welcher AA, Sarmiento UM, Schultz HJ, Chute HT;

DR WPI; 2002-130881/17.

XX NPI; 2002-130881/17.

PT New BT-like polypeptides, polynucleotides and their modulators, useful proliferative disorders, e.g. cancer and arteriosclerosis.

PT for disgnosing, preventing and treating reproductive immune and proliferative disorders, e.g. cancer and arteriosclerosis.

The invention relates to an isolated BT-like (BT-L) polypeptide (I). CC Conditions including reproductive disorders (e.g. infertility as conditions including reproductive disorders (e.g. infertility conditions including reproductive disorders (e.g. infertility, conditions including senior) and conditions (e.g. infertility) and extracellular domains and other regulators of BT-L polypeptides are growth and maintenance of cancer regulators of BT-L polypeptide (e.g. cancer including senior) and cancers of haematopoletic system. BT-L polypeptide (e.g. cancer including senior) and cancers of haematopoletic system. BT-L polypeptide conditions and cancers and autonomous both of the bases. T-cell cancer including attribution graft versus bost disease. T-cell cancer including attribution graft symptoms associated with the purpose of the prolong graft symptoms associated with the care of the prolong graft symptomic and cancer and autonomous diseases. The molecules are also cancer included and passing and passing and passing and treatment of diseases and utcerative collitis, and claimater of diseases and utcerative and organical conditions, and for emphasions, and for emph
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                                                                                                                                                                                                                                                                                                                                         Matches 173;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                             112 -----TVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHS
252 EGGSYVVKHLTTVEVNGTLNIPSNNLIVTEGEPCNVTCYAVGWTSLPDISWELEVPVSHS
                                                            192 IHDVQPSDSGSVQCSLQNSHGFGSAFLSVQVYDIANNYSFSLLGLILSDRGTYTCVVQRY 251
                                                                                                                          132 LSCDYKFCSEEQSIHRIYWQKHDKMYLSVISGYPEVWPKYKNRTTYASYNSTDSFISELI 191
                                                                                                                                                                                        72 VGOVSKSVRNYTYLKDSEAHFNCTVTHGWKLLMWTLNOMYVLSLTTQGPIITNNRFEKAL 131
                                                                                                                                                                                                                                                     12 LVÍLAQLTASGSSYQTÍEGÞOMAYSCQPLQESPLLGFPRLRFTHLFVLLLVGLLQISSGI
                                                                                                                                                                                                                       22 -----NATVLKGSQARENCTYSQGWKLIMWALSDMYVLSVRPMEPIITNDRE----
                                                                                                                                                                                                                                                                                              3 LVIF--LHGSGSGNEVIEGPQ-----
                                                                                                                                                                                                                                                                                                                                                            Loca
                                                                                                     IHNVEPSDSGNIRCSLQNSRLHGSAYL-----
                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                      28.3%; Score 583.5; DB 23; Length 631; 26.9%; Pred. No. 1.2e-39;
                                                                                                                                                                                                                                                                                                                           43; Mismatches 111;
                                                                                                                                                           TSQRYDQGGNFTSEMI
                                                                                                                                                                                                                                                                                       Indels 317; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse B7-like protein, B7-L_m2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endocrinopathy; lymphoproliferative disorder.
The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polypuclectide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and
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                                                                                                                                                                                                                                                                      Welcher AA,
                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
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28-NOV-2000; 2000US-0729264
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                                                                                                           Claim 13; Fig 6; 135pp; English.
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AAU75546 RESULT 9

AAU75546 standard; Protein; 223

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They are also meeful as immunocomprosition according for home married and according to the second seco
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                                                                                                355 QRPPRPASHPQASFNLASPEKVSNTTVV 382
                                                                                                                                                                                                                      185 NMRTNKADDETKLKSGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSSL--PYQELN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 KYGLGLAGIMLLIPICILIIRCCCCRRRCCGCNCCCRCCFCCRKRGFRIOFO---KKSE 297
243 KHOPGPATHPRVSFDIASPQKVRNVTLV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 PIITNNRFTYASYNSTDSFISELIIHDVQPSDSGSVQCSLQNSHGFGSAFLSVQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELF 120
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                                                                                                                                                                                                                                                                                                                      KEKTNK---ETETESGNENSGYNSDEOKTTDTASLPPKSCESSDPEQRNSSCGPPHQRAD 354
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pred. No. 1.8
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Seminal vesicle hyperplasia in transgenic mice overexpressing B7-L CC seminal vesicle hyperplasia in transgenic mice overexpressing B7-L CC cancer including seminal vesicle cancer. Jung, brain, breast, ovarian, cc cancer including seminal vesicle cancer. Jung, brain, breast, ovarian, cc pathway can be manipulated to regulate cytotoxic T-lymphocyte response cc in allograft transplantation, graft versus host disease, T-cell cc molecules are useful for alleviating the symptoms associated with cd diseases involving chronic immune cell dysfunction or to treat caucoimmune diseases such as systemic lupus erythematosus, rheumatoid cc arthritis, multiple sclerosis, diabetes, immune thrombocytopenic confiammatory bowel disease (Crohn's disease and allecrative colitis), confiammatory bowel disease (Crohn's disease and allecrative colitis), can also useful as immunocunnessiva sonets for bone marrow.
treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (crave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the amino acid sequence of mouse B7-L_m3.
                                                                                                                                                                                                                          proliferation, including arterioscierosis and vaccination of toxic Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for any and humarsensitivity reactions,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
The present invention describes a material for extracorporeal circulation
                                    Claim 1; Page 31-32; 36pp; Japanese.
                                                                        Material for extracorporeal circulation, applicable in selective elimination of diabetic complication factors such as carbonyl stress products caused by abnormally promoted carbonyl stress from excretor.
                                                                   dysfunction in vascular lesions
                                                                                                                                              WPI; 2001-290314/30.
                                                                                                                                                                                                        (TORA ) TORAY IND INC
                                                                                                                                                                                                                                      08-SEP-1999;
                                                                                                                                                                                                                                                               08-SEP-2000; 2000WO-JP06172.
                                                                                                                                                                                                                                                                                               15-MAR-2001.
                                                                                                                                                                                                                                                                                                                           WO200118060-A1
                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                           Extracorporeal circulation; carbonyl stress product; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                       Extracorporeal circulation material receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                   diabetes; vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB81925 standard; protein; 404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB81925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 PGPATHPRVSFDIASPQKVRNVTLV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 TNKADPETKLKSGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSSL--PYQELNKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 TNK---ETETESGNENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQRP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 PRPASHPQASFNLASPEKVSNTTVV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 KVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCECCRRKRGFRIQFQKKSEKEK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 IPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 LVILAQLTASGSSYQIIEGPQNVTVLKDSEAHFNCTVTHGWKLLMWTLNQMVVLSLTTQG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LVIF--LHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPME 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIITNNRFTYASYNSTDSFISELIIHDVQPSDSGSVQCSLQNSHGFGSAFLSVQ-----
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                                                                                                                                                                          Kubota M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 AA;
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                                                                                                                                                                                                                                     99JP-0254463
                                                                                                                                                                                                                                                                                                                                                                              lesion; excretory dysfunction.
                                                                                                                                                                         Akiyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.0%; Score 494; DB 23; 31.9%; Pred. No. 7.7e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --RKSANM----
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                                                                                                                                                                         Usui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ESTY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 178;
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                                                                          from excretory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which is made from a water-insoluble carrier immobilized with a protein having the sequence shown here. The materials of the invention, including adsorbents, are for extracorporeal circulation, which are applicable in the selective elimination of diabetic complication factors from a body fluid, and are therefore useful in treating vascular lesions like arteriosclerosis due to carbonyl stress products caused by abnormally promoted carbonyl stress from excretory dysfunction.
                                                                                                                                                                                                                                                                                                  Human; Receptor for advanced glycosylation end product; RAGE; cardiant; tissue growth; neointimal formation; blood vessel; restenosis; diabetes; myocardial infarction; angioplasty; peripheral vascular surgery; angina; transgenic animal; acute thrombotic stroke; venous thrombosis.
                                                                                                                                                                                                                               WO200230889-A2
                                                                                                                                                                                                                                                                                                                                                                                             Human receptor for advanced glycosylation end product (RAGE) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE23219 standard; Protein; 404 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 IP----SVNLVVAENEP------CEVTCLPSHWTRLPDISWELGLLVSHSSY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 KEQTRRHPETGLFTLQSELM---VTPARGGDPRPTFSCSFSPGLPRHRALRTAPIQPRVW 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 EIVDSASELTA--GVPNKVGTCVSEGSYPAGTLSWHLDG-----KPLVPNEKGVSV 173
                                       Stern DM,
                                                                                                                13-OCT-2000; 2000US-0687528.
                                                                                                                                                    12-OCT-2001; 2001WO-US32036
                                                                                                                                                                                         18-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 CRCCFCCRRKRGFRIQFQKKSEKEKT--NKETETESGNENSGYNSDEQKTTDTASLPPKS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 PGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT-----PTCTLTIRCCCCRRRCCGCNCC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 -GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISIIE-PGEEG-----
                                                                           (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 CESSDPEQRNSSCGPP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 ---- QRYDQGGNFT--SEMIHNVEPSDSGNIR---- CSLQNSRLHGSAYLTVQVMGELF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVIEGPQNATVLKGSQARFNCTVSQG----WKLIMWALSDMVVLSVRPMEPIITNDRFTS- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIHWMKD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QSEEPEAGESSTGGP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%;
Similarity 22.6%;
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                                         Schmidt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----QRRGEERKAPENQEEEEERAELN---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PTAGSVGGSGLGTLALALGILGGLGTAALLIGVILWQRR----- 366
                                           Marso S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Mismatches 114; Indels 137; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 147.5; DB 2
Pred. No. 0.00076;
                                         Topol E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 404;
                                             Lincoff AM;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    advanced glycation/glycosylation end product (RAGE), so as to inhibit new tissue growth or neointimal formation in subject's blood vessels and preventing restenosis in the subject. The method is useful for inhibiting new tissue growth or neointimal formation in blood vessels in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD36952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 like non-human animal, a transgenic non-human animal or a human suffering from diabetes, acute thrombotic stroke, venous thrombosis, unstable angina, myocardial infarction, abrupt closure following anciopiasty or stent placement, or thrombosis as a result of peripheral vascular surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          blood vessel injury and preventing exaggerated restenosis in a diabetic subject. The method comprises administering an inhibitor of receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for inhibiting new tissue growth or neointimal formation in blood vessels in a subject that has experienced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The method is also useful for preventing restenosis and for determining whether a compound inhibits new tissue growth in a blood vessel in a subject. The present sequence is human receptor for advanced glycosylation end product (RAGE) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 16; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
Receptor for advanced glycation end product; RAGE; receptor: amyloid beta peptide; blood-brain barrier; neurovascular str
                                                              Human receptor for advanced glycosylation end product (RAGE).
                                                                                                                                                                                                  AAU77543 standard; Protein; 404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 EIVDSASELTA--GVPNKVGTCVSEGSYPAGTLSWHLDG-----KPLVPNEKGVSV 173
                                                                                                            05-JUN-2002
                                                                                                                                                        AAU77543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 KEQTRRHPETGLFTLQSELM----VTPARGGDPRPTFSCSFSPGLPRHRALRTAPIQPRVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 YFYPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINI 222
                                                                                                                                                                                                                                                                                                                 390
                                                                                                                                                                                                                                                                                                                                                        334 CESSDPEQRNSSCGPP 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 ----ORYDQGGNFT--SEMIIHNVEPSDSGNIR----CSLQNSRLHGSAYLTVQVMGELF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 EVIEGPQNATVLKGSQARFNCTVSQG---WKLIMMALSDMVVLSVRPMEPIITNDRFTS- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IP----SVNLVVAENEP-------CEVTCLPSHWTRLPDISWELGLLVSHSSY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS----PQIHWMKD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                           CRCCFCCRRKRGFRIQFQKKSEKEKT--NKETETESGNENSGYNSDEQKTTDTASLPPKS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISIIE-PGEEG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT-----PTCTLTIRCCCCRRRCCGCNCC 275
                                                                                                                                                                                                                                                                                                               -QSEEPEAGESSTGGP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
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                                                                                                               (first entry)
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Pred. No. 0.00076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and decreasing cerebral vasoconstriction in subject suffering from the composition of receptor for advanced glycation end product (RAGE) (I) inhibits transcytosis of amyloid beta peptides across blood-brain (CC transcytosis of amyloid beta peptides across blood-brain (CC transcytosis of amyloid beta peptides across blood-brain (CC transcytosis) are subject, decreasing cerebral vasoconstriction and increasing (CC subject, decreasing cerebral vasoconstriction and increasing (CC subject, decreasing cerebral vasoconstriction in a transgenic non-human (CC animal (preferably, transgenic mouse overexpressing mutant human amyloid beta precursor protein) or a human, suffering from chronic or acute (CC cerebral amyloid angiopathy, preferably, Alzheimer's disease, and for (CC amino acid sequence of human receptor for advanced glycation end (CC cembra disease, aging, Down's syndrome, head trauma or stroke. This is the conduct (page) and properly described in the invariant conduction and conduction and conduction of human receptor for advanced glycation end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
276 CRCCFCCRRKRGFRIQFQKKSEKEKT--NKETETESGNENSGYNSDEQKTTDTASLPPKS 333
                                                                                  223 PGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT-----PTCTLTIRCCCCCRRRCCGCNCC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product (RAGE) described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a method of ameliorating neurovascular stress,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ameliorating neurovascular stress and decreasing cerebral vasoconstriction in subject suffering from chronic/acute cerebral amyloid angiopathy, by administering inhibitor of receptor for ad
                                                                                                                                                                                                               231 EPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIHWNKD-----
                                                                                                                                                                                                                                                                                                  174 KEQTRRHPETGLFTLQSELM----VTPARGGDPRPTFSCSFSPGLPRHRALRTAPIQPRVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 16; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    125 EIVDSASELTA--GVPNKVGTCVSEGSYPAGTLSWHLDG------KPLVPNEKGVSV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABK10856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-2000; 2000US-0638648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001WO-US25416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerebral vasoconstriction suppressor; cerebral blood flow enhancer; cerebral amyloid angiopathy; transgenic animal; amyloid beta precursor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200214519-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease; Down's syndrome; head trauma; stroke; human.
                                                                                                                                                                                                                                                                                                                                          71 ---- ORYDOGGNET--SEMIIHNVEPSDSGNIR----CSLQNSRLHGSAYLTVQVMGELF 120
                                                                                                                                                                                                                                                                                                                                                                                                                            15 EVIEGPQNATVLKGSQARFNCTVSQG---WKLIMWALSDMVVLSVRPMEPIITNDRFTS- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                               -GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISIIE-PGEEG-----
                                                                                                                                                                     YFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINI 222
                                                                                                                                                                                                                                                       IP----SVNLVVAENEP-------CEVTCLPSHWTRLPDISWELGLLVSHSSY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-257610/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                              -PTAGSVGGSGLGTLALALGILGGLGTAALLIGVILWQRR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.28;
22.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yan SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 147.5; DB 2
Pred. No. 0.00076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zlokovic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23; Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        advanced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ъ
                                                                                                                                                                               Matches
                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                               useful for rapid, high-throughput identification of compounds that modulate RAGE. The compounds are useful for treating symptoms of diabetes and symptoms of diabete. Late complications, amyloidoses, Alzheimer's disease, cancer, inflammation, kidney failure, systemic lupus nephritis or inflammatory lupus nephritis, erectile dysfunction and
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                               The invention relates to detecting receptor for advanced glycated endproducts (RAGE) modulators comprises determining the amount of RAGE protein or its fragment bound to the pre-adsorbed ligand by measuring the amount of anti-RAGE antibody bound to the solid surface. The method is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a receptor for advanced glycated endproducts (RAGE) modulators, for treating e.g., cancer, diabetes or inflammation, comprises measuring the amount of bound anti-RAGE antibody -
     121 IP----SVNLVVAENEP-----
                                 174 KEQTRRHPETGLFTLQSELM----VTPARGGDPRPTFSCSFSPGLPRHRALRTAPIQPRVW
                                                                                                             125
                                                                                                                                                                                                                                                                          atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 2; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-114372/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000;
05-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; RAGE; receptor for advanced glycated endproduct; receptor; antidiabetic; neuroprotective; cytostatic; antiinflammatory; vaso nephrotropic; dermatological; antiarteriosclerotic; nootropic; disease; cancer; inflammatton; kidney failure; systemic lupus; nephritis; erectile dysfunction; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2001; 2001WO-US17447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TRAN-) TRANS TECH PHARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-2001.
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                                                                                                                                15 EVIEGPQNATVLKGSQARFNCTVSQG---WKLIMWALSDMVVLSVRPMEPIITNDRFTS- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human RAGE protein SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM48745 standard; protein; 404 AA.
                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 -QSEEPEAGESSTGGP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 CESSDPEQRNSSCGPP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367
                                                                ----QRYDQGGNFT--SEMIIHNVEPSDSGNIR----CSLQNSRLHGSAYLTVQVMGELF 120
                                                                                                    EIVDSASELTA--GVPNKVGTCVSEGSYPAGTLSWHLDG-----
                                                                                                                                                                            85;
                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                            404 AA;
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-207342P
2001US-0799152
                                                                                                                                                                                      7.2%;
22.6%;
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                                                                                                                                                                      40;
------CEVTCLPSHWTRLPDISWELGLLVSHSSY 162
                                                                                                                                                                                    Score 147.5; DB 2
Pred. No. 0.00076;
                                                                                                                                                                      Mismatches
                                                                                                                                                                                                  DB 23; Length 404;
                                                                                                                                                                      114;
                                                                                                                                                                 Indels 137; Gaps
                                                                                                   --KPLVPNEKGVSV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nootropic; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vasotropic;
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RESULT 14
ABB75751
ID ABB75
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Human; GP354; immunoglobulin; pancreas; central nervous system; diagnosis; gene therapy; pancreatitis; inflammation; tumour; cancer; autoimmune disease; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       senile dementia; migraine; epilepsy; neurasthenia; neuropathy; neural degeneration; antiinflammatory; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunoglobulin superfamily member GP354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB75751 standard; Protein; 592 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 YEVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                  anticonvulsant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 PGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT-----PTCTLTIRCCCCRRRCCGCNCC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 EPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIHWMKD------ 274
                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppressive; antiparkinsonian; neuroprotective; antimigraine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390 -QSEEPEAGESSTGGP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 CESSDPEORNSSCGPP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 CRCCFCCRRKRGFRIQFQKKSEKEKT--NKETETESGNENSGYNSDEQKTTDTASLPPKS 333
                                                                                                                              WO200198360-A2.
                                                                                                                                                               Domain
                                                                                                                                                                                      Domain
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                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                         Peptide
(LUKA/) LUKASHIN A V. (KILB/) KILBURN D R.
           (BIOJ ) BIOGEN INC.
(CARU/) CARULLI J P.
(LUKA/) LUKASHIN A V
                                                                               22-JUN-2001; 2001WO-US19904.
                                                          22-JUN-2000; 2000US-213611P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISIIE-PGEEG----- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------PTAGSVGGSGLGTLALALGILGGLGTAALLIGVILWQRR-----
                                                                                                                                                                                                                                                                                                      /note= "extracellular domain"
35..102
                                                                                                                                                                                                                                                                                                                             /label= Mature_protein 19..507
                                                                                                                                                                                                                                                                                                                                                   /label= Signal_peptide
19..592
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                      323..374
                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                          /note=
                                                                                                                                                    /note=
                                                                                                                                                                           'note=
                                                                                                                                                                                                   'note=
                                                                                                                                                                                                                                                                      note:
                                                                                                                                                                                                              ..485
                                                                                                                                                                                                                                                                                 . 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QRRGEERKAPENQEEEEERAELN-----------
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                                                                                                                                                       "intracellular domain"
                                                                                                                                                                                                                                                                                           "Ig domain"
                                                                                                                                                                             "transmembrane domain"
                                                                                                                                                                                                  "Ig domain"
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                                                                                                                                                                                                                                                                     "Ig domain"
                                                                                                                                                                                                                                               "Ig domain"
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    KW XXX DXXX
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                                                                                                                                                                                                                                                          ABB75753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid or Gp354 polypeptide are used in the treatment of pancreatic injury and abnormal or disease conditions that relate to the pancreas, such as acute or chronic pancreatitis, pancreatic influence, pancreatic endocrine and hormonal imbalance, pancreatic tumours and pancreatic endocrine and hormonal imbalance, pancreatic tumours and eassociated cancers, and autoimmune disorders which affect the associated cancers, and autoimmune disorders which affect the pancreas. They are also used in the treatment of an injury to the CNS, and abnormal or disease conditions that relate to the CNS, including Alzheimer's disease, Parkinson's disease, senile dementia, migraine, epilepsy, neuritis, neurasthenia, neuropathy, neural degeneration and neural tumours (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     indicate a role in cell-cell recognition, binding, signalling and adhesion events in the pancreas and CNS. The present invention provides GP354 polypeptides and gP354 polynucleotides, as well as vectors, host cells, antibodies and related diagnostic and therapeutic methods. Claimed compositions comprising a gP354 therapeutic methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid sequence encoding a member of immunoglobulin superfamily, designated GP354, useful for the treatment of Alzheimer's disease, Parkinson's disease, senile dementia, migraine and epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carulli JP, Lukashin AV, Kilburn DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at low levels in central nervous system (CNS) tissue. It share more than 30% amino acid identity with any previously described protein. The protein structure and tissue distribution of GP35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the protein sequence of human GP354, a novel member of the immunoglobulin superfamily. GP354 is a pancreas enriched integral membrane protein, which is also detected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABL53873, ABL53875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-329171/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUNC/) SUN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Fig 1; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Human; GP354; immunoglobulin; pancreas; central nervous system; diagnosis; gene therapy; pancreatitis; inflammation; tumour; cancer; autoimmune disease; Alzheimer's disease; Parkinson's disease; senile dementia; migraine; epilepsy; neurasthenia; neuropathy;
                                                                                                         Human pancreas GP354.
                                                                                                                                                                                                                                      ABB75753 standard; Protein; 594 AA
                                                                                                                                                      24-JUN-2002 (first entry)
                                                                                                                                                                                                ABB75753;
                                                                                                                                                                                                                                                                                                                                                177
                                                                                                                                                                                                                                                                                                                                                                                    168 --PSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDT 216
                                                                                                                                                                                                                                                                                                                                                                                                                            122 APQVLGG---PSVSLVA--GVPANLTCRSRGDARPTPELLWFRDGVLLDGTTFHQTLLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 -- QVMGELFIPSVNLVVAENEPCEVTCLPSHWTR-LPDISW-ELGLLVSHSSYY--FVPE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LFCFRGSAGPSPHFLQQPEDLVVLLGEEARLPCALGAYWGLVQWTKSGLALGGQR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LVIFLHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPI 62
                                                                                                                                                                                                                                                                                                                                           GTPGSVESTLTLTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---DLPGWSRYWISGNAANGQHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVLVPPE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITNDRFTSQRYDQGGNFTS---EMIIHNVEPSDSGNIRCSLQNSRLHG-SAYLTV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        592 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.7%;
23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 138; DB 23
Pred. No. 0.0075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sun C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
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The present sequence is the protein sequence of human panéreatic CC GP354, a novel member of the immunoglobulin superfamily. GP334 is CC a pancreas-enriched integral membrane protein, which is also CC detected at low levels in central nervous system (CNS) tissue. The CC protein structure and tissue distribution indicate a role for GP334 CC in the pancreas and CNS. The invention provides GP354 polypeptides CC and GP354 polypucleotides, as well as vectors, host cells, CC antibodies and related diagnostic and therapeutic methods. Claimed CC compositions comprising a gP354 nucleic acid or GP354 polypeptide CC are used in the treatment of pancreatic injury and abnormal or CC disease conditions that relate to the pancreas, such as acute or CC chronic pancreatitis, pancreatic inflammation, pancreatic encorine insufficiency, pancreatic endocrine and hormonal imbalance, CC which affect the pancreas. They are also used in the treatment of the CNS, including Alzheimer's disease conditions that relate CC confice the CNS and abnormal or disease conditions that relate CC confice the CNS and abnormal or disease conditions that relate CC confice the CNS and abnormal or disease conditions that relate CC confice the CNS and abnormal or disease conditions that relate CC confice the confic
                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         senile dementia, migraine, epilepsy, neuritis, neurasthenia, neuropathy, neural degeneration and neural tumours (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BIOJ ) BIOGEN INC.
(CARU/) CARULLI J P.
(LUKA/) LUKASHIN A V.
(KILB/) KILBURN D R.
114 --QVMGELFIPSVNLVVAENEPCEVTCLPSHWTR-LPDISW-ELGLLVSHSSYY--FVPE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid sequence encoding a member of immunoglobulin superfamily, designated GP354, useful for the treatment of Alzheimer's disease, Parkinson's disease, senile dementia, migraine and epilepsy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Fig 8; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-329171/36.
N-PSDB; ABL53877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carulli JP, Lukashin AV, Kilburn DR, Sun C;
                                                  65 ---DLPGWSRYWISGNAANGQHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVLVPPE 121
                                                                                                63 ITNDRFTSQRYDQGGNFTS---EMIIHNVEPSDSGNIRCSLQNSRLHG-SAYLTV----- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-2001; 2001WO-US19904.
                                                                                                                                                   10 LFCFRGRAGPSPHFLQQPEDLVVLLGEEARLPCALGAYWGLVQWTKSGLALGGQR----- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUNC/) SUN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-2000; 2000US-213611P
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immunosuppressive; antiparkinsonian; neuroprotective; antimigraine;
                                                                                                                                                                                                3 LVIFLHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                            594 AA;
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Signal_peptide
19..594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                            6.6%;
                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                      Score 136; DB 2
Pred. No. 0.011;
                                                                                                                                                                                                                                                           Mismatches 106;
                                                                                                                                                                                                                                                                                                            DB 23; Length 594;
                                                                                                                                                                                                                                                      Indels 30; Gaps
                                                                                                                                                                                                                                                      10;
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Ş В Q Ъ Q

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Search completed: April 28, 2003, 18:14:28 Job time: 43.0676 secs
                                                                       밁
                                                                                                    QΥ
                                                                                                                                     В
                                                         177 GTPGSVESTLTLTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVT 227
                                                                                       168 --PSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDT 216
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Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                         Result
                                                                                                                                                                                                                No.
                                                                                                                                                                                                                                                                         pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
136.5
135.5
134.5
133.5
132.5
129.5
129.7
127.1
125.5
125.5
                                                                                                                                                                          1692
566.5
                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          April 28, 2003, 16:24:32; Search time 37.1283 Seconds (without alignments) 2142.147 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVAGAMENRDPPGSGSGNEV......HPQASFNLASPEKVSNTTVV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-729-264-4
2088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671580 segs, 206047115 residues
                                                                                                                                                                                                                Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPTREMBL_21:*
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Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
 81.
6.27.
6.66.
6.11.
6.66.
6.00.
6.00.
                                                                                                                                                                                                                             Query
                                                                                                                                                                                                                                                                                                                                                                                                                           sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_archea:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_mhc:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                             sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                         sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                     sp_rvirus:*
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                                                                                                                                                                                                                                                                                                                                                                  sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                               sp_plant:*
                                                                                      1445
1427
871
881
 869
164
197
166
344
697
                                                                           Q61988
O15146
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                                                                                                                                                                                          Q9NSI5
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                                      Q95QY1
                                                              Q22048
                                                                                                  Q61987
                                                                                                                                      Q9D4K2
                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                   098892 mus musculu
090912 mus musculu
092626 homo sapien
09044k2 mus musculu
063155 rattus norv
091562 xenopus lae
061987 mus musculu
                                                                                                                                                                                            Q9nsi5 homo sapien
                                                                                                                                                                                                                     Description
                           Q95qy1 caenorhabdi
Q9df61 gallus gall
                                                                 015146 homo sapien
Q22048 caenorhabdi
                                                   017641
                                                                                           Q61988 mus musculu
   Q9dbp0 mus musculu
Q9z290 mus musculu
                                                       caenorhabdi
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Q9NSI5 RESULT 1

Q9NSI5

PRELIMINARY;

PRT;

315 AA

Q9NSI5;

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010400 IOIIO	_		26926	5.5	114.5	45
OTOA ARADO	062319		531	5.5	114.5	44
CC319	_		152	5.5	114.5	43
caen			808	υ. υ	115	42
5 mus	_	. 4	344	1 U	115	41
homo sal	000131		1047	10.	T15.5	40
Q8qhl3 gallus gal			1 2 2 2	n (
3 torped			946	л (0 0
1100			868	JI JI		ب د د
COLOCULAR SING COLOCALA			860	5.5	•	3 7
mus mu			677	5.5	115.5	36
מאוטוו	0		390	5.5	•	ω Մ
	_		975	5.6	116	34
097174 drosophila			896	5.6	116	ω
09w4t9 drosophila			900	٠	116	32
09n9v9 drosophila			0 0	١.	T10.0	٤
Q9wu51 mus muscuru			878	л	116 5	ى ر د
	0		364	л	1165) t
100	Q9R094		868	ر.	117	20
	062838		868	ம	118	28
a rat	DAPKM/		5636	ر ت	118.5	27
O O	0046600		- 344	5.7	119	26
\circ	1071		6632	5.7	119.5	25
001761 caenorhabdi	COLORD	٦L	T 2 9 0	ı ı	1.20	24
Q9w213 drosophila	nows13		1005	n (1 1 0 0	2.0
044924 drosophila	044924		1 205	л : 7	100) t
4	093242		344	5.7	120	၁ ၁
ral luc	CTSCIEC		315	5.7	120	21
gallus	05/396	L	313	5.7	120	20
gall	CALINO		455	5.8	120.5	19
homo	CAMPO	4	6620	5.8	122	18
096aa2 homo sapien	2000	- ())))	1 (T22.3	1
caenc	018238	л	198	n O	'n	,

ALIGNMENTS

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ACCOMPAND DE CONTROL D
                                                                                                                          RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.S.,
RA Toyoda A., Ishii K., Totoki Y., Choi D.K., Soeda E., Ohki M.,
RA Toyoda A., Ishii K., Totoki Y., Choi D.K., Soeda E., Ohki M.,
RA Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Raichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Rosenthal A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.L.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

REMBL; AL163280; CAB90447-1;
DR InterPro; IPR0030561; EGF-like.
DR InterPro; IPR003096; IGG-like.
DR InterPro; IPR003096; IGG-like.
DR Ffam; PF00047; 14; 2.

DR SMART; SM00409; IG; 2.

SMART; SM00409; IG; 2.

DR SMART; SM00409; IG; 2.

DR PROSITE; PS00022; EGF1; UNKNOWN_1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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           315
315 AA;
                34599 MW; B69DCB23570FA3D1 CRC64;
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ocal

Similarity

81.0%; 99.7%;

DB 4; Length 315;

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RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gassterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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       EMBL; AK008060; BAB25436.1; EMBL; BC004806; AAH04806.1;
                                                Strausberg R.,
Submitted (MAR
                                                                                    SEQUENCE FROM N.A.
                                                                                                                   Wature 409:685-690(2001).
                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (Trembirel, 1/, Last Luncourter, 2010003D20Rik protein (RIKEN CDNA 2010003D20 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9D8G2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNENSGYNSDEQKTT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEKTNKETETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNENSGYNSDEQKTT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEKTNKETETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENEPCEVTCLPSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRFT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVNGELFTPSVNLVVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314;
                                    (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1692; DB 4;
Pred. No. 3.6e-148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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             RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchononi L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
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DR
DR
SQ
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  Wynshaw-Boris A., Yoshida K., Hasegawa Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=TESTIS; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4931420D14RIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4931420D14Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9D9T2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9D9I2
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InterPro; IPR003006; Ig_MHC.
SMART; SMO0409; IG; 1,
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 270 AA; 29604 MW; A39C273DAA950DFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 ETKLKSGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSSL--PYQELNKHQPGPATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 PRVSFDIASPQKVRNVTLV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 POASENLASPEKVSNTTVV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 MLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRKRGFRIQFQ---KKSEKEKTNK--- 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 ENEPCEVTCLPSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 CVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 YASYNSTDSFISELIIHDVQPSDSGSVQCSLQNSHGFGSAFLSVQ------ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 SQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 SGSGNEVIEGPQNARVLKGSQARENCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRFT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 SGSSYQIIEGPQNVTVLKDSEAHFNCTVTHGWKLLMWTLNQMVVLSLTTQGPIITNNRFT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETETESGNENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASH 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLIIVLIIIFCCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.1%; Score 566.5; DB 1 34.6%; Pred. No. 3.3e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------DSIGEEGPALPTWAIILLAVAFS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---CASRREKEESTYQNEIRKSANMRTNKADP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 AA
Kawaji H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 135;
Kohtsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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SORRERA
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Q92626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:685-690(2001).
EMBL; AK006892; BAB24782.1;
MGD; MGI:1913992; 4931420D14Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q92626 PRELIMINARY; PKT; 1490 AA.
Q92626;
Q92626;
Q1-FEB-1997 (TrEMBLrel. 02, Created)
Q1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97191544; PubMed-9039502;
Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KIAAQ20T-KIAAQ280) deduced by analysis of cDNA clones from ceil line KG-1 and brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYELOBLAST KIAA0230 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 LTRSQLELIEPE--PTMALEPSEITVAFFSHKNANVSDP----EEVPECLDSDPFPNGDL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 NENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQASENL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 CTLTIRCCCCRRRCCGCNC-CCRCCCCCCRKKRGFR----IQFQKKSEKEKTNKETETESG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 AS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606
                                                                                                                                  Mitchell M.S., Kan-Mitchell J., Minev B., Edman C., Deans R.J.; "Identification of a novel melanoma gene (MG50) - likely the ger II-1 receptor antagonist - which encodes epitopes recognized by cytolytic T lymphocytes."; submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                       "Assignment of a human melanoma associated gene MG50 (D2S448) to chromosome 2p25.3 by fluorescence in situ hybridization.";
                                                                                                                                                                                                                                                                                                                 Weiler S.R., Taylor S.M., Deans R.J., Kan-Mitchell J., Mitchell M.S.,
                                                                                                                                                                                                                                                                                                                                 MEDLINE=95048383; PubMed=7959781;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 CSLSRSCCCCRCRCC-CHCRCCRC--CCSRSRRFRSRTTLKFFQITEKGEQSLQRRIRRQ 111
                                                                                                                                                                                                                                                                                                         Trent J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           Genomics 22:243-244(1994).
                                                                                                                                                                                                                  TISSUE=MELANOMA;
                InterPro;
                                InterPro;
                                                          InterPro;
                                                                            InterPro;
                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                       D86983; BAA13219
                                                                                                          AF200348;
                                                                                                                                                                                                                                                                                                                                                                                                   . 3:321-329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 AA; 18931 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
    IPR000372;
                                                               IPR003598;
                                                                            IPR002007; Anim_peroxidase
                 IPR000483;
                                  IPR001611;
                                                 IPR003006;
                                                                                              1CXP
                                                                                                          AAF06354.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 141; DB 11; 32.0%; Pred. No. 3.8e-05; ative 20; Mismatches 49
                                  Ig_MHC.
LRR.
      LRR_Nterm.
                 LRR_Cterm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1496 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 168;
                                                                                                                                                                      (MG50) - likely the gene for epitopes recognized by human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
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          OPD4K2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003591; LRR_typ.
InterPro; IPR001007; VWE_C.
Pfam; PP03098; An_peroxidase; 1.
Pfam; PF00047; 19; 4.
Pfam; PF00560; LRR; 5.
Pfam; PF001463; LRRCT; 1.
Pfam; PF001463; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00408; IGC2; 4.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRUT; 1.
SMART; SM00013; LRR_TYP; 4.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01208; VWFC; UNKNOWN_1.
Immunoglobulin domain.
NON_TER 1
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MEDLINE-21085660; PubWed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Chazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Saito T., Chazaki Y., Gojobori T., Batalov S., Casawat T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casawat T., Kadota K., Matsuda T., Gissi C., King B., Kochiwa H., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kughl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Staubli F., Suzuki R., Baldarelli R., Barsh G., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 PLPVDPRVNITPS------GG-----LYIQNVVQGDSGEYACSATNNIDSVHATAF 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 VAGEVKTQEVTLRYEGSPARPTEVIQPQNTEVLVGESVTLECSATGHPPPRISWTRGDRT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 IIVQALPQFTVTPQDRVVIEGQTVDFQCEAKGNPP-----PVIAWTKGGSQLSVDRRHLV 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 LTVQVMGELFTPSVNLVVAENE----PCEVTCLPSHWTWLPDISW-ELGLLVSHSSYYFV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9D4K2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9D4K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      809
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4931420D14RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4931420D14Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553 VEVGANVQLP----CSSQGEPEPAITWNKDGVQVTESGKFHISPEGFLTINDVGPADAG
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 RCCCCRRRCCG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 VLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNS--RLHGSÄY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GGGINIPGVLSSLPSLGFSLP--TWGKVGLGL--AGTMLLTPTCTLTI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSSGTLR--ISGVALHDQ--GQYECQAV--NIIGSQKVVAHLTVQPRVTPVFASIPSDTT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV-----IRCPQDT- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYECVARNTIG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167209 MW; E9B9A7069BF1ABFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 138; DB 4;
pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 1496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68;
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SMART; SM00060; FN3; 6.
                Pfam; PF00041; fn3; 6. Pfam; PF00047; 1g; 4. PRINTS; PR00014; FNTYPI
                                                              InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003961; FN_III.
InterPro; IPR003598; Ig_C2.
InterPro; IPR003600; Ig_Ilke.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                            EMBL; U68725; AAB41099.1; -.
EMBL; M32291; AAA41086.1; -.
HSSP; P56276; ITLK.
                                                                                                                                                                                                                                                                  MEDLINE=90100559; PubMed=2294591;
Fearon E.R., Cho K.R., Nigro J.M., Kern S.E., Simons J.W.,
Ruppert J.M., Hamilton S.R., Preisinger A.C., Thomas G., Kinzler K.W.,
                                                                                                                                                                                                                                                                                                                                                                              Keino-Masu K., Masu M., Hinck L., Leonardo E.D., Chan S.S.Y., Culotti J.G., Tessier-Lavigne M.; "Deleted in Colorectal Cancer (DCC) encodes a netrin receptor.";
                                                                                                                                                                                                                                  "Identification of a chromosome 18q gene that is altered in colorectal
                                                                                                                                                                                                                 Science 247:49-56(1990).
                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 387-420 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            Cell 87:175-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97015074; PubMed=8861902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colorectal tumor suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q63155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 PNGDLAS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
EMBL; AK016467; BAB30253.1; -
EMBL; MGI:1913992; 4931420D14R1K.
MGD; MGI:1913992; 4931420D14R1K.
MGD; MGI:1913992; 4931420D14R1K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 ASFNLAS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 QRRIRRQLTRSQLELIEPEPTMALEPSEITVAFFSHKNANVSDP----EEVPPCLDSDPF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 GYNSDEQKTTD-----TASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQ 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 CTLTIRGCCCRRRCCGCNC-CCRCCFCCRRKRGFRIQFQKKSEKEKTNKETETESGNENS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 CSLSRSCCCCRCRCC-CYCRCCRC--CCSRSRRFRSRTTLRVRDPKFFQ--ITEKGEQSL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.5%; Score 136.5;
31.5%; Pred. No. 0.00
ative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1445 AA.
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Thes 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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ACCOCK SQUARES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
Q91562
                                                                              Matches
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                                                                                                              Query Match
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                                                                                                                                                 PRINTS; PRO0014; FNTYPEIII
SMART; SM00060; FN3; 6
SMART; SM00408; IGC2; 3
SMART; SM00410; IG_11ke; 2
Immunoglobulin domain; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                        InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003961; FN_III.
InterPro; IPR003598; Ig_C2.
InterPro; IPR003600; Ig_Ilke.
InterPro; IPR003006; Ig_MHC.
217 PGSARVGNEAELRILSESGLHRQQVFLQRPSNVVAIEGQDAVLECAVS-GYPTPTIVWMQ 275
                                                                                                                                                                                                                                                                                                                                                    Dev. Biol. 166:654-665(1994).
EMBL; U10986; AAA70168.1; -.
                              12 PGSGS-GNEV------IEGPQNARVLKGSQARFNCTVSQGW--KLIMWAL 52
                                                                                                                                                                                                                                                                                                                                                                                                                          Pierceall W.E., Reale M.A., Candia A.F., Wright C.V., Cho K.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95113183; PubMed=7813784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                           "Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the nervous system of developing Xenopus embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91562;
Q91562;
                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor suppressor
                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378 QIVGGSNLR----ILGVVKSDEGFYQCVAENEAGNAQSSA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00408; IGc2; 3. SMART; SM00410; IG_like; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 FVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 ISASAELTVLVPPWFLNHPSNLYAYESMDIEFECAVSGKP-VPTVNWMKNGDVVIPSDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin domain; Repeat. SEQUENCE 1445 AA; 157940 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTWLPDISW-ELGLLVSHSSYY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 LRGEEVI------QLRSKKYSLLGG--SNLLISNVTDDDSGTYTCVVTYKNEN 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 RNPASTRTGNEAEVRILSDPGLHRQLYFLQRPSNVIAIEGKDAVLECCVS-GYPPPSFTW 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 ALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 RDPPGSGSGNEV-------IEGPQNARVLKGSQARFNCTVSQGW--KLIMW 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                 PF00041; fn3; 6. PF00047; ig; 4.
                                                                              65;
                                                                                                                                                                                                                                                                                                                                               P40189; 1BQU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 6.5%; Score 135; DB 11; Lengtn 1. Similarity 25.5%; Pred. No. 0.0023; Similarity 25.5%; Pred. No. 0.0023; Indels
                                                                                                                             1427 AA; 156533 MW; 61FEA12C8A674972 CRC64;
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                        6.4%; Score 134.5; DB 13; Leng...
25.4%; Pred. No. 0.0025;
73. Mismatches 93; Indels
                                                                                                                                                      Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    084F625954481988 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1427 AA
                                                                                             DB 13; Length 1427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 1445;
                                                             65; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                             15;
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53 SDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLH 110

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                                                                                                                                                                                                                      Priam: PF00069; pKinase; 1.

Prints; PR00109; TYRKINASE.

PRINTS; PR001091; Euk_Pkinase; 1.

ProDom: PD000001; Euk_Pkinase; 1.

SWART; SM00408; IGC2; 2.

R SWART; SM00410; IG_11ke; 1.

R SWART; SM00219; TYFKC; 1.

PROSITE; PS00038; FZ; 1.

PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS001108; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS001108; PROTEIN_KINASE_TYR; 1.
Matches
                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUSK On MOUSE).
Mus musculus (Mouse).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nsk2 protein precursor MUSK OR NSK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ganju P., Walls E., Brennan J., Reith A.D.; "Cloning and developmental expression of Nsk2, a novel receptor tyrosine kinase implicated in skeletal myogenesis,."; oncogene 11:281-290(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q61987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X86444; CAA60165.1;
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 YFQIVDGSNLR----ILGLVKSDEGYYQCIAENEAGNIQTYAQLIIPDPAVPSSSILPSA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 FSADLTVMVPPQFLNHPANLYAYESMDIEFECAVSGKPS-----PTVKWTKNGEVVIPSD 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 GSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTWLPDISW-ELGLLVSHSS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95349951; PubMed=7624144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-MYOBLAST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432 PRDV-----VPVLVSS 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01392; Fz; 1.
Pfam; PF00047; ig; 3.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                           PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS00108; PROTEIN_KINASE_ST; 1 PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; PS00228; TUBULIN_B_AUTOREG; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003600;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        œ
                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                           Signal; Transferase
                                                                                                                                                                         ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GD-----EPVPIRTR----KYSVLGG--SNLLISNVTDDDAGAYTCVATYKNENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQDTGGGINIPGVLSS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YYFVPEPSDLQSAVSILALTPQSNGTLTCVA-----TWKSLKARKSATVNLTVI-RC 216
                     ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:103581; Musk.
  73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000024; Fz_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001245; Tyr_pkinase.
                                                                                             1 21 F
871 AA; 97047 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
     Conservative
                                                                                                                                                                      Immunoglobulin domain; Serine/threonine-protein kinase
                        6.4%;
21.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta_tubulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig_MHC.
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. 01, Last sequ
. 20, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
     45;
                                                Score 133.5;
                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                Pred.
                                                                                                     F3C53DC6AFE702AB CRC64;
     Mismatches
                                o
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                                0.0016;
                                                     DB 11; Length 871;
          127;
          Indels
          93;
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             Gaps
                  17;
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QΥ

4 GAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRP 62

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QY
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Qy
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01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ganju P., Walls E., Brennan J., Reith A.D.; "Cloning and developmental expression of Nsk2, a novel receptor "Cloning and developmental expression of Nsk2, a novel receptor tyrosine kinase implicated in skeletal myogenesis,."; Oncogene 11:281-290(1995).

Oncogene 11:281-290(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q61988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUSK OR NSK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nsk2 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 EVLGRILRAPESHNVTFGSFVTLRCTEIGIP-----VPTISWIENGNAVSSGSIQESVKD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118
           PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO0101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_TY; 1.
PROSITE; PS00109; PROTEIN_KINASE_TY; 1.
PROSITE; PS00109; TUBULIN_B_AUTOREG; 1.
ATP-binding; Immunoglobulin domain; Serin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95349951; PubMed=7624144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 EALLCYHLFLECSPGVVPTPMPICREYCLAVKELFCAK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 RVIDSRLQLFITKP---GLYTCIATNKHGEKFSTÄKAAATVSIAEWSKSQKDSQGYCAQY 320
                                                                                    SMART; SM00408; IGC2; 2.
SMART; SM00410; IG_11Ke; 1.
SMART; SM00219; TYIKC; 1.
PROSITE; PS50038; FZ; 1.
PROSITE; PS00107; PROTEIN_K.
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X86445; CAA60166.1; -. HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-MYOBLAST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 MEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-----LTV 117
                                                                                                                                                                 Pfam; PF001392; Fz; 1.
pfam; PF00047; 19; 3.
pfam; PF00069; pkinase; 1.
pRINTS; PR00109; TYRKINASE.
proDom; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                        InterPro; IPR003600;
InterPro; IPR003006;
InterPro; IPR002290;
                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:103581; Musk.
                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                        InterPro; IPR000024; Fz_domain.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      و
Signal; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVMGELFIPSVNLVVAENEPCEVTC----LPSHWTWLPDISW-ELGLLVSHSSYYFVPEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDLQSAVSILALTPQSNGTLTCVAT----WKSLKARKSATVNLTVIR------CPQD 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -NALRENSRIAALE-----SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKLVKLEV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RCCCCRRRCCGCN-----CCCRCC-----FCCR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGEGVLMQGPGEKMLLVFLPTTSHRDPEDAQELLIHTAWNEL-----KAVSPLCRPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGINIPG-----VLSSLPSLGFSLP-----TWGKVGLGLAGTMLLTPTCTLTI 264
                                                                                                                                                                                                                                               IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
              Immunoglobulin domain; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                             Ig_MHC.
Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                        Beta_tubulin
                                                                                                                                                                                                                                                                                            Ig_like.
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01,
20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                881 AA
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3DDC20E179FA010C CRC64;

DB 4;

Mismatches

178; Indels 105; Gaps Length 869;

20;

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RESULT 10
015146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-96009854; PubMed=7546737;

Valenzuela D.M., Stitt T.N., DiStefano P.S., Rojas E., Mattsson K.,

Compton D.L., Nunez L., Park J.S., Stark J.L., Gles D.R., Thomas S.,

LeBeau M.M., Fernald A.A., Copeland N.G., Jenkins N.A., Burden S.J.,

Glass D.J., Yancopoulos G.D.;

"Receptor tyrosine kinase specific for the skeletal muscle lineage:

expression in embryonic muscle, at the neuromuscular junction, and
                                                                                                                                                                                                       Valenzuela D.M., Rojas E., Yancopoulos G.D., Submitted (MAY-1997) to the EMBL/GenBank/DDE EMBL; AF0006464; AAB63044.1; -.
                                                                                                                                                                                                                                                                                        after injury.";
Neuron 15:573-584(1995):
                                               ofam; PF00069; pkinase; 1.
                                                                                                   InterPro;
InterPro;
                                                                                                                              InterPro;
                                                                                                                                                                              InterPro;
                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O15146 PRELIMINARY; PRT; 869 . 015146; O1-JAN-1998 (TrEMBLrel. 05, Created) O1-JAN-1998 (TrEMBLrel. 05, Last sequence Muscle specific tyrosine kinase receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 EALLCYHLFLECSPGVVPTPMPICREYCLAVKELFCAK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 RVIDSRLQLFITKP---GLYTCIATNKHGEKFSTAKAAATVSIAEWSKSQKDSQGYCAQY 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 SDLQSAVSILALTPQSNGTLTCVAT----WKSLKARKSATVNLTVIR------CPQD 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 EVLGRILRAPESHNVTFGSFVTLRCTEIGIP-----VPTISWIENGNAVSSGSIQESVKD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 QVMGELFIPSVNLVVAENEPCEVTC----LPSHWTWLPDISW-ELGLLVSHSSYYFVPEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 GALQVKMKP-----KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD------ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 MEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY----LTV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GAMENRDPPGSGSGNEVIEGPQNARVLKGSQARENCTVSQGWK-LIMWALSDMVVLSVRP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                           PF01392; Fz; 1.
PF00047; 1g; 3.
                                                                                                                                                                                                P11362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCCCCRRCCGCN-----CCCRCC-----FCCR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGINIPG-----VLSSLPSLGFSLP------TWGKVGLGLAGTMLLTPTCTLTI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGEGVLMQGPGEKMLLVFLPTTSHRDPEDAQELLIHTAWNEL-----KAVSPLCRPAA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -NALRENSRIAALE------SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKLVKLEV 208
               PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73;
                                                                                      IPR003598; Ig_c2.
IPR003006; Ig_MHC.
IPR001245; Tyr_pkinase.
                                                                                                                                          IPR000719; Euk_pkinase. IPR000024; Fz_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                          IPR002453; Beta_tubulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        881 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                   TYRKINASE
                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98435 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 133.5; DB Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. ; EA0D0282E9B28ED7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           869 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                 DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
EMBL; Z66499; CAA91301.1;
             investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                    Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                 none;
                                                                             MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                   Sims M.A
                                                                                                                                                                                                                                                                                     01-NOV-1996 (TremBLrel.
01-NOV-1996 (TremBLrel.
01-MAR-2002 (TremBLrel.
                                      "Genome sequence of the nematode C.elegans: A platform for
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea
Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                               T01B7.8
                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                       T01B7.8 protein.
                                                                                                                                                                                                                                                                                                                                                        022048
                                                                                                                                                                                                                                                                                                                                                                                                                                    483 SSSFSVS 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 QASFNLA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430 SVPECSKLPSMHWDPTACARLP-----HLDYNKENLKTFPP--MTSSKPSVDIPNLPSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 SGNENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQRP----PRPASHP 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 LCNHIFQECSPGVVPTPIPICREYCLAVKELFCAKE----WLVMEEKTHRGLYRSEMHLL 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00408; IGc2; 3.
SMART; SM00219; TyrKc; 1.
PROSITE; PS50038; FZ; 1.
PROSITE; PS50010; PROTEIN_KINASE_ATP;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
PROSITE; PS00228; TUBULIN_B_AUTOREG; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 ----INIPGVLSSLPSLGFSL------PTWGKVGLGLAGTMLLTPTCTLTIRCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 RVIDSRLQLFITKP----GLYTCIATNKHGEKFSTAKAAATISIAEWSKPQKDNKGYCAQY 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 SDLQSAVSILALTPQSNGTLTCVAT----WKSLKARKSATVNLTVIRCPQDTGGG----- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 -SPLRENSRIAVLE------SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKVVKLEV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 GALQVKMKP-----KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD------ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 MEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GAMENRDPPGSGSGNEVIEGPONARVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCRRCCGCN------CCCCCCC-----FCCRRKRGFRIQFQKKSEKEKTNKETETE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGEVCNAVLAKDALVFLNTSYADPEEAQELLVHTAWNEL-----KVVSPVCRPAAEAL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELFIPSVNLVVAENEP------CEVTCLPSHWTWLPDISW-ELGLLVSHSSYYFVPEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVFARILRAPESHNVTFGSFVTLHCTATGIP-----VPTITWIENGNAVSSGSIQESVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                               Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97056 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3%; Score 132.5; DE 20.8%; Pred. No. 0.002;
                                                                                                                                                                                                                                                                                      01,
01,
20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55;
                                                                                                                                                                                                                                                                                   Last annotation update)
                                                                                                                                                                                                                                                                                                      Last sequence update)
                                                                                                                                                                                                                                                                                                                       Created)
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PRT;

164 AA.

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RESULT 12
Q17641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 LGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
PROSITE; PS00269; DEFENSIN; UNKNOWN_1.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01208; VMFC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 20.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q17641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q17641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
Anderson K., Chissoe S.;
"The sequence of C. eleg
                                                                                                                                                                         "Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                 PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
PROSITE; PS00269; DEFENSIN; UNKNOWN_1.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01208; VWFC; UNKNOWN_1.
                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                           Submitted (APR-1996) to the
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                       Hypothetical SEQUENCE 19
                                                                                                                                    InterPro;
                                                                                                                                                               EMBL; U55854; AAK68161.1;
                                                                                                                                                                                                       Waterston R.;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                         investigating biology.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 CRTCCCTRCCTCCR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 -- NCCC-RCCFCCR 287
                                                                                                          InterPro;
                                                                                                                       InterPro;
                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 PODTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCCRRRCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 KRQGGCGCGCGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAILLAIGTFIAV----SQVQSAV-----LPVSSTELATVGTDVSTASTAIDTLGNSSSRV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000561; EGF-li
IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001450; 4Fe4S_ferredoxin.
IPR001271; Defensin_mammal.
                                                                                                         IPR000561;
IPR001007;
                                                                                                                     IPR001450; 4Fe4S_ferredoxin.
IPR001271; Defensin_mammal.
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                           197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16499 MW;
                                                                                                                                                                                                                                                                        elegans cosmid C04G6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; Score 129.5; 32.1%; Pred. No. 0.
                           20596 MW; FB5F9457BFB9B8AD CRC64;
                                                                                                          VWF_C
6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 0.00043; 11; Mismatches 53
                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
 Score 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C002D48D36C9FCED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GCCGCGGGGG--CGCCCCRPRCCCCCRRCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
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Query Match

RESULT 14
Q9DF61
ID Q9DF6
AC Q9DF6
DT 01-MA
DT 01-MA
DT 01-DE

Q9DF61

PRELIMINARY;

344 ₽

Q9DF61; 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,

Last sequence update)
Last annotation update)

Created)

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                                                                                                                           Query Match
Best Local :
                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
01-mAR-2002 (TremBLrel.
Hypothetical 17.0 kDa pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q95QY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a plinvestigating biology. The C. elegans Sequencing Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BRISTOL N2;
Anderson K., Chissoe S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       None;
                                                                                                                                                                                                     Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                         PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
PROSITE; PS000269; DEFENSIN; UNKNOWN_1.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01208; VWFC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-2001) to the EMBL/GenBank/DDBJ EMBL; U55854; AAK68158.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147
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                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO01450; 4Fe4S_ferredoxin
InterPro; IPR001271; Defensin_mammal.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001007; VWF_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
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                                                 260 CTLTIRCCCCRRCCGC--NCCC-RCCFCCR 287
86 CCCRPRCCCCCRRCCTCCRTCCCTRCCTCCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of C.
                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                          166 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elegans cosmid C04G6."; ) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                             16971 MW; 9D9D130351BB50F1 CRC64;
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                                                                                                                                Score 125.5;
Pred. No. 0.0
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                                                                                                          Mismatches
                                                                                                                                   No. 0.001;
        116
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                                                                                                                                                            DB 5;
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OBCAM alpha 1 isoform.

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RESULT 15
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Best Local
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
                                                                                                                 STRAIN=C57BL/6J; TISSUE=LUNG; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                    01-JUN 2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Solute carrier family 34 (sodium phosphate), member 2.
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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SMART; SM00408; IGc2; 3.
SMART; SM00410; IG_like; 2.
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Lodge A.P., Howard M.R., McNamee C.J., Moss D.J.;
"Co-localisation, heterophilic interactions and regulated expression of IgLON family proteins in the chick nervous system.";
Brain Res. Mol. Brain Res. 82:84-94(2000).
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 ---WEKEDTRLA 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 AENEPCEVTCL----PSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQS 188
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IPR003600; Ig_like.
IPR003006; Ig_MHC.
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25.4%; Pred. No. 0.0029;
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                                                                                                                                                                                                                                                                                                                                InterPro; IPR003841; Na_Pi_cotrans.
Pfam; PF02690; Na_Pi_cotrans; 1.
TIGRRAMS; TIGR01013; 2a58; 1.
SEQUENCE 697 AA; 76244 MW; 2A7B9384857EF16F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1342284; Slc34a2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
EMBL; AK004832; BAB23600.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wynshaw-Boris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
672 SKEC--
                                 347 NSSCGPPHQRADQRPPRPASHPQASFNLASPEKVSNTTV 385
                                                                                       645 R----
                                                                                                                                                            593 LPLWMHSLKPWDNV-----ISLATTC-FORRCCCCCRVCCRVCCMVCGCKCCRCSKCC 644
                                                                                                                                                                                                     233 LPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCG-----CNC-CCRCCFCC 286
                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                    RRKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKTTDTASLPPKSCESSDPEQR 346
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
-----QDEGKGQVEVLSMKALSNTTV 696
                                                                                                                                                                                                                                                                      6.0%;
25.8%;
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                                                                              ----DQGEE-----EEEKEQD---IPVKASGAFDNAAM 671
                                                                                                                                                                                                                                                                            Score 125;
Pred. No. 0.
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Search completed: April 28, 2003, 21:07:38 Job time: 41.1283 secs

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OM protein - protein search, using sw model
                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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2088
1 MVAGAMENRDPPGSGSGNEV......HPQASFNLASPEKVSNTTVV 386
                                                                                                                                                                                                                      112892 segs, 41476328 residues
  SwissProt_40:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

30 31 33 33	. No	Result
102.5 102.5 102.5 102 100.5	Score 145.5 136 132 126 127 128 129 114.5 111.5 111.5 111.5 111.5 111.5 110.5 110.5 110.5 110.5 110.5 110.5 110.5 110.5 110.5	}
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SREC_HUMAN KLK8_RAT FAS2_DROME CONT_CHICK VGL1_CVPMI KMLS_CHICK DJC5_MOUSE SY62_DISOM LAMP_CHICK TY03_MOUSE TY03_RAT KMLS_RABIT
Q14162 homo sapien p36374 rattus norv p34082 drosophila p14781 gallus gall p33470 porcine tra p11799 gallus gall p54101 mus musculu p24506 discopyge o Q98919 gallus gall p55144 mus musculu p55146 rattus norv p29294 oryctolagus

ALIGNMENTS

RA R	RAN	OS OC	RESULT RAGE_H ID R ID Q AC Q DT 0 DT 0 DT 1 DE A GN A
SEQUENCE FROM N.A. (ISOFORM 2). SEQUENCE FROM N.A. (ISOFORM 2). Malherbe P., Richards J., Gaillard H., Thompson A., Diener C., Malherbe P., Richards J., Gaillard H., Thompson A., Diener C., Schuler A., Huber G., Schuler A., Huber G., "CDNA cloning of a novel secreted isoform of the human Receptor for advanced Glycation End products (RAGE) and characterization of cells advanced Glycation End products (RAGE) and characterization of cells co-expressing cell-surface scavenger receptors and Swedish mutant amyloid precursor protein."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. [6] SEQUENCE FROM N.A. (ISOFORM 1).	SEQUENCE FROM N.A. (ISOFORM 1). SEQUENCE FROM N.A. (ISOFORM 1). SUGAYA K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A., Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A., Inoko H., Ikemura T.; "Three genes in the human MHC class III region near the junction with the class II: gene for receptor of advanced glycosylation end products, PBX2 homeobox gene and a notch homolog, human counterpart of mouse mammary tumor gene int-3."; Genomics 23:408-419(1994). SEQUENCE FROM N.A. (ISOFORM 1). Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E., Banta A., Spies T., Hood L.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases. [4] SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100. Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y., Yamamoto H.; "Molecular heterogeneity of the receptor for advanced glycation endproducts."; SUDMitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; . Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606; [1] SEQUENCE FROM N.A. (ISOFORM 1). TISSUB-Lung; MEDLINE=92340547; PubMed=1378843; MEDLINE=92340547; PubMed=1378843; Neeper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C., Elliston K., Stern D., Shaw A.; Elliston K., Stern D., Shaw A.; Elliston K., Stern D., Shaw A.; Biol. Chem. 267:14998-15004(1992). J. Biol. Chem. 267:14998-15004(1992).	UMAN AGE_HUMAN 15109; Q1527: 1-NOV-1997 (1-NOV-1997 (1-NOV-1997 (2-JUN-2002 (45-JUN-2002 for Receptor for RAGE.

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SMART; SM00408; IGC2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M91211; AAA03574.1; -. EMBL; D28769; BAA05958.1; -. EMBL; U89336; AAB47491.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mmunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hudson B.I., Futers T.S.;
"Novel polymorphisms in the receptor for advanced glycation end-products (RAGE) gene.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted (isoform 2).
ALTERNATIVE PRODUCTS: 2 ISOFORMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARE PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB036432; BAA89369.1; -. AJ133822; CAB43108.1; -. BC020669; AAH20669.1; -. AF208289; AAG35728.1; -.
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137
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259
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363
404
106
215
308
99
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POTENTIAL.
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/FTId=VAR_011338.
M -> G (IN REF. 1).
                                                   GACRTESVGGT
Q -> R.
                                                                                                            ESSTGGP -> VSDLERGAGRTRRGGANCRLCGRIRAGNSS
                                                                                                                                                           GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRA
VSISIIEPGEEGPTAGSVGGSGLGTLALALGILGGLGTAAL
                                                                                                                                                                                                             MISSING (IN ISOFORM 2).
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N-LINKED (GLCNAC. . .)
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IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
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Cho K.R., Oliner J.D., Simons J.W., Hedrick L., Preisinger A.C., Hedge P., Silverman G.A., Voge
                                                                                                            Nigro J.M., Cho K.R., Fearon E.R., Kern
                                                                                                                     MEDLINE=91121517; PubMed=1991322;
                                MEDLINE-94245241;
                                             GENE STRUCTURE,
                                                                       Cell 64:607-613(1991).
                                                                                                  Oliner J.D., Kinzler K.W.,
                                                                                                                                                                   colorectal cancers.";
Science 247:49-56(1990).
                                                                                                                                                                                                                                  SEQUENCE OF 1-750 FROM N.A. MEDLINE-90100559; PubMed-2294591; Fearon E.R., Cho K.R., Nigro J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995
01-NOV-1995
15-JUN-2002
                                                                                     "Scrambled exons
                                                                                                                                                                                                                  Fearon E.R., Cho K.R., Nigro J.M., Kern S.E., Ruppert J.M., Hamilton S.R., Preisinger A.C.,
                                                                                                                                                                                           "Identification of a chromosome 18q
                                                                                                                                                                                                               Vogelstein B.;
                                                                                                                                                                                                                                                                                          Genes Dev. 8:1174-1183(1994).
                                                                                                                                                                                                                                                                                               "The DCC gene product in cellular differentiation and colorectal tumorigenesis.";
                                                                                                                                                                                                                                                                                                                                     Vogelstein B.;
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(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
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                               AND VARIANTS CARCINOMA HIS-1375.

1; PubMed=8188295;
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Thomas G., K
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           Fearon
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metastasis."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miyake S., Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y., "Point mutations and allelic deletion of tumor suppressor gene DCC in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT CARCINOMA THR-168, AND VARIANT GLY-201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 19:525-531(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer Res. 54:3007-3010(1994).
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PIR; A38442; A38442.
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                                                                                                                                                          Glycoprotein; Immunoglobulin domain; Transmembrane; Signal; Repeat; Anti-oncogene; Disease mutation; Polymorphism.

SIGNAL 1 25 POTENTIAL.
                                                                                                                                                                                                          SMART; SM00060; FN3; 6.
SMART; SM00410; IG_like; 2.
SMART; SM00408; IGC2; 3.
                                                                                                                                                                                                                                         PRINTS; PRO0014; FNTYPEIII. SMART; SM00060; FN3; 6.
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Pfam; PF00047; ig; 4.
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SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: FOUND IN AXONS OF THE CENTRAL AND PERIPHERAL NERVOUS SYSTEM AND IN DIFFERENTIATED CELL TYPES OF THE INTESTINE.

DISEASE: COLORECTAL TUMORS THAT LOST THEIR CAPACITY TO DISEASE: THO MUCUS PRODUCTING CELLS UNIFORMLY LACK DCC DIFFERENTIATE INTO MUCUS PRODUCTING CELLS UNIFORMLY LACK DCC EXPRESSION, INACTIVATION OF DCC DUE TO ALLELIC DELETION AND/OR POINT MUTATIONS MAY CAUSE BOTH LYMPHATIC AND HEMATGENOUS POINT MUTATIONS MAY CAUSE BOTH LYMPHATIC AND HEMATGENOUS POINT MUTATIONS OF DESOPHAGEAL SQUAMOUS CELL CARCINOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL; X76132; CAA53735.1; -.

LL; M32292; AAA5275.1; -.

LL; M32288; AAA52174.1; -.

LL; M32288; AAA52175.1; ALT_SEQ.

LL; M32290; AAA52176.1; -.

LL; M63696; AAA52177.1; -.

LL; M63702; AAA52178.1; -.

LL; M63702; AAA52178.1; -.

LL; M63702; AAA52179.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
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                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:2701; DCC.
                                                                                                                                                                                                                                                                                                       | IPR003961; FN_III.rep
| IPR003962; FNIII.rep
| IPR00306; Ig_HHC:
| IPR003598; Ig_c2:
| IPR003600; Ig_like.
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                  POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 4.

FIBRONECTIN TYPE-III 1.
                                                                                                                                            TUMOR SUPPRESSOR PROTEIN DCC.
                                                                                                                               EXTRACELLULAR (POTENTIAL)
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ID DCC_M
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GN DCC.
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01.NOV-1997 (Rel. 35, Created)

01.NOV-1997 (Rel. 35, Last seq

15-JUN-2002 (Rel. 41, Last ann
                                      Cooper H.M., Armes P., Britto J., Gad J., Wilks A.F.:
"Cloning of the mouse homologue of the deleted in colorectal cancer gene (mDCC) and its expression in the developing mouse embryo."; oncogene 11:2243-2254(1995).
                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS A: B
STRAIN-BALB/C; TISSUE-Brain;
MEDLINE=96112625; PubMed=8570174;
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCC_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 RNPASSRTGNEAEVRILSDPGLHRQLYFLQRPSNVVAIEGKDAVLECCVS-GYPPPSFTW 273
                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                        Tumor suppressor protein DCC precursor
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                                                                                                                                                                                                                         NCBI_TaxID=10090;
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25:1%;
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Last annotation update)
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FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 6
BY SIMILARITY.
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BY SIMILARITY.
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MISSING (IN REF. 3).
MISSING (IN REF. 3).
WW; 4A8612766ED0471F CRC64;
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P -> H (IN A COLORECTAL CARCINOMA).
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Pfam; PF00047; 19; 4.
PRINTS; PR00014; FNTYPE
SMART; SM00060; FN3; 6.
SMART; SM00410; IG_1ke
SMART; SM00408; IGC2; 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X85788; CAA59786.1; -. HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are produced by alternative initiation. A third isoform: C is Produced by alternative splicing.

TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN THE BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS. ISOFORM C IS EXPRESSED ONLY IN THE EMBRYO.

EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION AND REMAIN AT THIS LEVEL IN THE ADULT.

AND REMAIN AT THIS LEVEL IN THE ADULT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:94869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR003600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FNTYPEIII.
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BY SIMILARITAL

GLCNAC...) (POTENT

N-LINKED (GLCNAC...) (POTENT

N-LINKED (GLCNAC..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FnIII_repeat.
; Ig_MHC.
; Ig_c2.
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IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 3.
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FIBRONECTIN TYPE-III
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG-LIKE C2-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
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cloning, sequencing, expre
Genomics 29:562-570(1995).
                        "The human myosin light chain kinase
                                       Potier M.-C., Chelot E., Pekarsky Y., Turnell W.G.;
                                                                    TISSUE=Hippocampus;
MEDLINE=96121365; PubMed=8575746;
                                                                                                SEQUENCE OF 923-1914 FROM N.A.
                                                                                                                       Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                 REVISIONS
Birukov K.
                                                                                                                                                                                    Lazar V.L., Garcia J.G.N.;
"A single human myosin lig
Genomics 57:256-267(1999).
                                                                                                                                                                                                                           MEDLINE=99216419; PubMed=10198165;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 2; 3A;
                                                                                                                                                                                                                                            TISSUE=Umbilical vein;
                                                                                                                                                                                                                                                                                      Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                        Birukov
                                                                                                                                                                                                                                                                                                                                                                                           Garcia J.G.N., Lazar V.L., Gilbert-Mcclain L.I., Gallagher P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Myosin light chain kinase, smooth muscle and non-muscle isozymes
(EC 2.7.1.117) (MLCK) [Contains: Telokin (Kinase related protein)
                                                                                                                                                                                                                                                                                                                    REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Umbilical vein endothelial cells; MEDLINE=97304466; PubMed=9160829;
                                                                                                                                                                                                                                                                                                                                                               regulation.
                                                                                                                                                                                                                                                                                                                                                                Myosin light chain kinase in endothelium: molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                        Verin A.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYLK OR MLCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KMLS_HUMAN S
Q15746; Q14844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 QIVGGSNLR----ILGVVKSDEGFYQCVAENEAGNAQSSA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 FVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTWLPDISW-ELGLLVSHSSYY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 LRGEEVI------QLRSKKYSLLGG--SNLLISNVTDDDSGTYTCVVTYKNEN 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 RNPASIRTGNEAEVRILSDPGLHRQLYFLQRPSNVIAIEGKDAVLECCVS-GYPPPSFTW 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 ALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSR 108
                                                                                                                                                                                                                                                                                                                                           J. Respir. Cell Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOCS I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 RDPPGSGSGNEV------IEGPQNARVLKGSQARFNCTVSQGW--KLIMW 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISASAELTVLVPPWFLNHPSNLYAYESMDIEFECAVSGKP-VPTVNWMKNGDVVIPSDYF
                                                                                                                                              NS (ISOFORM 2).
K.G., Garcia I
                                                                                                                                                                                                                                                                                                       K.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1447 AA;
                                                                                                                                            Garcia J.G.N.;
                                                                                                                                                                                                                                                                                                  Garcia J.G.N.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q16794; 095796;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISOFORM 1)
             expression,
                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.5%;
                                                                                                                                                                                           _light chain kinase gene (MLCK; MYLK).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158298 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 132; DB 1; Length 1447; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                        16:489-494(1997).
      nase (MLCK) from hippocampus:
and localization to 3qcen-q21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      095797; 095798; 095799; Q9UBG5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0D1F1097C22D5B9F CRC64;
                                                                                                                                                                                                                                                      3B AND 4).
                                              Gardiner K., Rossier J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1914 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Watterson D.M., Schavocky J.P., Guo L., Weiss C., Chlenski A., Shrinsky V.P., Van Eldik L.J., Haiech J.; Shrinsky V.P., Van Eldik L.J., Haiech J.; and the kinase-related protein gene found at human chromosome 3q21 in a multi-gene cluster: organization, expression, alternative splicing and nolumorphic marker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watterson M.D.;

Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR SUBMITTED.

IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC.) AN EVERT THAT IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC.) AN EVERT THAT FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS. CENTRAL DETERMINANT IN THE DEVELOPMENT OF VASCULAR PERMEABILITY AND TISSUE DEDMA FORMATION. IN THE NERVOUS SYSTEM IT HAS BEEN SHOWN TO CONTROL THE GROWTH INTIATION OF ASTROCYTIC PROCESSES IN CULTURE AND TO PARTICIPATE IN TRANSMITTER RELEASE AT SYNAPSES FORMED BETWEEN CULTURED SYMPATHETIC GANGLION CELLS. CRITICAL PARTICIPANT IN SIGNALING SEQUENCES THAT RESULT IN FIBROBLAST APOPTOSIS.

-1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin light-chain]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         splicing and polymorphic marker.";
J. Cell. Biochem. 75:481-491(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20007838; PubMed=10536370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Lung, and Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1614-1914 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1456-1914 FROM N.A.
Genew; ....
Genew; ....
WTM; 600922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rissuE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               EMBL;
EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3B, 4 AND DEL-1790; ARE PRODUCED BY ALTERNATIVE SPLICING.
3B, 4 AND DEL-1790; ARE PRODUCED BY ALTERNATIVE SPLICING.
3B, 4 AND DEL-1790; ARE PRODUCED BY ALTERNATIVE SPLICING.

FISSUE SPECIFICITY: SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES ARE
EXPRESSED IN A WIDE VARIETY OF ADULT AND FETAL TISSUES AND IN
RETHER TISSUE- NOR DEVELOPMENT-SPECIFIC. NON-MUSCLE ISOFORM 2 IS
FIRE DOMINANT SPLICE VARIANT EXPRESSED IN VARIOUS TISSUES. TELOKIN
HAS BEEN FOUND IN A WIDE VARIETY OF ADULT AND FETAL TISSUES.
HAS BEEN FOUND IN A WIDE VARIETY OF ADULT AND FETAL TISSUES.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; A NON-MUSCLE FORM (THE LONGEST FORM), A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH NO CATALYTIC ACTIVITY); ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              light-chain] phosphate.
SUBUNIT: TELOKIN BINDS CALMODULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L; U48959; AAC18423.2; -.
L; AF069601; AAD15921.2; -.
L; AF069602; AAD15922.1; -.
L; AF069603; AAD15923.1; -.
L; AF069604; AAD15924.1; -.
L; X85337; CAAS9685.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; 1 (SHOWN HERE), 2, 3B, 4 AND DEL-1790; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                  AF096771; AAD51380.1; 
AF096766; AAD51380.1; 
AF096767; AAD51380.1; 
AF096768; AAD51380.1; 
AF096769; AAD51380.1; 
AF096770; AAD51380.1; 
AF096771; AAD54018.1; 
AF096771; AAD54018.1; 
AF096772; AAD51381.1; 
AF096776; AAD51381.1; 
                                                         HGNC:7590; MYLK.
   IPR000719; Euk_pkinase.
                                                                                          CAA62378.1;
1A06.
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InterPro;
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ACT_SITE
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00060; FN3; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00408; IGC2; 8.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0014; FNTYPEIII. Prodom; PD000001; Euk_pkina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 8.
Pfam; PF00069; pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003600;
InterPro; IPR002290;
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PS00108; PROTEIN_KINASE_ST; 1
PS50011; PROTEIN_KINASE_DOM; 1
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IPR003598;
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Serine/threonine-protein kinase; Calmodulin-binding; Phosphorylation; Immunoglobulin domain; Repeat;
                                                                                                                1162
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ig_like.
ser_thr_pkinase.
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FnIII_repeat.
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MYOSIN LIGHT CHAIN KINASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              I-5 (INCOMPLETE).
6 x 12 AA APPROXIMATE TANDEM REPEATS.
II-1 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE
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     V T - > G
C C C C
                                                                                                                                                              MISSING (IN ISOFORM 3A AND ISOFORM 3B)
MISSING (IN ISOFORM DEL-1790).

V -> M (IN REF. 5).
S -> P (IN REF. 3; AAD15922).
P -> A (IN REF. 5).
                                                                                                                                                                                                                                                                                ISOFORM 3B AND ISOFORM 4).
GKFGQVFRLVEKKTRKVWAGKFFKAYSAKEKENIRQEISIM
                                                                                                                                                                                                                                                                                                                             VSGIPKPEVAMFLEGTPVRRQEGSIEVYEDAGSHYLCLLKA
RTRDSGTYSCTASNAQGQVSCSWTLQVER -> G (IN
ISOFORM 2 AND ISOFORM 3B).
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                                                                                                                                  KPM ->
P -> L
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                                                                    AAD15924).
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                                                                                                                                                                                                                                                   (IN ISOFORM 4)
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                                                                                  (IN REF. ) (IN REF. ) (IN REF. )
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AAD15922/AAD15923/
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Wilson D.J.A., Kim D.-S., Clarke G.A., Marshall-Clarke S., Moss D.J. A family of glycoproteins (GP55), which inhibit neurite outgrowth, are members of the Ig superfamily and are related to OBCAM, neurotrimin, LAMP and CEPU-l.";
J. Cell Sci. 109:3129-3138(1996).
                                                                                                                                                                                                                                                                                                                                                            G55A_CHICK
                                                                        MEDLINE=97157768; PubMed=9004047;
                                                                                         TISSUE-Brain
                                                                                             SEQUENCE OF 64-337 FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                         Lodge A.P., Kim D.-S., Howard M.R., McNamee C.J., Smith N., "Cloning of CEPU-s, a secreted isoform of CEPU-1, and OBCAM chick: structural diversity of IgLON family proteins."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                   TISSUE-Brain,
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurite inhibitor GP55-A precursor (OBCAM protein gamma isoform).
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                   Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                    Q98892;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 LLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSA-----TVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEOKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQR----PPRPASHPQASFNLASPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSASAVETRPSIWGECPPKFATKLGRVVVKEGQMGRFSCKITGRPQ-----PQVTWLKGN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PI-----PSV-----NLVVAENE----PCEVTCLPSHWTWLPDISWELG- 158
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I -> T (IN REF. 5)
A -> P (IN REF. 5)
G -> R (IN REF. 5)
GY -> D (IN REF. 3)
AAD15924).
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                                                                                                                                                                                                                                                                                                                                                          337 AA.
                                                       Marshall-Clarke S., Moss D.J.;
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0.047;
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. 5).
. EF. 3; AAD15922/AAD15923/
                                                                                                                                                                                                                                            Phasianidae; Phasianinae;
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                                                                                                                                                               Moss D.J.;
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       CEPU_CHICK STAN
Q90773;
Q1-NOV-1997 (Rel. 3
Q1-NOV-1997 (Rel. 3
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                     240 LPTWGKVGLGLA 251
                                                                                                                                                                                                                               141 NEGSSVTLMCLAFGRPE-----PTVTWR----HLSGKGQGFVSEDEYLE----ITGITREQ 188
                                                                                                                                                                                                                                                           133 AENEPCEVTCL----PSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQS 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00410; IG_like; 1.
SMART; SM00408; IGc2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y08170; CAB41420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                  92
                                                                                                                                                                                                                                                                                                                 79 QGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRLHGSAYLTVQVMGELFIPSVNLVV 132
                                                                                                                                                                                                                                                                                                                                              37 NYTYRQGESATLRCTYDDRYRRYAW-LNRSTILYAGNDKWSIDNRYVILSN---TKTQY-
                                                                                                                                                                                                                                                                                                                                                                         26 NARVLKGSOARFNCTVSQGWKLIMWALSDMVVL-----SVRPMEPIITNDRFTSQRYD 78
                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               send an email to license@isb-sib.ch)
                                                                                                                                                                                                    NGTLTCVATWKSLKARKSATVNLTV----IRCPQDTGGGINIPGVL----SSLPSLGFS
                                                                                                                          ---WFKEDTRLA 256
                                                                                                                                                                         SGEYECSAV-NDVAVPDVRKVKVTVNYPPYISNAKNTGASVGQKGILQCEASAVPVAEFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELULIAR LOCATION: Attached to the membrane by a GPI-anchor. TISSUE SPECIFICITY: RESTRICTED TO THE NERVOUS SYSTEM.
DEVELOPMENTAL STAGE: INCREASES DURING DEVELOPMENT FROM VERY LOW LEVELS AT EMBRYONIC DAY 10 AND IS MOST ABUNDANT AFTER HATCHING.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
                                                                                                                                                                                                                                                                                       -----SIKIHNVDVYDEGPYTCSVQTDNHPKTSRVH----LIVQVPPQIVNISSDITV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: INHIBITS NEURITE OUTGROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003598; Ig_c2.
IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
317
337
115
201
295
108
194
288
133
277
285
                                                                                                                                                                                                                                                                                                                                                                                                                          6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36887 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell adhesion; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEURITE INHIBITOR GP55-A (
REMOVED IN MATURE FORM (PC
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 125; DB 1;
Pred. No. 0.0066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . . ) (POTENTIAL)
                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAE717551856651E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                 353
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                          97;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                 91
                                                                                                                                                                                                                                                                                                                                                                                                      14;
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15-JUN-2002

(Rel. (Rel.

35, 41,

Last annotation Last sequence update)

update)

35, Created)

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Ş
                                                                      Query Match
                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEPU-1 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Neurosci. 16:1770-1779(1996).

J. Neurosci. 16:1770-1779(1996).

-i- FUNCTION: IT MAY BE A CELLULAR ADDRESS MOLECULE SPECIFIC PURKINJE CELLS. IT MAY REPRESENT A RECEPTOR OR A SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developing cerebellar Purkinje cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spaltmann F., Bruemmendorf T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96370549; PubMed=8774445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "CEPU-1,
                                                                                                                                                                                                                                                                                                                                                                                    pfam; PF00047; 19; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00408; IGc2; 2.
Immunoglobulin domain; Cell adhesion; Glycoprotein; GPT-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 272497; CAA96578.1; -.
                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                          Repeat; Signal;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                          CARBOHYD
                                                                                                    SEQUENCE
                                                                                                                VARSPLIC
                                                                                                                                                CARBOHYD
                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. ALTERNATIVE PRODUCTS: 2 ISOFORMS; A MAJOR FORM AND A MINOR FORM (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: FOUND ON THE DENDRITES, SOMATA AND AXONS OF
         26 NARVLKGSQARFNCTVSQ-----GW---KLIMWALSDMVVLSVRPMEPIITNDRFTSQRY 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: EXPRESSED BY DEVELOPING CEREBELLAR PURKINJE CELLS. EXPRESSION COINCIDES WITH THE GROWTH OF THE DENDRITIC TREE AFTER PURKINJE CELLS HAVE FINISHED THEIR MIGRATION FROM THE VENTRICULAR ZONE (FROM E15 UNTIL E21). EXPRESSED IN THE ADULT. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
                                                         госат
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPING PURKINJE CELLS. UNDETECTABLE ON OTHER NEURONS LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOLGI OR GRANULE CELLS.
                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a novel immunoglobulin superfamily molecule, is expressed
                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003006;
                                         Conservative
                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                         Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
<u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig_MHC.
                                                          25.3%;
                                                                                                       38736 MW;
                                              36;
                                                                                                                                                                                                                                                                                                                                                                              splicing
                                                                                                                    N-LINKED (GLCNAC. . .) (POT
GPI-ANCHOR (POTENTIAL).
MISSING (IN MAJOR ISOFORM).
                                                                                                                                                                                                                                                                                    REMOVED IN MATURE FORM
IG-LIKE C2-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                               N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                              CEPU-1 PROTEIN.
                                                            Pred. No. 0.012;
                                                                            Score 122;
                                                                                                                                                                                                                                                                                                                                                                 POTENT LAL.
                                                                                                                                                                                                                                           POTENTIAL
                                              Mismatches
                                                                                                         2550C48591EBBBA6 CRC64;
   <del>::</del>
::
                                                                                                                                                                  (GLCNAC . . .)
                                                                            DB 1;
                                                 91;
    -
                                                                            Length 353;
                                                 Indels
                                                                                                                                                     .) (POTENTIAL)
                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DENDRITIC TREE,
                                                  56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF A
                                                  Gaps
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밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Neurotrimin precursor (GP65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning of neurotrimin defines a new subfamily of differentially expressed neural cell adhesion molecules.";

J. Neurosci. 15:2141-2156(1995).

I. PUNCTION: NEURAL CELL ADHESION MOLECULE.

I. SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

I. TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM.

I. DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN SEVERAL

III DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN SEVERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 INEGGNVSLTCIA---TGRPDPTITWR---HISPKAVGFISEDEYLE----ITGITREQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley;
MEDLINE=95198094; PubMed=7891157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTRI_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 GTLTCVATWKSLKARKSATVNLTV-----IRCPQDTGGGINIPGVL----SSLPSLGFSL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Struyk A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Eustachio P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 PTWGK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 --WYK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 NVTVRQGESATLRCSVDNRVTRVAWLNRSSILYAGNDKWCLDPRVVLLANTKTQYSIQ--
                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
                                                                                                                                                      Interpro; IPR003006; Ig_MHC.
Interpro; IPR003598; Ig_c2.
Interpro; IPR003600; Ig_like
                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                         EMBL; U16845; AAA67445.1;
                                 CHAIN
                                                                                                      SMART;
                                                                                                                                         Pfam; PF00047; ig;
                                                     SIGNAL
                                                                  Repeat; Signal
                                                                                  [mmunoglobulin domain; Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAENEPCEVTCLPSHWTWLPD--ISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----IHDVDVYDEGPYTCSVQTDNHPKTSRVH----LIVQVSPKITETSSDIS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRLHGSAYLTVQVMGELFIPSVNLV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEYECSAS-NDVAAPVVQRVKVTVNYPPYISDAKSTGVPVGQKGILMCEASAVPSADFQ-
                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPING PROJECTION SYSTEMS: IN NEURONS OF THE THALAMUS, SUBPLATE, AND LOWER CORTICAL LAMINAE IN THE FOREBRAIN AND IN TRONTINE NUCLEUS, CEREBELLAR GRANULE CELLS, AND PURKINJE CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                     THE HINDBRAIN
                                                                                                    SM00410; iG_like; 1.
SM00408; iGc2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND SEQUENCE OF 217-229
   31
321
344
122
                                                                                                                                                          Ig_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
     REMOVED IN MATURE FORM IG-LIKE C2-TYPE DOMAIN
                                      NEUROTRIMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 AA
                                                                                                                                                                                                                                                                                                                     There are no restrictions on
                           (POTENTIAL)
                                                                                                 GPI-anchor;
                                                                                                                                                                                                                                                                                          and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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DOMAIN

CARBOHYD CARBOHYD

150 236 57 157 243 44 70 152 216 2216 2284 292 305

CARBOHYD

DISULFID DISULFID

DOMAIN DISULFID

POTENTIAL. IG-LIKE C2-TYPE IG-LIKE C2-TYPE

DOMAIN

ωΝ

DOMAIN

CARBOHYD CARBOHYD

152 216 284 292

CARBOHYD

Matches Query Match

59;

a collaboration

Local

Similarity

SEQUENCE CARBOHYD

A

LIPID

```
TISSUE-Fibroblast;

MEDLINE-97037064; PubMed-8882711;

Park S.-K., Lee H.-S., Lee S.-T.;

"Characterization of the human full-length PTK7 cDNA encoding characterization control characterization characteriz
                                                                                                              receptor protein tyrosine kinase-like
chick KLG.";
                                                                                                                                                                                                                                                                                                                                                             TISSUE=Colon carcinoma, and Placenta;
MEDLINE=96074849; PubMed=7478540;
MOSSIE K., Jallal B., Alves F., Sures I., Plowman G.D., Ullrich A.;
TColon carcinoma kinase-4 defines a new subclass of the receptor
tyrosine kinase family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTK7_HUMAN STANDARD; PRT; 1070 AA. Q13308; Q13417; 1070 AA. 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tyrosine-protein kinase-like 7 precursor (Cole
                                                                                                                                                                                                                                                                                                                                                   Oncogene 11:2179-2184(1995).
                                                                              Biochem. 119:235-239(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 NARVLKGSQARFNCTVSQGWKLIMWALSDMVVLS-----VRPMEPIITNDRFTSQRYDQ 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEYECSAS-NDVAAPVVRRVNVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTLTCVATWKSLKARKSATVNLTVIRCP----QDTGGGINIPGVL----SSLPSLGFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGNNISLTCIATGRPE-----PTVTWR----HISPKAVGFVSEDEYLE----IQGITREQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENEPCEVTCL----PSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SIEIQNVDVYDEGPYTCSVQTDNHPKTSRVH----LIVQVSPKIVEISSDISIN 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRLHGSAYLTVQVMGELFIPSVNLVVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSN---TQTQY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.

N-LINKED (GLCNAC...) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 121; DB 1
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
N-LINKED
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
GPI-ANCHOR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor (Colon carcinoma kinase-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches .
                                                                                                                          molecule closely related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00219; RECEPTOR_TYR_KIN_II; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00410; IG_like; 2.
SMART; SM00408; IGc2; 5.
SMART; SM00219; TYPKC; 1.
                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00109; TYRKINASE. ProDom; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig;
Pfam; PF00069; pkir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002011; RTKinaseII.
InterPro; IPR001245; Tyr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U33635; AAA87565.1; -
EMBL; U40271; AAC50484.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND REVISION TO 834.

Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: MAY FUNCTION AS A CELL ADHESTON MOLECULE. LACKS PROBABLY

THE CATALYTIC ACTIVITY OF TYROSINE KINASE. MAY BE CONNECTED TO THE

PATHOPHYSIOLOGY. OF COLON CARCINOMAS AND/OR MAY REPRESENT A TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÷÷
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SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER, PANCREAS, KIDNEY, PLACENTA AND MELANOCYTES. WEAKLY EXPRESSED IN THYROID GLAND, OVARY, BRAIN, HEART AND SKELETAL MUSCLE ALSO EXPRESSED EXTHROLEUKENIA CELLS. BUT NOT EXPRESSED IN COLON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERYTHROLEUKEMIA CELLS. BUT NOT EXPRESSED IN COLON.
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601890;
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AF447167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF447171;
AF447173;
AF447174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF447176; AAL39062.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF447170;
AF447171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGNC:9618; PTK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000719; Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pkinase; 1
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Ig_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Glycoprotein; Cell adhesion;
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 6.
IG-LIKE C2-TYPE DOMAIN 7.
PROTEIN KINASE; INACTIVE.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                   TYROSINE-PROTEIN KINASE-LIKE
                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
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255 --WFK 257

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SEQUENCE FROM N.A.

PTK7 OR CCK4.

SEQUENCE FROM N.A.

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CD22_MOUSE
ID CD22_M
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DT 01-FEB
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OC Mammal
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RP SEQUEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                   CD22_MOUSE STANDARD; PRT; 862 AA.
p35329;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
B-cell receptor CD22 precursor (Leu-14) (B-lymphocyte cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
              STRAIN-DBA/ZJ, and BALB/C; TISSUE-Liver;

MEDLINE=93315834; PubMed=8100843;

Law C.-L., Torres R.M., Sundberg H.A., Parkhouse R.M.,

Law C.-L., Copeland N.G., Jenkins N.A., Clark E.A.;

Brannan C.I., Copeland N.G., Jenkins N.A., Clark E.A.;

"Organization of the murine Cd22 locus. Mapping to chromosome 7 and characterization of two alleles.";

J. Immunol. 151:175-187(1993).

J. THE LOCALIZATION OF B-CELL B-CELL INTERACTIONS. MAY BE INVOLVED IN GLYCOPROTEINS; ONE OF WHICH IS CD45.

GLYCOPROTEINS; ONE OF WHICH IS CD45.
                                                                                                                                                                                                                                                                                                                      molecule) (BL-CAM).
                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                   CD22 OR LYB-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 TLTCVATWKSLKARKSATVNLTV-----IRCPQDTGGGINIPGVLSSL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 ----NGSLLLTQVRPRNAGIYRCIGQGQRGPPIILEATLHLAEIEDMPLFEPRVFTAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 VIEGPQNARVLKGSQARFNCTVS-QGWKLIMWALSDMVVLSVRPMEPIITNDRFTSQRYD 78
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                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CD22-ALPHA AND CD22-BETA (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- TISSUE SPECIFICITY: B-LYMPHOCYTES.
-:- SIMILARITY: BELLONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-:- SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-:- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
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SMART; SM00408; IGC2; 4.
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IPR003598; Ig_c2.
IPR003600; Ig_like.
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S -> R (IN BALB/C).

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Genomics 41:414-421(1997).
                                                                                            Vielmetter J., Chen x.-N., Miskevich F., Lane R.P., Yamakawa Korenberg J.R., Dreyer W.J.,
                                                                                                                                                                                                                                                                                                                      "Identification and characterization of neogenin, a DCC-related
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97236653; PubMed=9121761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                               Molecular characterization of human neogenin, a DCC-related protein.
                                                                                                                                                            MEDLINE-97312699; PubMed-9169140;
                                                                                                                                                                                            TISSUE=Fetal brain;
                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND
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NEO1 OR NGN.
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                                              the mapping of its gene (NEO1) to chromosomal
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M -> T (IN BALB/C).
S -> T (IN BALB/C).
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Pred. No. 0.15;
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SALA BARANA BARA
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SMART; SM00410; IG_11ke; 1.
SMART; SM00408; IGC2; 3.
Transmembrane; Immunoglobulin domain; Glycoprotein; Signal; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U61262; AAB17263.1; -. EMBL; U72391; AAC51287.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION MOLECULE IN A BROAD SPECTRUM OF EMBRYONIC AND ADULT TISSUES.
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003961; FN_III.
InterPro; IPR003962; FnIII_repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS-:- SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
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BY SIMILARITY
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IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
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OPCM_HUMAN
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16-OCT-2001 (Rel. 40, Last annotation update)
Opioid binding protein/cell adhesion molecule precursor (OBCAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q14982;
01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPCML OR OBCAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPCM_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding a human opioid-binding cell adhesion molecule (OBCAM). "; Gene 155:213-217(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 QAGAQL-IILEHAPATTGPLPSAPRDVVASLVSTRFIKLTW 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 KQPSPLVRVIGQDVVLPCVASGLPTPTIKWMKNEEALDTESSERLVLLAGGS-----LEIS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 DRVIKLPSGMLVISNATEGDGGLYRCVVESGGPP---KYSDEVELKVLPDPEVISDLVFL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shark K.B., Lee N.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95237612; PubMed-7721093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Occipital cortex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Opioid-binding cell adhesion molecule) (OPCML)
                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: BINDS OPICIDS IN THE PRESENCE OF ACIDIC LIPIDS; PROBABLY INVOLVED IN CELL CONTACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *Cloning, sequencing and localization to chromosome 11 of a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 NEVIEGPQNARVL----KGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITN---- 69
                               Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00408; IGc2; 2.
                                                                                                                                                             EMBL; L34774; AAA36387.1; -
                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 RKSATVNLTVIRCPQDTGGGINIP-GVLSSLPSLGFSLPTW 243
                                                                              Interpro; IPR003598; Ig_c2.
Interpro; IPR003600; Ig_like.
                                                                                                                                              Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
                                                                                                                InterPro;
             Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T----PTVKWVKNGDMVIPSDYFKIVKEHNLQ----VLGLVKSDEGFYQCIAENDVGNA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHWTWLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKA
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                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
                                                                                                                                                                                                                                                                                                                                                                             similarity)
                                                                                                                                600632;
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                                                                                                                                              HGNC:8143; OPCML.
 Signal
                                                                                                              IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Advanced glycosylation end product-specific receptor precursor
                                                                                                                                                                                                                                                                                                                                          RAGE_BOVIN
Q28173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIAIT
                        "Cloning and expression of a cell surface receptor for advanced glycosylation end products of proteins.";
J. Biol. Chem. 267:14998-15004(1992).
-i. FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGED. THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
                                                                                                                                                                                         Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                             AGER OR RAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 AENEPCEVTCL----PSHWTWLPDISWELGLLVSHSSYY----FVPEPSDLQSAVSILAL 184
                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                    Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                          (Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 KRDQSGEYECSAL-NDVAAPDVRKVKITVNYPPYISKAKNTGVSVGQKGILSCEASAVPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 TPQSNGTLTCVATWKSLKARKSATVNLTV----IRCPQDTGGGINIPGVL----SSLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 NEGSSVTLLCLAIGRPE-----PTVTWR------HLSVKEGQGFVSEDEYLE----ISDI 192
- i- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                        Neeper M., Schmidt
                                                                                                                                    MEDLINE=92340547; PubMed=1378843;
                                                                                                                                                                                                                                                                                                                                                                                                                         252 AEFQ---WFKEETRLATGLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 LGFSLPTWGK----VGLGLAG 252
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                  RATE IN DIABETES
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                                                                                                          chmidt A.M., Brett
Stern D., Shaw A.;
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                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                          Brett J., Yan S.D., Wang F., Pan Y.C.,
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IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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OPIOID BINDING PROTEIN/CELL ADHESION
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N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                            Ruminantia; Pecora; Bovoidea;
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Best Local
01-OCT-1989 (Rel. 12, Created)
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                                                       OPCM_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                336 EGTTAGSVEGPG----LETLALTLGILG--GLG------TVALLIGVIVWHRR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                              277 NCCCRCCFCCRRKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKTTDTASLPPK 336
                                                                                                                                                                                                                                                                                                                                                                                                                219 D--TGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCCRRRCCGC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 -IKDGRPLPLPPGPMLLLPEVG-----PEDQGTYSCVATHPSHGPQESRAVSVTIIETGE 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 LLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 TKRHPKTGLFTLHSELM----VTPARGGALHPTFSCSFTPGLPRRRALHTAPIQLRVWSEH 232
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_11ke.
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SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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                                                       STANDARD;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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IG-LIKE C2-TYPE DOMAIN 2.
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SPECIFIC RECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003006; InterPro; IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S03199; S03199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X12672; CAA31192.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The second of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY, IGLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Opioid binding protein/cell adhesion molecule precursor (OBCAM)
(Opioid-binding cell adhesion molecule) (OPCML).
79 QGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRLHGSAYLTVQVMGELFIPSVNLVV 132
                                                  44 NVTVRQGESATLRCTIDDRVTRVAW-LNRSTILYAGNDKWSIDPRVIILVN---TPTQY- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBO J. 8:489-495(1989).

-i- FUNCTION: BINDS OPIOIDS IN THE PRESENCE OF ACIDIC LIPIDS; PROBABLY INVOLVED IN CELL CONTACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein with potential roles in opioid binding and cell contact.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schofield P.R., McFarland K.C., Hayflick J.S., Wilcox J.N., Cho T.M., Roy S., Lee N.M., Loh H.H., Seeburg P.H., "Molecular characterization of a new immunoglobulin superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                          26 NARVLKGSQARFNCTVSQGWKLIMWALSDMVVL-----SVRPMEPIITNDRFTSQRYD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89251576; PubMed-2721489;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Bovinae; Bos.
                                                                                                                                                                              Local
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SM00408;
                                                                                                                                                                         Similarity
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322
                                                                                                                                                                       5.3%;
25.0%;
                                                                                                                                                                                                                                            37914 MW;
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                                                                                                                                                 31; Mismatches
                                                                                                                                                                  Score 111.5; DB Pred. No. 0.084;
                                                                                                                                                                                                                                                             GPI-ANCHOR (POTENTIAL)
                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
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GLCNAC . .)
GLCNAC . .)
GLCNAC . .)
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                                                                                                                                             Indels
                                                                                                                                                                                        Length 345;
                                                                                                                                                                                                                                                                                                   ) (POTENTIAL).
) (PROBABLE).
) (POTENTIAL).
                                                                                                                                                                                                                                                                                (POTENTIAL)
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InterPro; IPROUSEON; Ig_11...

R InterPro; IPROUSEON; Ig_11...

R Pfam; PF00041; fn3; 6.

P Pfam; PF00047; ig; 4.

DR PAINTS; PR00014; FNTYPEIII.

DR SMART; SM00060; FN3; 6.

DR SMART; SM00410; IG_11ke; 2.

DR SMART; SM00410; IG_2; 2.

Transmembrane; Immunoglobulin domain; Glycoprotein; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RC STRAIL-White leghorn; TISSUE-Embryonic brain;

RX MEDLINE-95105243; PubMed-7806578;

RA Vielmetter J., Roman J.M., Dreyer W.J.;

RV vielmetter J., Roman J.M., Dreyer W.J.;

RV vielmetter J., Roman J.M., Dreyer W.J.;

RT vielmetter J., Roman J.M., Dreyer W.J.;

RT suppressor molecule deleted in colorectal cancer.";

RI J. Cell Biol. 127:2009-2020(1994).

RL J. Cell Biol. 127:2009-2020(1994)

CC -:- FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE TRANSITION OF UNDIFFERENTIATED FOLLFERATING CELLS TO THEIR CLLS TO THE THE CLLS TO THEIR CLLS TO THE THE AXONS.

C -- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC

-- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHICK
                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                  EMBL; U07644; AAC59662.1; -. HSSP; P11276; 2MFN.
                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252
                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                          InterPro;
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SIMILARITY:
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                                                                                                                                                                                                                                                                                          IPR003961; FN_III.
IPR003962; FnIII_x
                                                                                                                                                                                                                                                                       IPR003006;
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Q92154;
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                                                                                                                                          Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                          SMP
                                                      Dulac C., Tropak M.B., Cameron-Curry P., Rossier J., Marshak D.R.,
                                                                                                                                                                                  Schwann cell myelin protein precursor.
                                                                           MEDLINE=92153423; PubMed=1739462;
                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                     NCBI_TaxID=93934;
                                                                                                                                         Archosauria; Aves;
                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                         372 GFYQCIA 378
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                                                                                                                                                                                                                                                                                                                                                                           265 LRAGGS----LLISDVTEEDVGTYTCIADNENETIEAQAELAVQVPPEFLKRPANIYAHE
                                                                                                                                                                                                                                                                                                                                                                                                                   218 VRQPSSLTKVTGQNAVFPC-VAGGFPTPYVRWTKNG--
                                                                                                                                                                                                                                                                                                                                                                                               78
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                                                                                                                                                                                                                                                                                                                                                                                              -DQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSAYLTVQVMGELFIPSVNLVVAE 134
                                                                                                                                                                                                                                                                                                              GTLTCVA 196
                                                                                                                                                                                                                                                                                                                                 SMDIVFECEVTGKPT-----PTVKWVKNGDVVIPSDYFKIVKEHNLQ-----VLGLVKSDE 371
                                                                                                                                                                                                                                                                                                                                                     NE----PCEVTCLPSHWTWLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                        STANDARD;
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376
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25.7%;
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IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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BY SIMILARITY.
N-LINKED (GLCN
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 111.5;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        558C6795579C0E26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 0.49;
                                    Schwann cell myelin immunoglobulin super
                                                                                                   18-28; 120-132;
                                                                                                                                                                                                                                         620 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                     yelin protein, superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                     135-157
                                                                                                                                              Phasianinae;
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SPECIFICITY: EXCLUSIVELY EXPRESSED BY MYELINATING AND

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    437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 2.
SMART; SM00410; IG_like; 1.
SMARR; SM00408; IGc2; 2.
Myelin; Glycoprotein; Cell adhesion; Transmembrane; Signal; Repeat;
                                                                                                                                 186
                                                                                                                                                                            344
                                                                                                                                                                                                         140 VTCLPSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAV---SILALT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                        234 P--SLGFSLPT 242
                                                                                                                                                                                                                                                  286 NL--RLLLSNVGPDDGGSFSCVAENRHGRHNRSLQLRVAYAPRAPVINGSLWVVSGDPVS 343
                                                                                                                                                                                                                                                                                                                                        246 GP--TEVVEGSDVELGCEAEGRPAPLISWFRGSEVL------REEPGR 285
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                                                                                                                                                                                                                                                                                                                                                                                 23 GPQNARVLKGSQARFNCTV-SQGWKLIMWALSDMVVLSVRPMEPIITNDRFTSQRYDQGG 81
                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NONMYELINATING SCHWANN CELLS AND OLIGODENDROCYTES.

DEVELOPMENTAL STAGE: FIRST SYNTHESIZED AT EMBRYONIC DAY 5, 1

REMAINS EXPRESSED BY CULTURED SCHWANN CELLS.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                            PARPEDGGTYSCVA--ENQHGASSTSFNISVEYPPLVLPASRCTAG-GDGVRCVCMVNSI
                                                                                                                   ---PQSNGTLTCVATWKSLKARKSATVNLTV-----IRCPQDTGGGINIPGVLSSL 233
                                                                                                                                                                                                                                                                                             NFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVN--LVVAENEPCE 139
PDSSLVFELPT 447
                                                                                                                                                                            VTCRAE ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S83711; AAB21466.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003006; Ig_MHC.
IPR003598; Ig_c2.
IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        620 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260
346
420
431
222
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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304
391
429
488
222
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516
536
620
106
223
311
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                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
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IG-LIKE V-TYPE DOMAIN 1

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 4.

BY SIMILARITY

BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 111; DB Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC...) (P. N-LINKED (GLCNAC...) (P. N-LINKED (GLCNAC...) (P. N-LINKED (GLCNAC...)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                --SEPAAILTVLRGGKVMAAAIYEDHVTMEMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                              84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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                                                                                                                                                                                                           185
                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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Search completed: April 28, 2003, 18:09:41 Job time : 14.3692 secs

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
                                                                               Database
                                                                                                                                                               Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-729-264-4
2088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                April 28, 2003, 18:09:54; Search time 19.0659 Seconds
                                                                                                                                                                                                                                                                                                                 283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                 PIR_73:*
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                                                                                                                                           Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                      MYAGAMENRDPPGSGSGNEV.....HPQASFNLASPEKVSNTTVV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
pir3:*
pir4:*
                                                         pir1:*
                                       pir2:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (without alignments)
1946.300 Million cell updates/sec
                                                                                                                                                                                                                                                                             283224
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	IJ	. Description
	145.5		404	- :	161596	advanced glycosyla
N I	ω.	6 5	1447	N	A54100	suppressor
ω	134.5		1427	2	151669	
4	133.5		871	٢	I48696	
տ	ω		881	<u></u>	I48697	
6	129.5	6.2	164	N	T24272	
7	122.5	5.9	188	N	T15651	~
8	121	5.8	344	N	I56551	imin - rat
9	119.5	5.7	6642	N	T29757	
10	119	5.7	1070	ν	JC4593	osine
11	115.5	5.5	946	ш	A47299	ror-related recept
12.	114.5	.5.5	152	N	T18975	netical p
13	114.5	5.5	531	Ν	S20900	tin - mouse (i
14	114.5	٠. ت	862	N	I49583	וורדמרדסוו
15	114.5	ნ	26926	ب	I38344	cardiac mu
16	112.5	5.4	345	N	JC4025	opioid-binding cer
17	112.5	5.4	416	Н	A42879	advanced grycosyra
18	112	5.4	868	N	A46512	CD22 nomolog/B lym
19	111.5	5.3	345	2	S03199	outpo
20	111.5	5.3	1443	N	I50600	CKE
21		•	6805	N	S20901	ibbit (I
22	111		620	N	JH0593	- ⊢
23	111	•	693	N	S49228	sodium-dependent p
24	110.5	•	338	N	JC1238	opioid-binding pro
25	110.5	5.3	345	Ŋ	JC1239	oid-bi
26	110.5	•	4391	N	A38096	n prec
27	109.5		364	N	A30521	, <u>–</u>
28	109		3375	ນ	T19821	prot
29	107		391	2	T09058	butyrophilin nomol

Query Match

7.0%;

Score 145.5;

DB 1; Length 404;

444	42	39 40	38	37	ω ω	ယ (၁	ω A	3 3	32	31	30
101.5	102.5	103.5	104	104	104.5	105.5	106	106.5	106.5	106.5	106.5
4.4.	- - - 0	, u, u	5.0	5.0	5. O	5.1	5.1	5.1	5.1	5.1	5.1
215 1449	890 721	2491	2295	764	1177	662	1092	1272	841	802	487
888	0 H K) H K	N	2	N	2	Н	N	Ν	2	2
T16542 S47423	A53743	A28372	C88369	A49448	T16594	T16525	JN0635	S26180	JC5894	T13149	\$65133
hypothetical prote E2 glycoprotein pr	protein-tyrosine k hypothetical prote	insulin-like growt henaran sulfate pr	protein unc-52 [im	irregular chiasm C	hypotherical proce	hypothetical prote		ascin			===

ALIGNMENTS

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A;Cross-references: GB:D28769; NID:g561657; PIDN:BAA05958.1; PID:g561659
R;Neeper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.;
J. Biol. Chem. 267, 14998-15004, 1992
A;Title: Cloning and expression of a cell surface receptor for advanced glycosylation
A;Reference number: A42879; MUID:92340547; PMID:1378843
A;Accession: B42879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprot C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C;Accession: 161596; B42879; S27968
C;Accession: 161596; B42879; S27968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: sequence extracted from NCBI backbone (NCBIP:109438)
C;Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly c;Comment: function, thus contributing to tissue lesions in diabetes.
C;Comment: This receptor appears also to mediate the effects of amyloid beta peptide ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterpart of mouse mammary tumor gene int-3. A; Reference number: A55562; MUID:95137587; PMID:7835890 A; Accession: I61596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Sugaya, K.; Fukagawa, T.; Matsumoto, K.; MITa, K.; Takadashi, E., Ando, A., Ando, A., Ando, A., Ando, A., Title: Three genes in the human MHC class III region near the junction with the classifile: Three genes in the human MHC class III region near the junction with the classifile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               advanced glycosylation end-products receptor precursor human
                                                                                                                                                                                                                                                                              A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-404/Product: advanced glycosylation end products receptor #status predicted <MAT F;23-344/Domain: extracellular #status predicted <EXT>
F;31-101/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 'G',2-99,'R',101-404 <NEE>
A;Cross-references: EMBL.M91211; NID:g190845; PIDN:AAAO3574.1; PID:g190846
A;Experimental source: lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-404 < RES>
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F;345-362/Domain: transmembrane #status predicted <TMM>
F;363-404/Domain: intracellular #status predicted <INT>
F;25,81/Binding site: carbohydrate (Asn) (covalent) #statu:
F;38-99,144-208,259-301/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 6p21.3-6p21.3
A;Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I61596
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                                                                                                                                                                                          F;137-210/Domain: immunoglobulin homology <IM2>F;252-303/Domain: immunoglobulin homology <IM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:306354; OMIM:600214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB: AGER
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                                                                    (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: transmembrane protein; tumor suppressor F;1-25/Domain: signal sequence #status predicted <SIG>F;26-1447/Product: tumor suppressor protein DCC #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:119838; OMIM:120470
A; Map position: 18q21.1-18q21.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-750 <FEA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Identification of a chromosome 18q gene that is altered in colorectal cancers. A;Reference number: A40098; MUID:90100559; PMID:2294591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X76132; NID:g453209; PIDN:CAA53735.1; PID:g453210 R;Fearon, E.R.; Cho, K.R.; Nigro, J.M.; Kern, S.E.; Simons, J.W.; Ruppert, J.M.; Hamilt. Science 247, 49-56, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Homo sapiens (man)
C:Daccies: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 05-Nov-1999
C:Accession: A54100; A4008
R:Hedrick, L.; Cho, K.R.; Fearon, E.R.; Wu, T.C.; Kinzler, K.W.; Vogelstein, B. Genes Dev. 8, 1174-1183, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: GDB:DCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M32292; NID:g181492; PIDN:AAA35751.1; PID:g181493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A40098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A54100; MUID: 95011532; PMID: 7926722
A; Accession: A54100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: The DCC gene product in cellular differentiation and colorectal tumorigenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor suppressor protein DCC precursor - human
N.Alternate names: colorectal cancer suppressor DCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-1447 <HED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
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                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                             109 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTWLPDISW-ELGLLVSHSSYY 167
                                                                              274 LRGEEVI------QLRSKKYSLLGG--SNLLISNVTDDDSGMYTCVVTYKNEN 318
                                                                                                                                                                                     215 RNPASSRTGNEAEVRILSDPGLHRQLYFLQRPSNVVAIEGKDAVLECCVS-GYPPPSFTW 273
                                                                                                                                  51 ALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 KTTDTASLPPKSCESSDPEQRNSSCGPP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 E-PGEEG-------PTAGSVGGSGLGTLALALGILGGLGTAALLIGVI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 AYLTVQVMGELFIP----SVNLVVAENEP------CEVTCLPSHWTWLPDIS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 KPLVPNEKGVSVKEQTRRHPETGLFTLQSELM----VTPARGGDPRPTFSCSFSPGLPRHR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 LWQRR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 RCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT------PTCTLTIRCC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 WELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 ALRTAPIQPRVWEPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIH 270
                                                                                                                                                                                                                                      9 RDPPGSGSGNEV-------IEGPQNARVLKGSQARFNCTVSQGW--KLIMW 50
                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 EPIITNDRFTS-----ORYDQGGNFT--SEMIIHNVEPSDSGNIR----CSLQNSRLHGS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCRRCCGCNCCCCCCCCCRKRGFRIQFQKKSEKEKT--NKETETESGNENSGYNSDEQ 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----QSEEPEAGESSTGGP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WMKD------GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISII 321
                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                       Conservative
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25.1%;
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                                                                                                                                                                                                                                                                                                                             Score 136; DB 2; Length 1447; Pred. No. 0.051;
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                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                               101; Indels
     <u>::</u> :: - ::
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                                                                                                                                                                                                                                                                                               50;
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                                                                                                                                                                                     N;Contains: protein-tyrosine kinase nsk2 precursor, splice form 4
C;Species: Mus musculus (house mouse)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
C;Accession: 148696; 560738
R;Ganju, P.; Walls, E.; Brennan, J.; Reith, A.D.
Oncogene 11, 281-290, 1995
A;Title: Cloning and developmental expression of Nsk2, a novel receptor tyrosine kina
        A;Cross-references: EMBL:X86444; NID:g929723; PIDN:CAA60165.1; PID:g929724 A;Experimental source: splice form 2
                                                                                                                                                  A; Reference number: I48696; MUID:95349951; PMID:7624144 A; Accession: I48696
A; Accession: S60738
                                                                                                               A; Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine kinase (EC 2.7.1.112) nsk2 precursor, splice form 2 - mouse N.Alternate names: receptor-type tyrosine kinase
                                                                                                       A; Molecule type: mRNA
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                                                                         A; Residues: 1-871 <GAN1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor suppressor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U10986; NID:g606873; PIDN:AAA70168.1; PID:g606874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Expression of a homologue of the deleted in colorectal cancer (DCC) gene in A; Reference number: 151668; MUID:95113183; PMID:7813784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: I51669
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A; Residues: 1-1427 <PIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 FSADLTVMÝPPQFLNHPANLYAYESMDIEFECAVSGKPS-----PTVKWTKNGEVVIPSD 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 GSAYLTYQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTWLPDISW-ELGLLVSHSS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 PQDTGGGINIPGVLSS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 PGSARVGNEAELRILSESGLHRQQVFLQRPSNVVAIEGQDAVLECAVS-GYPTPTIVWMQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 QIVGGSNLR----ILGVVKSDEGFYQCVAENEAGNAQTSAQLIVPKPAIPSSS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 ISASAELTVLVPPWFLNHPSNLYAYESMDIEFECTVSGKP-VPTVNWMKNGDVVIPSDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 SDMYVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLH 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 PGSGS-GNEV------IEGPQNARVLKGSQARFNCTVSQGW--KLIMWAL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFQIVDGSNLR----ILGLVKSDEGYYQCIAENEAGNIQTYAQLIIPDPAVPSSSILPSA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYFVPEPSDLQSAVSILALTPQSNGTLTCVA-----TWKSLKARKSATVNLTVI-RC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GD------EPVFIRTR----KYSVLGG--SNLLISNVTDDDAGAYTCVATYKNENTS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRDV-----VPVLVSS 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4%; Score 134.5; DB 25.4%; Pred. No. 0.065;
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C;Superfamily: mouse ror-related receptor; immunoglobulin homology; protein kinase homol C;Keywords: ATP; glycoprotein; phosphotransferase; receptor; transmembrane protein; tyrc F;1-21/Domain: signal sequence #status predicted <SIG> F;22-871/Product: protein-tyrosine kinase nsk2, splice form 2 #status predicted <MAT2>
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A; Residues: 1-456, 'A', 466-871 <GAN2>
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F;22-856, A', 466-871/Product: protein-tyrosine kinase nsk2, splice form 4 #status predif;42-101/Domain: immunoglobulin homology <IMM1>
F:42-101/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics
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F:583-591/Region: protein kinase ATP-binding motif
F:222,462/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F; 226-284/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000 C;Accession: I48697; S60740 R;Ganju, P; Walls, E; Brennan, J.; Reith, A.D.
                                                                                                                                                                                                                                                                                                                Oncogene 11, 281-290, 1995 A; Title: Cloning and developmental expression of Nsk2, a novel receptor tyrosine kinase A;Reference number: 148696; MUID:95349951; PMID:7624144
A;Accession: 148697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Contains: protein-tyrosine kinase nsk2 precursor, splice form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-tyrosine kinase (EC 2.7.1.112) nsk2 precursor, splice form 1 - mouse N;Alternate names: receptor-type tyrosine kinase
A;Accession: S60740
A;Molecule type: DNA
A;Residues: 1-456, 'A', 466-881 <GAN2>
A;Cross-references: EMBL:X86445; NID:g929725
A;Experimental source: splice form 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Mus musculus (house mouse)
                                                                                                                                                                                   A;Cross-references: EMBL:X86445; NID:g929725; PIDN:CAA60166.1; PID:g929726
                                                                                                                                                                                                                           A; Residues:
                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                      A;Status: nucleic
                                                                                                                                                         A; Experimental source: splice form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 SDLQSAVSILALTPQSNGTLTCVAT----WKSLKARKSATVNLTVIR------CPQD 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 QVMGELFIPSVNLVVAENEPCEVTC----LPSHWTWLPDISW-ELGLLVSHSSYYFVPEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 -NALRENSRIAALE-----SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKLVKLEV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 EALLCYHLFLECSPGVVPTPMPICREYCLAVKELFCAK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 RGEGVLMQGPGEKMLLVFLPTTSHRDPEDAQELLIHTAWNEL------KAVSPLCRPAA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 TGGGINIPG-----VLSSLPSLGFSLP------TWGKVGLGLAGTMLLTPTCTLTI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 RVIDSRLQLFITKP---GLYTCIATNKHGEKFSTAKAAATVSIAEWSKSQKDSQGYCAQY 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 EVLGRILRAPESHNVTFGSFVTLRCTEIGIP-----VPTISWIENGNAVSSGSIQESVKD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192/Domain: immunoglobulin homology <IMM2>
84/Domain: immunoglobulin homology <IMM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 MEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-----LTV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RCCCCRRCCGCN------CCCRCC-----FCCR 287
                                                                                                                                                                                                                       1-881 <GAN1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                         acid sequence not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         splice forms see PIR: I48697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4%; Score 133.5; DE 21.6%; Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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F;22-456,'A',466-881/Product: protein-tyrosine kinase nsk2, splice form 3 #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Keywords: ATP; glycoprotein; phosphotransferase; rect
F;1-21/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: mouse ror-related receptor; immunoglobulin homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: MGI:103308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Comment: For alternate splice forms see PIR:148696
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;135-192/Domain: immunoglobulin homology <IMM2>F;226-284/Domain: immunoglobulin homology <IMM3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;498-518/Domain: transmembrane #status predicted
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A; Accession: T24272
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                             R;Sims,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T01B7.8 - Caenorhabditis elegans
                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z66499; PIDN:CAA91301.1; GSPDB:GN00020; CESP:T01B7.8
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                                                                                                                                          A; Introns: 20/3;
                                                                                                                                                                                         A; Gene: CESP:T01B7.8
                                                                                                                                                                                                                     C; Genetics
                                                                                                                                                                                                                                      A; Experimental source: clone T01B7
                                                                                                                                                                                                                                                                                     A;Residues:
                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                     A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 EVLGRILRAPESHNVTFGSFVTLRCTEIGIP-----VPTISWIENGNAVSSGSIQESVKD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 QVMGELFIPSVNLVVAENEPCEVTC----LPSHWTWLPDISW-ELGLLVSHSSYYFVPEP 172
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157 LGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 EALLCYHLFLECSPGVVPTPMPICREYCLAVKELFCAK 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 MEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-----LTV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRP 62
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                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCCCCRRRCCGCN------CCCRCC-----FCCR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGEGYLMQGPGEKMLLVFLPTTSHRDPEDAQELLIHTAWNEL------KAVSPLCRPAA 373
                                                                                                                                                                                                                                                                                       1-164 <WIL>
                                                                            Similarity
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21.6%;
                                                                          6.2%; Score 129.5; DB 32.1%; Pred. No. 0.015;
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Pred. No. 0.046;
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                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127;
                                                                                                     DB 2;
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                                                           53;
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                                                                                                     Length 164;
                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                 A;Cross references: EMBL:U16845; NID:g755184; PIDN:AAA67445.1; PID:g755185
                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Neurosci. 15, 2141-2156, 1995
A;TItLe: Cloning of neurotrimin defines a new subfamily of differentially expressed neural, Reference number: 156551; MUID:95198094; PMID:7891157
                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-344 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: I56551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep.1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U58760; NID:g1330384; PID:g1330389; PIDN:AAB00710.1; GSPDB:GN00A;Experimental source: strain Bristol N2; clone C27A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-188 <NHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C27A2
A;Reference number: Z18382
A;Accession: T15651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ
    149 EGNNISLTCIATGRPE-----PTVTWR----HISPKAVGFVSEDEYLE----IQGITREQS 196
                                          134 ENEPCEVTCL----PSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 CTLTIRCCCCRRRCCGC--NCCC-RCCFCCR 287
                                                                                                                                       80
                                                                                                                                                                44 NYTYROGESATIRCTIDNRYTRYAWLNRSTILYAGNDKWCLDPRYYLLSN---TQTQY-- 98
                                                                                                                                                                                                      26 NARVLKGSQARFNCTVSQGWKLIMWALSDMVVLS-----VRPMEPIITNDRFTSQRYDQ 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 CCCRPKCCCCCRRCCTCCRTCCCTRCCTCCR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 CRTCCCTRCCTCCR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 -- NCCC-RCCFCCR 287
                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 PQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 KRQGGCGCCGCGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CESP:C27A2.5
                                                                                    -----SIEIQNVDVYDEGPYTCSVQTDNHPKTSRVH----LIVQVSPKIVEISSDISIN 148
                                                                                                                          GGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRLHGSAYLTVQVMGELFIPSVNLVVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19/3; 91/2
                                                                                                                                                                                                                                                               59;
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                                                                                                                                                                                                                                                                       5.8%; Score 121; DB 2
24.1%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.9%; Score 122.5; DB 61.3%; Pred. No. 0.057;
                                                                                                                                                                                                                                                         37;
                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                          DB 2; Length 344;
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                                                                                                                                                                                                                                                      93;
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                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                  56;
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A; Map position: 6p21.1-6p12.2
                                          A; Gene: GDB: PTK7
                                                                                                                                                                                                                                              R;Park,
                                                                                                                                                                                                                                                             C; Accession: JC4593
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                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-6642 < DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: Z20679
A; Accession: T29757
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                                                                                                                                                                                                                   Park, S.K.; Lee, H.S.; Lee, S.T.
Biochem. 119, 235-239, 1996
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-1070 <PAR>
A;Cross-references: GB:U40271; NID:g1322231; PIDN:AAC50484.1; PID:g1322232
C;Comment: This protein is a member of receptor protein tyrosine kinase family, but p
                                                                                                                                                                                                                                                                                                                                                               A;Title: Characterization of the human full-length PTK7 cDNA encoding a receptor prot A;Reference number: JC4593; MUID:97037064; PMID:8882711 A;Accession: JC4593
                                                                                            A;Cross-references: GDB:134760; OMIM:601890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 16-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-tyrosine kinase-related receptor PTK7 precursor - human
N;Alternate names: receptor protein tyrosine kinase-like protein (RPTK)
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A;Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1
/3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2132 ------LKISNAKIEQTGTVKVTAQNSAGQDSKQADLKVEPNVKAPKFKSQLTDKVA 2182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2077 VYDGPKSYTIKETETAEFKATIS-GFPAPTVKWTINEKIVEESRTITTIKTEDVYT---- 2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 NGTLTCVATWKSLKARKSATVNLT-----VIRCPQD 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 AENEPCEVTCL---PSHWTWLPDISWEL-GLLVSHSSYYFVPEPSDLQSAVSILALTPQS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 DQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPS-----VNLVV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 VIEGPQNARVLKGSQARFNCTVSQGW--KLIMWALSDMVVLSVRPMEPIITNDRFTSQRY 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 5.7%; Score 119.5; Local Similarity 23.4%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGTLTAKAKNAAGECETSAKVTVNGGNKKPEFVQAPQN 2277
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                                                                                                          Matches
                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 869 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/644,
FILING DATE: 10-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Valenzuela, et al.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
TITLE OF INVENTION: AND LIGANDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 SVPECSKLPSMHWDPTACARLP-----HLDYNKENLKTFPP--MTSSKPSVDIPNLPSSS 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 SGNENSGYNSDEOKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQRP----PRPASHP 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 LCNHIFQECSPGVVPTPIPICREYCLAVKELFCAKE----WLVMEEKTHRGLYRSEMHLL 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 CCRRRCCGCN------CCCRCC-----FCCRRKRGFRIQFQKKSEKEKTNKETETE 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 RVIDSRLQLFITKP---GLYTCIATNKHGEKFSTAKAAATISIAEWSKPQKDNKGYCAQY 320
                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: RETELECOMMUNICATION INFORMATION: 914-345-7400
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                                                                                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 QASFNLA 375
                                  113 GALQVKMKP-----KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD----- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Kegence....
cmpreT: 777 Old Saw Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: USSN 60/008,657 FILING DATE: 15-DEC-1995
63 MEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMG 121
                                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Cobert, Robert J
REGISTRATION NUMBER: 36,108
                                                                    4 GAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRP 62
                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tarrytown
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                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diskette
                                                                                                          6.3%; Score 132.5; DB 2; 20.8%; Pred. No. 0.0018; ative 55; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/644,271
                                                                                                                                                                                                                                                                                                            .29:
                                                                                                                                                                                                                                                                                                                                                                                                     REG 195A
                                                                                                                                                DB 2; Length 869;
                                                                                                                 Indels 105;
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US-09-077-955-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/077,955A CURRENT FILING DATE: 1998-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Valenzuela et al., David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: PCT/US96/20696 EARLIER FILING DATE: 1996-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: REG195-B-PCT-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1995-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/008,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1996-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 08/644,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 EVFARILRAPESHNVTFGSFVTLHCTATGIP-----VPTITWIENGNAVSSGSIQESVKD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 ELFTPSVNLVVAENEP-----CEVTCLPSHWTWLPDISW-ELGLLVSHSSYYFVPEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430 SVPECSKLPSMHWDPTACARLP-----HLDYNKENLKTFPP--MTSSKPSVDIPNLPSSS 482
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                                                                                                           173 SDLQSAVSILALTPQSNGTLTCVAT----WKSLKARKSATVNLTVIRCPQDTGGG----- 223
                                                                                                                                                                   209 EVFARILRAPESHNVTFGSFVTLHCTATGIP-----VPTITWIENGNAVSSGSIQESVKD 263
                                                                                                                                                                                                                                                                        159 -SPLRENSRIAVLE------SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKVVKLEV 208
224 ----INIPGVLSSLPSLGFSL------PTWGKVGLGLAGTMLLTPTCTLTIRCC 267
                                                       264 RVIDSRLQLFITKP---GLYTCIATNKHGEKFSTAKAAATISIAEWSKPQKDNKGYCAQY 320
                                                                                                                                                                                                                    122 ELFIPSVNLVVAENEP-----CEVTCLPSHWTWLPDISW-ELGLLVSHSSYYFVPEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                             63 MEDIITNDRETSORYDOGGNETSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRP 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.3%; Score 132.5; DB 20.8%; Pred. No. 0.0018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 869;
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                                                                                                           Query Match
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LIBRARY: GenBar
CLONE: 1532042
            414 GTCTCTGT---
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                              190 GTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGI----NIPGVLSSLPSLGFSLPTWGK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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ADDRESSEE: Incyte Ph
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APPLICANT: Greenwald, Sara
APPLICANT: Greenwald, Sara
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: CARBONIC ANHYDRASE VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                            Local Similarity
es 37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 QASFNLA 375
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                                                                           Conservative
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                                                                     1; Mismatches
                                                                                    Score 128.5; DB 2; Pred. No. 0.0077;
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                                                                     41; Indels
                                                                                                    Length 1345;
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                                                                  Gaps
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GENERAL INFORMATION:
APPLICANT: Green et al
TITLE OF INVENTION: POLY
TITLE OF INVENTION: Lymp
TITLE OF INVENTION: POLY
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                                                                                                          Sequence 4, Application US/09651200 Patent No. 6429303
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LENGTH: 340
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CURRENT APPLICATION NUMBER: US/09/651,200
PRIOR ADDITORMANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-12-21
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PRIOR FILING DATE: 2000-02-18
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                                                                                                                                                                                                                                      329 SDSKEDD 335
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                                                                                                                                                                                                                                                                                                            289 ---ALAFYCWRK-----IKQSCEEENAGAEDQDG-----EGEGSKTALQPLKH 328
                                                                                                                                                                                                                                                                                                                                                 278 CCCRCCFCCRRKRGFRIQFQKKSEKEKINKETETESGNENSGYNSDEQKTTDTASLPPKS 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Ver. 2.0
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Polynucleotides Encoding Members of the Human Lymphocyte Activation Antigen B-7 Family and Polypeptides Encoded Thereby
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CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
PRIOR APPLICATION NUMBER: 60/183578
PRIOR FILING DATE: 2000-02-18
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                    SOFTWARE: Pa
SEQ ID NO 6
LENGTH: 534
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Best Local Similarity
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APPLICANT: Green e
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                                                                                                                                                                                                                                                     TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and FITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
CURRENT FILING DATE: 2000-08-30
                                                                                                        PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-02-18
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                                                                                           NUMBER OF SEQ ID NOS:
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TYPE: PRT
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US-09-651-200-24
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                                                                                                                                                                                                                                                                                   SEQ ID NO 24
LENGTH: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Green et al TITLE OF INVENTION: Polynucleotides Encoding Members of the Human TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 15966-562 (CURA-62) CURRENT APPLICATION NUMBER: US/09/651,200 CURRENT FILING DATE: 2000-08-30 CURRENT FILING DATE: 2000-08-30
                                                                                Best Local 511
                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/.
PRIOR FILING DATE: 2000-02-18
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR ETITING DATE: 1999-12-21
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                                                                                                                                                                                                                                            ORGANISM: Unknown
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239 PQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLV---- 294
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78; Conserv
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RESULT 12
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                                                   Sequence 15, Application US/09540245A Patent No. 6270984 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/062,365
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schmidt, Ann Marie
APPLICANT: Stern, David
TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A
TITLE OF INVENTION: SUBJECT
FILE REFERENCE: 55424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                  300 E-PGEEG-------PTAGSVGGSGLGTLAL 321
                                                                                                                                                                                                                                                             249 WMKD------GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISII 299
                                                                                                                                                                                                                       215 RCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLL 256
                                                                                                                                                                                                                                                                                                155 WELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVI 214
                                                                                                                                                                                                                                                                                                                                        197 ALRTAPIQPRVWEPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIH 248
                                                                                                                                                                                                                                                                                                                                                                             113 AYLTVQVMGELFIP----SVNLVVAENEP------CEVTCLPSHWTWLPDIS 154
                                                                                                                                                                                                                                                                                                                                                                                                                    140 KPLVPNEKGVSVKEQTRRHPETGLFTLQSELM---VTPARGGDPRPTFSCSFSPGLPRHR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 EPIITNDRFTS-----QRYDQGGNFT--SEMIIHNVEPSDSGNIR----CSLQNSRLHGS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         523 SDSKEDD 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483 ---ALAFYCWRK-----IKQSCEEENAGAEDQDG------EGEGSKTALQPLKH 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 CESSDPE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 CCCRCCFCCRKKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKTTDTASLPPKS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 QDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCN 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 VSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCP--- 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 FGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTTTC--SSYRGYPEAEVFWQDGQGVPL 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 -----HSFTEGR-DQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV-SIRD 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 EPIITNDRFTSQRYDQGGNF-----TSEMITHNVEPSDSGNIRCSLQNSRL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDAHGSVTITGQPMTFPPEAL----WVTVGLSVCLIALLV------- 482
              Kid, Thomas
                                 Goodman, Corey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.8%; Score 121.5; DB 25.7%; Pred. No. 0.0048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Indels 69; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-08-374-834-1
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SEQ ID NO 15
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APPLICANT:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                   COUNTRY:
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US-09-540-245A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
    FILING DATE: 21-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1395
TYPE: PRT
ORGANISM: Drosophila melanogaster
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TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Valenzuela, et al.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 PPPSVFWTKEGV 383
                                               APPLICATION NUMBER: US 08/095,658 FILING DATE: 21-JUL-1993
                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 QSNGTLTCVA--TWKSLKARKSATV----NLTVIRCPQDTGGGINIPGVLSSLPSLGFSL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 YGQTATFHCSVGGDPP-----PKVLWKKEEGNIPVSRARILHD-----EKSLEISNITP 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 IVDGGN----LLISNVEPIDEGNYKCIAQNLVGTRESSYAKLIVQVKPYFMKEPKDQVML 267
                                                                                                                                               FILING DATE:
                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             STREET: 7// Old
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 ENEP----CEVTCLPSHWTWLPDISW----ELGLLVSHSSYYFVPEPSDLQSAVS:LALTP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 PKDTRVAKGETALLECGPPKGIPEPTLIWIKDGVPLDDLKAMSFGASSRV-----R 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 YDQGGNFTSEMIIHNVEPSDSGNIRCSLQN---SRLHGSAYLTVQVMGELFIPSVNLVVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 PQNARVLKGSQARFNCTVSQG--WKLIMW-----ALSDMVVLSVRPMEPIITNDRFTSQR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                      777 Old Saw Mill River Road
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                                                                                                                                          19-JAN-1995
Robert
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                                                                                                                                                            US/08/374,834
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; MOLECULE TYPE: protein US-08-374-834-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08644271 Patent No. 5814478
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 868 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Valenzuela, et al.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
TITLE OF INVENTION: AND LIGANDS
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 GALQVKMKP-----KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGDSALRE--- 163
                 PRIOR APPLICATION DATA:
                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 -----NSRIAVLE------SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKLVKLEV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 RVIDSRLQLFITKP---GLYTCIATNKHGEKFSTAKAAATVSIAEWSKSQKESKGYCAQY 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 SDLQSAVSILALTPQSNGTLTCVAT----WKSLKARKSATVNLTVIR------CPQD 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ELFIPSVNLVVAENEP------CEVTCLPSHWTWLPDISW-ELGLLVSHSSYYFVPEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 RGLYRSGMH------FLPVPECSKLPSMHQDP 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 SGNENSGYNSDEQKTTDTASLPPKSCES-----SDP 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 CCRRRCCGCN------CCCRCC-----FCCRRKRGFRIQFQKKSEKEKTNKETETE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 RGEVCDAVLVKDSLVFFNTSYPDPEEAQELLIHTAWNEL-----KAVSPLCRPAAEAL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 TGGGINIPGVLSSLPSLGFSLP------TWGKVGLGLAGTMLLTPTCTLTIRCC 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 MEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRP 62
                                                            APPLICATION NUMBER: US/08/644,271 FILING DATE: 10-MAY-1996
                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                               ZIP: 10591
                                                                                                                                                                                                                                                                                              CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Regeneron Pharmaceuticals, STREET: 777 Old Saw Mill Road
                                            CLASSIFICATION:
                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                     COUNTRY:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 868 amino acids amino acid
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                                                                                                                                                                                                                                                        USA
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                                                                                                                          FastSEQ Version 2.0
                                                                                                                                                                     IBM Compatible
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345-7721

NO: 1:
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21.0%; Pred. No. 0.037;
                                                                                                                                                   Dos
    USSN 60/008,657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --KEWLAMEGKTH 418
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                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09077955A Patent No. 6413740
                                             SEQ ID NO 1
LENGTH: 868
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/077,955A CURRENT FILING DATE: 1998-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS FILE REFERENCE: REG195-B-PCT-US
                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: PCT/US96/20696
EARLIER FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 08/644,271
                                                                                          SOFTWARE: Patentin Ver. 2.0
                                                                                                                      NUMBER OF SEQ ID NOS: 36
                                                                                                                                        EARLIER APPLICATION NUMBER: 60/008,657 EARLIER FILING DATE: 1995-12-15
                                                                                                                                                                                          EARLIER FILING DATE: 1996-05-10
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Valenzuela et al., David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 914-345-7400
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LENGTH: 868 amino acids
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ATTORNEY/AGENT INFORMATION:
ORGANISM: Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 -----NSRIAVLE------SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKLVKLEV 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 RVIDSRLQLFITKP---GLYTCIATNKHGEKFSTAKAAATVSIAEWSKSQKESKGYCAQY 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 SDLQSAVSILALTPQSNGTLTCVAT----WKSLKARKSATVNLTVIR------CPQD 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Cobert, Robert J
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 LCNHLFQECSPGVLPTPMPICREYCLAVKELFCA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 TGGGINIPGVLSSLPSLGFSLP------TWGKVGLGLAGTMLLTPTCTLTIRCC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 EVFARILRAPESHNVTFGSFVTLRCTAIGMP-----VPTISWIENGNAVSSGSIQENVKD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 MEPIITNDRFTSORYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMG 121
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1	Оy	Db Qy	Qу	Дb	Qу	Дy	Оy	¥. 8 0
•	313 419	268 374	220 321	173 264	122 209	63 164	4 113	Query Match Best Local Matches 8
	SGNENSGYNSDEQKTTDTASLPPKSCESSDP 343	CCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEKTNKETETE 312	TGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCC 267	SDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQD 219:	ELFIPSVNLVVAENEPCEVTCLPSHWTWLPDISW-ELGLLVSHSSYYFVPEP 172	MEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMG 121	GAMENRDPPGSGSGNEVIEGPONARVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRP 62 ::: ::: : : : : : : : : : : : : : :	9.7%; Score 118; DB 4; Length 868; Best Local Similarity 21.0%; Pred. No. 0.037; Matches 83; Conservative 42; Mismatches 151; Indels 120; Gaps 19;

Search completed: April 28, 2003, 21:12:19 Job time : 19.0485 secs

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OM protein - protein search, using sw model
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Maximum DB
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Listing first 45 summaries
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                    /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:
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1337.141 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Welcher AA,

Sarmiento UM, Schultz HJ,

Chute HT;

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ALIGNMENTS	AAU00905	AAU00904	AAR84094	AAU84351	ABB75752	AAU29315	ABB75753	ABB75751	ABG16336	AAB68421	AAG77856	AAG77858	AAG77857	AAW26506	AAW26611	AAW62572	AAR84091	AAW62573	AAR84092	AAW62568	AAR84087	AAW62583	AAW62569	AAR94982	AAW62575	AAR13144	069	AAY33498	AAR68553	ABB11587	AAY70469	AAW81030	AAM48745	AAU77543	AAE23219	
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ALIGNMENTS

AAU75541 standard; Protein; 386 AA

23-APR-2002 (first entry)

AAU75541;

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Human; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder.
                                                                                                                                                                                                                                                                                                                                 Human B7-like protein, B7-L_h2.
                                                                                                                         03-JAN-2002
                                                                                                                                                    WO200200710-A2
                            (AMGE-) AMGEN INC
                                                      28-JUN-2000;
28-NOV-2000;
                                                                                              28-JUN-2001; 2001WO-US20719
                                                                                                                                                                                Homo sapiens.
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2000US-0729264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc seminal vesicle hyperplasia in transgenic mice overexpressing B7-L CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian, cc cancer including seminal vesicle cancer, lung, brain, breast, ovarian, cc cancer and cancers of haematopoiettic system. B7-L polypeptide cancer and cancers of haematopoiettic system. B7-L polypeptide cc in allograft transplantation, graft versus host disease, T-cell ecl mediated diseases and autoimmune diseases. B7-L cc diseases involving chronic immune call dysfunction or to treat consumune diseases such as systemic lupus erythematosus, rheumatoid cc purpura and psoriasis, chronic inflammatory disease such as creating the symptoms associated with cc arthritis, multiple sclerosis, diabetes, immune thrombocytopenic cc inflammatory bowel disease, chronic inflammatory disease such as consumpressive agents for bone marrow and organ cc useful for disease stransplantation or to prolong graft survival. B7-L molecules are also useful for disease for any treating the survival and creative called a simulnosuppressive agents for bone marrow and organ creating the survival and creating and also are also a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and (extrinsic alveolitis), vasculopathies, coeliac disease, various pneumopathies thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the amino acid sequence of human B7-L_h2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                        241
                                                                                   241
                                                                                                                                           181
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                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                          121 GELFIPSVNLYVAENEPCEVTCLPSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for enhancing the immune response to tumours. (1) plays a regrowth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                         61 RPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prollferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVAGAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVAGAMENROPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSV 60
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                              PTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCCCCCCRRKRGFRIQFQKKS 300
PTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKS
                                                                                                               ILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSL 240
                                                                                                                                                                                                                                  GELFIPSVNLVVAENEPCEVTCLPSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVS
                                                                                                                                                                          ILALTPOSNGTLTCVATWKSLKARKSATVNLTVIRCPODTGGGINIPGVLSSLPSLGFSL
                                                                                                                                                                                                                                                                                                                                                    RPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 2088; DB 23; 100.0%; Pred. No. 8.8e-165;
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                molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic
                                                                                    seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L
purpura and psoriasis, chronic inflammatory
                                                                                                                                                                                                                                proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a rol growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                              conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) an
                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polypucleotide encoding it and antibody against (I) useful for treating B7-like polypeptide related disease, disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for diagnosing, preventing and treating reproductive, immu proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Fig 1; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New B7-like polypeptides, polynucleotides and their modulators,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Welcher AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABK13028
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28-NOV-2000; 2000US-0729264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-2001; 2001WO-US20719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W0200200710-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endocrinopathy; lymphoproliferative disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; B7-like protein; B7-L; antiinfertility; gynaecological; antiinformour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human B7-like protein, B7-L_h1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 PPRPASHPQASFNLASPEKVSNTTVV 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 EKEKTNKETETESGNENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQR 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sarmiento UM, Schultz HJ, Chute HT;
            diabetes, immune thrombocytopenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory bowel disease (Grohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restemosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of allergy, asthma and hypersensitivity reactions, treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the amino acid sequence of human B7-L_h1.
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                                                                                                                  Human; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antillcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; toxic shock syndrome; allergy; nephropathy; skin disorder;
                                                                                                                                                                                                                                                                                                                                Human B7-like protein, B7-L_h3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU75542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU75542 standard; Protein; 386 AA.
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                                                  Homo sapiens.
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                                                                                             endocrinopathy; lymphoproliferative disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSQRYDQGGNETSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRF 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGNENSGYNSDEOKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQASF 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.0%;
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Query Match Best Local Similarity Matches 371;

95.8%; 99.2%;

Length 386; Indels

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Conservative

 Mismatches Score 2000; DB 23; Pred. No. 1.7e-157;

В

133 AENEPCEVTCLPSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTL 192

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28-JUN-2000; 2000US-214512P.
28-NOV-2000; 2000US-0729264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seminal vesicle hyperplasia in transgenic mice overexpressing B7-L seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of polypeptide. Hence modulators of (I) are useful for the treatment of polypeptide in cancer and cancers of haematopoietic system. B7-L polypeptide testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L molecules are useful for alleviating the symptoms associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role in growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The polypeptide, polynucleotide encoding it and antibody against () useful for treating B7-like polypeptide-related disease, disorders conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Fig 3; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABK13030
                                      Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions, reatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the amino acid sequence of human B7-L_h3.
                                                                                                                                                                                                                                                                        are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis.
                                                                                                                                                                                                                                                                                                                                                                                 arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis) grave's disease, Hashimoto's thyroiditis and diabetes mellitus. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to an isolated B7-like (B7-L) polypeptide (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sarmiento UM,
     386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schultz HJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chute HT;
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RESULT 4
AAU75543
AID 75543
AID 75543
AID 75543
AID 75643
AID 75643
AID AAU77
AIC AAU7
AIX AAU7
AIX Huma
AIX Huma
AIX AAU7
AIX Huma
AIX AAU7
AIX AA
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                 The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) as useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role growth and maintenance of cancer cells based on the observation of
seminal vesicle hyperplasia in transgenic mice overexpressing
                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Fig 4; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antiinflammatory; dermatological; antipsoriatic; netallergic; antiasthmatic; nephrotropic; antithyroid; antiulcer; antiallergic; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABK13031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Welcher AA, Sarmiento UM,
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28-NOV-2000; 2000US-0729264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human B7-like protein, B7-L_h4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 NLASPEKVSNTTVV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 NLASPEKVSNTTVV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 SGNENSGYNSDEQKTTETASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQASF 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 TMLLTPTCTLTIRCCCCRRCCGCNCCCRCCFCCRKRGFRIQFQKKSEKEKINKETETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-130881/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
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                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
             Homo sapiens
                                                                                                                               Novel human diagnostic protein #28160.
                                                                                                                                                                                   18-FEB-2002 (first entry)
                                                                                                                                                                                                                                             ABG28169;
                                                                                                                                                                                                                                                                                    ABG28169 standard; Protein; 463
                                                                                                                                                                                                                                                                                                                                                                                                                      298
                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 EKEKTNKETETESGNENSGYNSDEQKTTDTASLP 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GELFIPSVNLVVAENEPCEVTCLPSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RPMEPIITNDRETSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVAGAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVAGAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKS
                                                                                                                                                                                                                                                                                                                                                                                                         QTKKLRQKVEMKT---PATIQMNKRPQTPLLSLP 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPMEPIITNDRFTSQRYDQGGNLTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.5%; Score 1576; DB 23; 88.6%; Pred. No. 2.4e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnosetics foreneins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 58528; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                           109 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTWLPDISWELGLLVSHSSYYF 168
                                                                            121 VPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPG 180
                                                                                                                                                                               169 VPEPSDLQSAVSILALTEQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPG 228
                                                                                                                                                                                                                                      61 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYF 120
                                                                                                                                                                                                                                                                                                                                                          49 MWALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSR 108
241 KRG
                                        289 KRG 291
                                                                                                                                                                                                                                                                                                                                                                                                                     Loca.
                                                                                                                                                                                                                                                                                                                   1 MWALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSR 60
                                                                                                                   VLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRR 288
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          63.1%;
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Score 1318; DB 22;
pred. No. 7.6e-101;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT 6

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AAU75544
ID AAU7
              seminal vesicle hyperplasia in transgenic micro overexpressing B7-L cc seminal vesicle hyperplasia in transgenic micro overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cc cancer including seminal vesicle cancer, lung, brain, breast, ovarian, cc cancer including seminal vesicle cancer, lung, brain, breast, ovarian, cc maintenance and cancers of haematopoietic system. B7-L polypeptide cc pathway can be manipulated to regulate cytotoxic T-lymphocyte response cc pathway can be manipulated to regulate cytotoxic T-lymphocyte response cc molecules are useful for alleviating the symptoms associated with cc diseases involving chronic immune cell dysfunction or to treat conformation of the conformation of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antitumour; cytostatic; immunosuppressive; antiatthrilic; antirheumatic; antiloflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antilocer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) are useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and miscarriage, preterm labour and delivery and endometriosis) are extracellular domains and other regulators of B7-L polypeptides are extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role in growth and maintenance of cancer cells based on the observation of growth and maintenance of cancer cells based on the observation.
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28-NOV-2000; 2000US-0729264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Fig 5; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-130881/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New B7-like polypeptides, polynucleotides and their modulators, to for diagnosing, preventing and treating reproductive, immune and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABK13032
nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schultz HJ, Chute HT;
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                                                                                                                                                                                                                               Rat; B7-like protein; B7-L; antiinfertility; gynaecological; antilumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antihyroid; antiulcer; antilalergic; antiasthmatic; nephrotropic; antibacterial; virucide; tunur; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder;
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            (AMGE-) AMGEN INC.
                                         28-JUN-2000; 2000US-214512p
28-NOV-2000; 2000US-0729264
                                                                                          28-JUN-2001; 2001WO-US20719
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                                                                                                                                                                                                                                                                                                                                                                                   Rat B7-like protein, B7-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU75547 standard; Protein; 631 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 PRVSFDIASPQKVRNVTLV 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 POASFNLASPEKVSNTTVV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 ETKLKSGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSSL--PYQELNKHQPGPATH 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the amino acid sequence of mouse B7-L_m1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 MLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRKRGFRIQFQ---KKSEKEKTNK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 CVAELKDLQASKSLTVNLTVVQPPPD------SIGEEGPALPTWAIILLAVAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 CVATWKSLKARKSATVNLTVIRCPODTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 ENEPCEVTCLPSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 SGSGNEVIEGPONARVLKGSQARENCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETETESGNENSGYNSDEOKTIDTASLPPKSCESSDPEORNSSCGPPHQRADQRPPRPASH 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGEPCNVTCYAVGWTSLPDISWELEVPVSHSSYNSFLEPGNFMRVLSVLDLTPLGNGTLT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSSYQIIEGPQNVTVLKDSEAHFNCTVTHGWKLLMWTLNQMVVLSLTTQGPIITNNRFT 80
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                                                                                                                                                                                                                             lymphoproliferative disorder.
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cc seminal vesicle hyperplasia in transgenic mice overexpressing B7-L CS seminal vesicle hyperplasia in transgenic mice overexpressing B7-L CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian, CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian, CC pathway can be manipulated to regulate cytotoxic T-lymphocyte response CC in allograft transplantation, graft versus host disease, T-cell CC diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid CC autoimmune diseases such as systemic lupus erythematosus, rheumatoid CC arthritis, multiple sclerosis, diabetes, immune thrombocytopenic CC diseases involving chronic inflammatory disease such as Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They CC are also useful as immunosuppressive agents for bone marrow and organ cuseful for diagnosis and treatment of diseases involving abnormal cell CC Antagonists of B7-L polypeptides are useful for allery asthma and hypersensitivity reactions, and for comphropathies (e.g. glomerulonephritis), skin disorders (pemphigous and cell furnombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and cell furnombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and cell symphoproliferative disorders such as multiple myeloma. The present xx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role in growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, disorders conditions including reproductive disorders (e.g. infertility,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and prolliferative disorders, e.g. cancer and arteriosclerosis
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(I) are

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Matches
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309 SHSLSVRADFPTPNITEYGNPSADIKRITCFASGGFPKPRLSWLENGRELNSYNSFLEPG 368
                                                                                   249 QRYEGGSYVVKHLTTVEVMGTLNIPSNNLIVTEGEPCNVTCYAVGWTSLPDISWELEVPV
                                                                                                                           116 -----TVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTWLPDISWELGLLV 161
                                                                 162 SHS----
                                                                                                                                                                      189 ELIIHDVQPSDSGSVQCSLQNSHGFGSAFLSVQVYDIANNYSFSLLGLILSDRGTYTCVV 248
                                                                                                                                                                                                                                                         129 KALLSCDYKFCSEEQSIHRIYWQKHDKWYLSVISGVPEVWPKYKNRTTYASYNSTDSFIS 188
                                                                                                                                                                                                               86 EMIIHNVEPSDSGNIRCSLONSRLHGSAYL------ 115
                                                                                                                                                                                                                                                                                                                                          69 SGIVGQVSKSVRNVTVLKDSEAHFNCTVTHGWKLLMWTLNQMVVLSLTTQGPIITNNRFE 128
                                                                                                                                                                                                                                                                                                                                                                                 14 SGSGNEVIEGPONARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRF- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.4%; Score 572.5; DB 27.8%; Pred. No. 7.1e-39
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                                                                                                                                                                                                                                                                                                      -----TSQRYDQGGNFTS
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                                             -----SYYFVPEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 631;
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     antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirherantiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antilicer; antiallergic;
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The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role growth and maintenance of cancer cells based on the observation of
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28-NOV-2000; 2000US-0729264.
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                                                                                                                                                                                                                              for diagnosing, preventing and treating reproductive, imm proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                 Welcher
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                                                                                                                                                                                          Claim 13; Fig 6; 135pp; English.
                                                                                                                                                                                                                                                                New B7-like polypeptides, polynucleotides and their modulators, useful
                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGKENYGYSSDECITVKFRRCFRRNEASRETNKNLYIGPVEAAAEQ 629
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                               plays a role in
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                                                                                                                                                                                                                                                                                                                                           дb
XEXTXXX
                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions, treatment of e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), crave's disease, Hashimoto's thyroiditis and diabetes mellitus. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             testicular cancer and cancers of haematopoletic system. B7-L polypeptic pathway can be manipulated to regulate cytotoxic T-lymphocyte response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecules are useful for alleviating the symptoms associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lymphoprolliferative disorders such as multiple myeloma. The present sequence represents the amino acid sequence of mouse B7-L_m2.
                    Mouse B7-like protein, B7-L_m3
                                                               23-APR-2002 (first entry)
                                                                                                                                                  AAU75546 standard; Protein; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 MLLTPTCTLTIRCCCCRRRCCGCNCCCCRCCFCCRRKRGFRIQFQ---KKSEKEKTNK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 CVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGT
                                                                                                                                                                                                                                                          252
                                                                                                                                                                                                                                                                                                                                             194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 SGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRFT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rocar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YASYNSTDSFISELIIHDVQPSDSGSVQCSLQNSHGFGSAFLSVQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGSSYQIIEGPQNVTVLKDSEAHFNCTVTHGWKLLMWTLNQMVVLSLTTQGFIITNNRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENEPCEVTCLPSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLT 193
                                                                                                                                                                                                                                                          PRVSFDIASPQKVRNVTLV
                                                                                                                                                                                                                                                                                                PQASFNLASPEKVSNTTVV 386
                                                                                                                                                                                                                                                                                                                                           ETKLKSGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSSL--PYQELNKHQPGPATH
                                                                                                                                                                                                                                                                                                                                                                                 ETETESGNENSGYNSDEOKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASH 367
                                                                                                                                                                                                                                                                                                                                                                                                                               LLLILIVLIIIFCCC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.18; 34.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 566.5; DB 23; Pred. No. 7.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                   --CASRREKEESTYQNEIRKSANMRTNKADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----DSIGEEGPALPTWAIILLAVAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /.7e-39;
71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            breast, ovarian,
m. B7-L polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307
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Qγ

Matches

118;

Conservative

37;

Pred. No. 3.4e-32; 7: Mismatches 45;

Indels

176;

Gaps

6

31.4%;

Best Local Similarity

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The polypertide, polypucies tide encoding it and antibody against (I) are C useful for treating B7-like polypeptide-related disease, disorders or CC conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and CC proliferative disorders. Antibodies, soluble proteins comprising CC extracellular domains and other regulators of B7-L polypeptides are CC useful for enhancing the immune response to tumours. (I) plays a role in CC growth and maintenance of cancer cells based on the observation of CC seminal vesicle hyperplasia in transgenic mice overexpressing B7-L CC polypeptide. Hence modulators of (I) are useful for the treatment of CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide CC pathway can be manipulated to regulate cytotoxic T-lymphocyte response CC in allograft transplantation, graft versus host disease. B7-L CC diseases involving chronic immune cell dysfunction or treat with CC diseases involving chronic immune cell dysfunction or treat treatment of conservations. The conservation of treatment of the conservation of the 
                                    nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the amino acid sequence of mouse B7-L_m3.
                                                                                                                                                                                                                                               proliferation, including arteriosclerosis and vascular rescenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoridasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They
                                                                                                                                                                                                                           treatment of allergy, asthma and hypersensitivity reactions
                                                                                                                                                                                                                                                                                                                                                                                       are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated B7-like (B7-L) polypeptide (I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Fig 7; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABK13034.
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28-NOV-2000; 2000US-0729264
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reproductive disorder; graft versus host disease; autoimmune disease;
toxic shock syndrome; allergy; nephropathy; skin disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiucer; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Welcher AA, Sarmiento UM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-130881/17
                                                                                                                                                                                                                                                                                                                           for diagnosis and treatment of diseases involving abnormal cell aration, including arteriosclerosis and vascular restenosis.
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Query Match

23.2%;

Score 485;

DB 23;

Length 223

Sequence

223 AA;

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8X 200000
                                                                                                                          DR PT PT XXX
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PI
XX
                                                                                                                                                                                                                                                                                                              Дb
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The present invention describes a material for extracorporeal circulation which is made from a water-insoluble carrier immobilized with a protein having the sequence shown here. The materials of the invention, including adsorbents, are for extracorporeal circulation, which are applicable in the selective elimination of diabetic complication factors from a body
                                                                                                                                   Material for extracorporeal circulation, applicable in selective elimination of diabetic complication factors such as carbonyl stress products caused by abnormally promoted carbonyl stress from excretory dysfunction in vascular lesions
                                                                                                     Claim 1; Page 31-32; 36pp; Japanese.
                                                                                                                                                                                                                                                            Shimizu S,
                                                                                                                                                                                                                           WPI; 2001-290314/30.
                                                                                                                                                                                                                                                                                            (TORA ) TORAY IND INC
                                                                                                                                                                                                                                                                                                                            08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                         08-SEP-2000; 2000WO-JP06172
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extracorporeal circulation; carbonyl stress product; receptor; diabetes; vascular lesion; excretory dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                            WO200118060-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracorporeal circulation material receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB81925 standard; protein; 404 AA
                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 SFDIASPQKVRNVTLV 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 TESGNENSGYNSDEOKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 MILTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEKINK---ETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 YASYNSTDSFISELIIHDVQPSDSGSVQCSLQNSHGFGSAFLSVQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 SGSGNEVIEGPONARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRFT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKSGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSSL--PYQELNKHQPGPATHPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFNLASPEKVSNTTVV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENEPCEVTCLPSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGSSYQIIEGPQNVTVLKDSEAHFNCTVTHGWKLLMWTLNQMVVLSLTTQGPIITNNRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kubota M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                          99JP-0254463
                                                                                                                                                                                                                                                       Akiyama н,
                                                                                                                                                                                                                                                         Usui M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --RTNKADPETK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fluid, and are therefore useful in treating vascular lesions like arteriosclerosis due to carbonyl stress products caused by abnormally promoted carbonyl stress from excretory dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human receptor for advanced glycosylation end product (RAGE) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE23219 standard; Protein; 404 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 AYLTYQVMGELFIP----SVNLVVAENEP------CEVTCLPSHWTWLPDIS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 KPLVPNEKGVSVKEQTRRHPETGLFTLQSELM---VTPARGGDPRPTFSCSFSPGLPRHR 218
                                                                                                                                                                                                                                                                                                                                                                    Human; Receptor for advanced glycosylation end product; RAGE; cardiant; tissue growth; neointimal formation; blood vessel; restenosis; diabetes; myocardial infarction; angioplasty; peripheral vascular surgery; angina; transgenic animal; acute thrombotic stroke; venous thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 RCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT-----PTCTLTIRCC 267
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                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 -----QSEEPEAGESSTGGP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 KTTDTASLPPKSCESSDPEQRNSSCGPP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 CCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEKT--NKETETESGNENSGYNSDEO 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 EPITTNDRETS-----QRYDQGGNFT--SEMIIHNVEPSDSGNIR----CSLQNSRLHGS 112
                                                                                                                                                                                                                 13-OCT-2000; 2000US-0687528.
                                                                                                                                                                                                                                                                              18-APR-2002
                                                                                                                                                                                                                                                                                                              WO200230889-A2
                                         Inhibiting new tissue growth or neointimal formation in blood vessels of subject suffering from diabetes, stroke and preventing restenosis, comprises administering inhibitor of receptor for advance glycation end
                                                                                                                                                     Stern DM, Schmidt A,
                                                                                                                                                                                                                                             12-OCT-2001; 2001WO-US32036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
Disclosure; Page 16; 43pp; English
                                                                                                        N-PSDB; AAD36952
                                                                                                                                                                                   (UYCO ) UNIV COLUMBIA NEW YORK.
                               product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WMKD-----GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISII 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALRTAPIQPRVWEPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIH 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77;
                                                                                                                         2002-426260/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               404 AA;
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                                                                                                                                                          Marso S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------QRRGEERKAPENQEEEEERAELN------
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                                                                                                                                                           Topol E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 404;
                                                                                                                                                             Lincoff AM;
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Ax The invention relates to a method for inhibiting new tissue growth or CC neointimal formation in blood vessels in a subject that has experienced CC blood vessel injury and preventing exaggerated restenosis in a diabetic CC subject. The method comprises administering an inhibitor of receptor for CC experience of system of the method comprises administering an inhibitor of receptor for CC preventing restenosis in the subject. The method is useful for inhibiting CC preventing restenosis in the subject. The method is useful for inhibiting CC like non-human animal, a transgenic non-human animal or a human suffering CC indiabetes, acute thrombotic stroke, venous thrombosis, unstable from diabetes, acute thrombotic stroke, venous thrombosis, unstable compand, myocardial infarction, abrupt closure following angioplasty or the method is also useful for preventing restenosis and for determining CC whether a compound inhibits new tissue growth in a blood vessel in a CC subject. The present sequence is human receptor for advanced CC glycosylation end product (RAGE) protein.
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AAU77543
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU77543 standard; Protein; 404 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 KPLVPNEKGVSVKEQTRRHPETGLFTLQSELM---VTPARGGDPRPTFSCSFSPGLPRHR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219
                                                                                                                                                                              cerebral vasoconstriction suppressor; cerebral blood flow enhancer; cerebral amyloid anglopathy; transgenic animal; amyloid beta precursor; Alzheimer's disease; Down's syndrome; head trauma; stroke; human
                                                                                                                                                                                                                                                                                                     Human receptor for advanced glycosylation end product (RAGE)
                                                                                                                                                                                                                                                                                                                                                                                             AAU77543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 WMKD-----GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISII
                                                                                                                                                                                                                                         Receptor for advanced glycation end product; RAGE; receptor; amyloid beta peptide; blood-brain barrier; neurovascular stress;
                                                                                                                                                                                                                                                                                                                                                      05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 E-PGEEG------PTAGSYGGSGLGTLALALGILGGLGTAALLIGVI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 RCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT------PTCTLTIRCC 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 CCRRRCCGCNCCCRCCFCCRKRGFRIQFQKKSEKEKT--NKETETESGNENSGYNSDEQ 325
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                                                             21-FEB-2002.
                                                                                                   WO200214519-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 KTTDTASLPPKSCESSDPEQRNSSCGPP 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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23.5%; Pred. No. 0.001;
1tive 34; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 404;
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14-AUG-2001; 2001WO-US25416

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a method of ameliorating neurovascular stress, CC and decreasing cerebral vasoconstriction in subject suffering from CC chronic or acute cerebral amyloid angiopathy, comprising administering CC an inhibitor (I) of receptor for advanced glycation end product (RAGE). CC harrier, thus decreasing cerebral vasoconstriction and increasing CC subject, decreasing cerebral vasoconstriction and increasing CC subject, decreasing cerebral vasoconstriction in a transgenic non-human CC animal (preferably, transgenic mouse overexpressing mutant human amyloid cerebral amyloid angiopathy, preferably, Alzheimer's disease, and for CC ameliorating neurovascular stress is caused by Alzheimer's disease, aging, Down's syndrome, head trauma or stroke. This is the CC amino acid sequence of human receptor for advanced glycation end
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                                  02-APR-2002 (first entry)
Human RAGE protein SEQ ID NO 1.
                                                                                 AAM48745;
                                                                                                           AAM48745 standard; protein; 404 AA.
                                                                                                                                                                                                          390 -----QSEEPEAGESSTGGP 404
                                                                                                                                                                                                                                               326 KTTDTASLPPKSCESSDPEQRNSSCGPP 353
                                                                                                                                                                                                                                                                                                              268 CCRRCCGCNCCCRCCFCCRKKRGFRIQFQKKSEKEKT--NKETETESGNENSGYNSDEQ 325
                                                                                                                                                                                                                                                                                                                                                    322 E-PGEEG------PTAGSVGGSGLGTLALALGILGGLGTAALLIGVI 361
                                                                                                                                                                                                                                                                                                                                                                                       215 RCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT-----PTCTLTIRCC 267
                                                                                                                                                                                                                                                                                                                                                                                                                               271 WMKD------GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 WELGILVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 ALRTAPIQPRVWEPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIH 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 AYLTVQVMGELFIP----SVNLVVAENEP------CEVTCLPSHWTWLPDIS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 KPLVPNEKGVSVKEQTRRHPETGLFTLQSELM---VTPARGGDPRPTFSCSFSPGLPRHR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 16; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amellorating neurovascular stress and decreasing cerebral vasoconstriction in subject suffering from chronic/acute cerebral amyloid angiopathy, by administering inhibitor of receptor for advanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 EPIITNDRFTS-----QRYDQGGNET--SEMIIHNVEPSDSGNIR----CSLQNSRLHGS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYCO ) UNIV COLUMBIA NEW YORK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 7.0%; Score 145.5; DB 23; LengLii 404, Similarity 23.5%; Pred. No. 0.001; 34; Mismatches 94; Indels 123; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to detecting receptor for advanced glycated endproducts (RAGE) modulators comprises determining the amount of RAGE protein or its fragment bound to the pre-adsorbed ligand by measuring the amount of anti-RAGE antibody bound to the solid surface. The method is modulate RAGE in the compounds are useful for rapid, high-throughput identification of compounds that and symptoms of diabette are useful for treating symptoms of diabettes disease, cancer, inflammation, kidney failure, systemic lupus nephritis or inflammatory lupus nephritis, erectile dysfunction and
          390 -----
                                326 KTTDTASLPPKSCESSDPEQRNSSCGPP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                  268 CCRRRCCGCNCCCRCCFCCRKRGFRIQFQKKSEKEKT--NKETETESGNENSGYNSDEQ 325
                                                                                                                                           322 E-PGEEG------PTAGSVGGSGLGTLALALGILGGLGTAALLIGVI 361
                                                                                                                                                                                215 RCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT-----PTCTLTIRCC 267
                                                                                                                                                                                                                                                         155 WELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVI 214
                                                                                                                                                                                                                    271 WMKD------GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISII 321
                                                                                                                                                                                                                                                                                                219 ALRTAPIQPRVWEPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIH 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a receptor for advanced glycated endproducts (RAGE) modulators, for treating e.g., cancer, diabetes or inflammation, comprises measuring the amount of bound anti-RAGE antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-114372/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; RAGE; receptor for advanced glycated endproduct; receptor; antidiabetic; neuroprotective; cytostatic; antiinflammatory; vasotropic; nephrotropic; dermatological; antiarteriosclerotic; nootropic; diabetes; Alzheimer's disease; cancer; inflammation; kidney failure; systemic lupus; nephritis; erectile dysfunction; atherosclerosis.
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05-MAR-2001; 2001US-0799152.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77;
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-QSEEPEAGESSTGGP 404
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                                                                 -QRRGEERKAPENQEEEEERAELN-----
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RESULT 14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MG50; melanoma gene-50; melanoma associated antigen; human;
T cell epitope; cancer; lung cancer; rhabdomyosarcoma; diagnosis;
                                                                                                                                                                                                                                                                                                          or an MG50 T cell epitope, recombinant vectors, and antigen presenting cells. Methods are provided for identifying an MG50 melanoma associated antigen in an individual and for identifying an immune response against an MG50 melanoma associated antigen, as well as methods of stimulating T lymphocytes that are reactive against cancer cells expressing MG50 and for treating an individual having cancer cells that express MG50. The products and methods can be used for the detection, treatment and prevention of MG50-expressing cancers, e.g. melanomas, lung cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide comprises a portion of a new human melanoma associated antigen, designated MG50. The amino acid sequence was deduced from a cDNA clone (see AAV9992) isolated from melanoma cell line MSM M-1 cDNA by subtractive hybridisation. The 5' region MG50 cDNA was not obtained. MG50 mRNA has been detected in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New MG50 melanoma associated antigen fragments - used to develop products for the detection, treatment and prevention of MG50-expressing cancers, e.g. melanoma, lung cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           melanoma, lung carcinoma and rhabdomyosarcoma cells, foetal brain, foetal heart and human placenta. The invention also provides T cell epitopes (see AAW81031-54) from MG50, including cytotoxic and helper T cell epitopes, antibodies that specifically bind to MG50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 45-49; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rhabdomyosarcoma
                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                rhabdomyosarcoma
115 LTVQVMGELFIPSVNLVVAENE----PCEVTCLPSHWTWLPDISW-ELGLLVSHSSYYFV 169
                                    399 PLPVDPRVNITPS------GG-----LYIQNVVQGDSGEYACSATNNIDSVHATAF 443
                                                                                                         339 VAGEVKTQEVTLRYFGSPARPTFVIQPQNTEVLVGESVTLECSATGHPPPRISWTRGDRT 398
                                                                                                                                            2 VAGAMENRDPP----GSGSGNEVIEGPQNARVLKGSQARFNCTVS-QGWKLIMWALSDMV 56
                                                                                                                                                                                                      Cal
                                                                     VLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNS--RLHGSAY 114
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kan-Mitchell J,
                                                                                                                                                                                                                                                             1496 AA;
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0870941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US11533.
                                                                                                                                                                                                      6.6%; Score 138; DB 20; Length 1496; 25.1%; Pred. No. 0.022;
                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minev BR,
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitchell MS;
                                                                                                                                                                                        127; Indels
                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region
                                                                                                                                                                                          Gaps
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QУ
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     Вb
The present sequence is the protein encoded by PRG2 gene, that is upregulated in response to induction of p53 activity in human colon cancer EB1 cells. This sequence is the human homologue (hPxn) of Drosophila peroxidasin gene dPxn, that is expressed in heart, placenta, spleen, ovary and intestines. PRG2 is involved in p53-mediated growth suppression pathways and plays a role in redox regulation. It is a suppression pathways and plays a role in redox regulation. It is a ham-peroxidase that increases the intracellular content of reactive oxygen species (ROS). They are potential targets of p53 regulatory activity and are useful for modulation of cellular proliferation. PRG2 gene is localised to human chromosome 2p24.3. The PRG target molecules, have cytostatic and immunomodulatory activity. PRG polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRG2; p53 target; human; modulate; cell proliferation; immunomodulatory; chromosome 2p24.3; cytostatic; gene therapy; tumour cell; inducer; diagnosis; therapeutic; proliferative disease; cell cycle arrest; cancer; treatment; apoptosis; knockout animal; cancer susceptibility; dPxn; hPxn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY70469 standard; Protein; 1496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human p53 target molecule, PRG2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY70469
                                                                                                                                                                                                                                                     New p53-inducible isolated nucleic acid molecule including open reading frame encoding human homolog of Drosophila melanogaster peroxidasin, useful e.g. in detection and treatment of cancer \dot{}
                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ51671
                                                                                                                                                                                                                                                                                                                                                                                  Horikoshi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200012526-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          608 RYECVARNTIG 618
                                                                                                                                                                                                                      Disclosure; Page 71-74; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   (UYPR-) UNIV PRINCETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEVGANVQLP-----CSSQGEPEPAITWNKDGVQVTESGKFHISPEGFLTINDVGPADAG 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSSGTLR--ISGVALHDQ--GQYECQAV--NIIGSQKVVAHLTVQPRVTPVFASIPSDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RCCCCRRRCCG 275
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                                                                                                                                                                                                                                                                                                                                                  2000-246724/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         redox-regulation; reactive oxygen species; ROS.
                                                                                                                                                                                                                                                                                                                                                                                    Shenk T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0098251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US19551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Mature_human_PRG2_protein
/note= "Homologue of Drosophila peroxidasin, dPxn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..1496
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Search completed: April 28, 2003, 18:14:31 Job time: 41.4662 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.6%; Score 138; DB 21; Length 1496; Best Local Similarity 25.1%; Pred. No. 0.022; Matches 78; Conservative 38; Mismatches 127; Indels 68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins and antibodies are useful as diagnostic and therapeutic agents for detection and treatment of cancer and other proliferative diseases. The gene/CDNA may be used for gene therapy, to restore a gene function downstream of p53, that cannot be activated in the p53-deficient tumour cell. Antibodies can be used as inducers of cell cycle arrest and/or apoptosis. The DNA sequences can be used to generate 'knockout' animals as a model of cancer susceptibility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                 608 RYECVARNTIG 618
                                                                                                                                                                                  553 VEVGANVQLP-----CSSQGEPEPAITWNKDGVQVTESGKFHISPEGFLTINDVGPADAG 607
                                                                                                                                                                                                                                                                            499 LSSGTLR--ISGVALHDQ--GQYECQAV--NIIGSQKVVAHLTVQPRVTPVFASIPSDTT 552
                                                                                                                                                                                                                                                                                                                                                                           444 IIVQALPQFTVTPQDRVVIEGQTVDFQCEAKGNPP-----PVIAWTKGGSQLSVDRRHLV 498
                                                                                                                                               265 RCCCCRRRCCG 275
                                                                                                                                                                                                               221 ---GGGINIPGVLSSLPSLGFSLP--TWGKVGLGL--AGTMLLTPTCTLTI------ 264
                                                                                                                                                                                                                                                                                                                             170 PEPSDLQSAVSILALIPQSNGTLTCVATWKSLKARKSATVNLTV------IRCPQDT- 220
                                                                                                                                                                                                                                                                                                                                                                                                                         115 LTVQVMGELFIPSVNLVVAENE----PCEVTCLPSHWTWLPDISW-ELGLLVSHSSYYFV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 PLPVDPRVNITPS-----GG-----LYIQNVVQGDSGEYACSATNNIDSVHATAF 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 VAGEVKTQEVTLRYFGSPARPTFVIQPQNTEVLVGESVTLECSATGHPPPRISHTRGDRT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 VLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNS--RLHGSAY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAGAMENRDPP----GSGSGNEVIEGPQNARVLKGSQARFNCTVS-QGWKLIMWALSDMV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1496 AA;
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GenCore version 5.1.4_p5_4578 copyright (c) 1993 - 2003 compugen Ltd.
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OM protein - protein search, using sw model

Run on: April 28, 2003, 16:24:32; Search time 37.1283 Seconds (without alignments) 2142.147 Million cell updates/sec

US-09-729-264-6 2077

Title:
Perfect score:
Sequence: 1 MERHLLTVPEAVGSGSGNEV......HPQASFNLASPEKVSNTTVV 386

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: Searched: 671580 seqs, 206047115 residues 671580

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:* sp_phage:*
sp_plant:*
sp_rodent:* sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:* sp_human:*
sp_invertebrate:* sp_organelle:* sp_mhc:* sp_mammal:* sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

Result No.	Score	Query Match	Length DB	DB	ID	Description
1	1694	81.6	315	4	Q9NSI5	OMO
N	579.5	27.9	270	11	Q9D8G2	Q9d8g2 mus musculu
ω	142.5	6.9	344	13	Q9DF61	Q9df61 gallus gall
4	141	6.8	168	11	Q9D9I2	Q9d9i2 mus musculu
U I -	137.5	6.6	315	13	Q9DGI5	
σ	137.5	6.6	344	11	Q99PJ0	
7	137.5	6.6	344	13	093242	
œ	136.5	6.6	173	11	Q9D4K2	Q9d4K2 mus musculu
9	135	6.5	1496	4	Q92626	Q92626 nomo sapien
10	133.5	6.4	344	4	Q9P121	Q9p121 nomo sapien
11	133	6.4	1427	13	Q91562	
12	131	6.3	697	11	Q9DBP0	Q9dbQ mus muscuru
13	131	6.3	697	11	Q9Z290	2222 mus muscuru
14	129.5	6.2	164	U	Q22048	Q22048 Caenornabur
15	129	6.2	6632	υī	001761	OUI/61 caenornabur
16	128	6.2	1445	11	Q63155	Q63155 Fattus norv

ALIGNMENTS

Length 315;

0;

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RA Kawal J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashizaki Y.;
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Best Local Similarity
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                     Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AK008060; BAB25436.1; - EMBL; BC004806; AAH04806.1; -
                                                                               Strausberg R.
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                           Nature 409:685-690(2001).
                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9D8G2;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9D8G2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 MLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEKTNKETETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLT
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MGI:1919308; 2010003D20Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNENSGYNSDEQKTT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLESLETWGKVGLGLAGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNENSGYNSDEQKTT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEKTNKETETES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGSGNEVIEGPQNARVLKGSQARENCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRFT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1694; DB 4; Pred. No. 7.3e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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DR
DR
SQ
                                                      InterPro; IPR003006; I9_MHC. Pfam; PF00047; 19; 3. SMART; SM00409; IG; 3. SMART; SM00408; IGC2; 3. SMART; SM00410; IG_1ike; 2.
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                                                                                                                                                                                                                                                                            MEDLINE-20499204; PubMed=11042360; Lodge A.P., Howard M.R., McNamee C.J., Moss D.J.; "Co-localisation, heterophilic interactions and regulated expression of IgLON family proteins in the chick nervous system."; Brain Res. Mol. Brain Res. 82:84-94(2000).

EMBL; AF292934; AAG01877.1; -...
                                                                                                                                                                        InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
         Immunoglobulin domain.
SEQUENCE 344 AA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBCAM alpha 1 isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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PROSITE; PS00290; IG_MHC; UNKNOWN 1.

SEQUENCE 270 AA; 29604 MW; A39C273DAA950DFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
SMART: SM00409; IG; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 QRPPRPASHPQASFNLASPEKVSNTTVV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 NMRTNKADPETKLKSGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSSL--PYQELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 IILLAVAFSLLLILIIVLIIIFCCCC------CASRREKEESTYQNEIRKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 KVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQ---KKSE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 TPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 IPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILAL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
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      37531 MW;
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16,
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Last annotation update)
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37FE6051CBF0E7B4 CRC64;
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PRESULT 4
Q9D912
ID Q9D9
ID Q9D9
AC Q9D9
DT Q1----
DT Q1---
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schaim I.M., Staubii F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazazarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashiraki Y.;
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Best Local Similarity
                                                                                                                                                       Matches
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-11217851;
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                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
EMBL; AK006892; BAB24782.1; -.
MGD; MGI:1913992; 4931420D14Rik.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHS 164
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 ----SVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 RLLFLVPAGVPVRSGDATFPKAMDNVTVRQGESATLRCTVDDRVRRVAW-LNRSTILYAG 78
3 RHLLTVPEAVGSGSGNEVI-EGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVL--- 58
                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDKWSIDNRVVILSN---TKTQY-----SIKIHNVDVYDEGPYTCSVQTDNHPKTSR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGASVGQKGILQCEASAVPVAEFQ---WFKEDTRLA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72; Conservative
                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                           168 AA;
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.9%; Score 142.5; DB 1
26.1%; Pred. No. 0.00014;
                                                                                                                                                                                                                                                                                                       18931 MW;
                                                                                                                                                                                      6.8%; Score 141; DB 11; Length 168; 32.0%; Pred. No. 7.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Mismatches 110; Indels 59; Gaps
                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                   7A2BD279612A5E94 CRC64;
                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 344;
                                                                                                                                                                       49;
                                                                                                                                                                       Indels
                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
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ij Q99PJ0 RESULT 6

099РJ0

Q99PJ0; 01-JUN-2001 (TrEMBLrel. 17, Created)

PRELIMINARY;

PRT;

344 AA

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Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003598; I9_C2.
InterPro; IPR003600; I9_11ke.
InterPro; IPR003006; I9_MHC.
InterPro; IPR003006; I]
Ffam; PF00047; Iq; 3.
SMART; SM00408; IGc2; 3.
SMART; SM00410; IG_11ke; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9DGI5;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9DGI5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterisation of CEPU-Se, a secreted isoform of the IgLON family protein CEPU-1.", Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF292936; AAG01879.1; "...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEPU-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEPU-Se alpha 1 isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 AS 167
                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain. SEQUENCE 315 AA; 34606 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 LTRSQLELIEPE--PTMALEPSEITVAFFSHKNANVSDP----EEVPPCLDSDPFPNGDL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 NENSGYNSDEQKTTETASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQASFNL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003599;
                                                                                                 166 YYFVPEDSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV----IRCDQDT 220
232 GVPVGQKGILMCEASAVPSADFQ---WYK 257
                                                                                                                                       127
                                                                                                                                                                        108
                                  221 GGGINIPGVL----SSLPSLGFSLPTWGK 245
                                                                                                                                                                                                         80
                                                                                                                                                                                                                                       54 DMYVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NS 107
                                                                                                                                                                                                                                                                          20 RLLELVPAGVPVRSGDATFPKAMDNVTVRQGESATLRCSVDNRVTRVAWLNRSSILYAGN 79
                                                                                                                                                                                                                                                                                                                                                        Match 6.6%; Score 137.5; DB 13; Length 315; Local Similarity 26.0%; Pred. No. 0.00036;
                                                                                                                                                                                                                                                                                                         3 RHLLTVPEAVGSGSGNEVI-EGPQNATVLKGSQARFNCTVSQ-----GW---KLIMWALS 53
                                                                                                                                                                    RLHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPD--ISWELGLLVSHSS 165
                                                                                                                                                                                                       DKWCLDPRVVLLANTKTQYSIQ------IHDVDVYDEGPYTCSVQTDNHPKTS 126
                                                                    VGFISEDEVLE----ITGITREQSGEYECSAS-NDVAAPVVQRVKVTVNYPPYISDAKST
                                                                                                                                      RVH----LIVQVSPKITEISSDISINEGGNVSLTCIA---TGRPDPTITWR---HISPKA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last
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                                                                                                                                                                                                                                                                                                                                                                                                                   68C5D27F0DDC6FB2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 AA
                                                                                                                                                                                                                                                                                                                                                    104; Indels
                                                                                                                                                                                                                                                                                                                                                      57;
                                                                                                                                                                                                                                                                                                                                                      Gaps
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DT 01-D
DE CEPU
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                    Kimura Y., Shirabe K., Fukushima M., Takeshita M., Tanaka H.; "CEPU-1: an Immunoglobulin Superfamily Molecule, Has Cell Adhesion Activity and Shows Dynamic Expression Patterns in Chick Embryonic
                           Submitted (MAR-1998) to the
EMBL; AB011810; BAA31514.1;
InterPro; IPR003598; Ig_c2.
                                            Spinal Cord."
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                 Gallus gallus (Chicken).
                                                                                                                                                                                                                    CEPU-1.
                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                    Archosauria; Aves;
                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                            093242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; 19; 3.
SMART; SM00409; IG; 3.
SMART; SM00408; IGc2; 3.
SMART; SM00410; IG_like; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous system.";
submitted (JUN-2000) to the
EMBL; AF282980; AAK00276.1;
                                                                                                                                                                                                                                                                                                                                                                       239
                                                                                                                                                                                                                                                                                                                                                                                                  228
                                                                                                                                                                                                                                                                                                                                                                                                                                184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003599; Ig. C2. InterPro; IPR003598; Ig. C2. InterPro; IPR003600; Ig_like. InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 --LIVQVSPKIVEISSDISINEGNNISLTCIATGRPE-PTVTWR---HISPKAVGFVSED 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 AYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ICR; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and expression of mouse neurotrimin gene in the denervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 ---PYAGNDKWCLDPRVVLLGNTQTQYSIEIQNVDVYDEGPYTCSVQIDNHPKTSRVH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 RHLLTVPEAVGSGSGNEVI-EGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocal
                                                                                                                                                                                                                                                                                                                                                                GTLQCEASAVPSAEFQ --- WFK 257
                                                                                                                                                                                                                                                                                                                                                                                             GVL----SSLPSLGFSLPTWGK 245
                                                                                                                                                                                                                                                                                                                                                                                                                     EYLQ----IQGITREQSGEYECSAS-NDVAAPVVPRVKVTVNYPPYFSEAKGTGVPVGQK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCP-----QDTGGGINIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PMEPIITNDRF-TSQRYDQGGNFTSE--MIIHNVEPSDSGNIRCSLQ-----NSRLHGS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 AA; 37924 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                    Neognathae;
                                                                                                                                                              Chordata; Craniata; Vertebrata; Eute
Weognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.6%; Score 137.5;
26.0%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                           EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3ECC6D5EE6C5C17D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                     344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115; Indels
                                                                                                                                                               Euteleostomi;
idae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wunchaw-Barie B. Vocakida K. Haseorawa V. Kawaii H. Zohteniki C., Wilming L.,
Kohteniki C., Wi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ωy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR DR DR DR DR DR DR DR
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                           EMBL; AK016467; BAB30253.1; -. MGD; MGI:1913992; 4931420D14Rik.
                                                 Nature 409:685-690(2001).
EMBL; AK016467; BAB30253.1; -
           SEQUENCE
                                                                                                                                                   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                          Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4931420D14RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4931420D14Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9D4K2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9D4K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART: SM00408: IGC2; 2.
SMART: SM00410; IG_like; 1.
Immunoglobulin domain:
SEQUENCE 344 AA; 37613 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003600; InterPro; IPR003006; Pfam; PF00047; ig; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 VGFISEDEYLE----ITGITREQSGEYECSAS-NDVAAPVVQRVKVTVNYPPYISDAKST 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 DMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 RLLFLVPAGVPVRSGDATFPKAMDNVTVRQGESATLRCSVDNRVTRVAWLNRSSILYAGN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 RHLLTVPEAVGSGSGNEVI-EGPQNATVLKGSQARFNCTVSQ-----GW----KLIMWALS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPD--ISWELGLLVSHSS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVPVGQKGILMCEASAVPSADFQ---WYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGINIPGVL----SSLPSLGFSLPTWGK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVH----LIVQVSPKITEISSDISINEGGNVSLTCIA---TGRPDPTITWR---HISPKA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKWCLDPRVVLLANTKTQYSIQ------IHDVDVYDEGPYTCSVQTDNHPKTS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 26.0970; Conservative
        173 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
        19581 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37613 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig_like.
Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.6%; Score 137.5;
26.0%; Pred. No. 0.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
147B6F155AC29FDF CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22CAA8F526A6B57E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .0004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Gaps
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ACCOCK PROBLET REPORT OF THE PROBLEM OF THE PROBLEM
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Q92626
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                                                               InterPro; IPRO0 Pfam; PF03098; Pfam; PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97191544; PubMed-9039502;
Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y. Tanaka A., Kotani H., Miyajima N., Nomura N.;
Tranaka A., Kawarabayasi Y.
Tranaka A., Kotani H., Miyajima N., Nomura N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYELOBLAST KIAA0230 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q92626;
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                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitchell M.S., Kan-Mitchell J., Minev B., "Identification of a novel melanoma gene (II-1 receptor antagonist - which encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Assignment of a human melanoma associated gene MG50 (D2S448) chromosome 2p25.3 by fluorescence in situ hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95048383; PubMed=7959781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 CTLTIRCCCCRRRCCGCNC-CCRCCFCCRKRGFRIQFQKKSEKEKTNKETETESGNENS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 22:243-244(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Irent J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weiler S.R., Taylor S.M., Deans R.J., Kan-Mitchell J., Mitchell M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-MELANOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166
                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FISSUE=MELANOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Res. 3:321-329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNGDLAS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASFNLAS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRRIRRQLTRSQLELIEPEPTMALEPSEITVAFFSHKNANVSDP----EEVPPCLDSDPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYNSDEQKTTE-----TASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQ 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ytic T lymphocytes.";
tted (OCT-1999) to the EMBL/GenBank/DDBJ databases
D86983; BAA13219.1; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                                                                                                                P05164; 1CXP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF200348;
                                     PF00560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                         IPR003591;
IPR001007;
                                                                                                                                                                                                                                             IPR003006; Ig_MHC.
IPR001611; LRR.
IPR000483; LRR_Cterm.
                                                                                                                                                                                                                                                                                                                                                     IPR002007; Anim_peroxidase
IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                  Au__
1g; 4.
   LRRCT;
                                                                                                    An_peroxidase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF06354.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.6%;
                                                                                                                                             LRR_typ.
                                                                                                                                                                                                                LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 136.5; DB 11,
Pred. No. 0.0002;
Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawarabayasi Y., Ohara O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      deduced by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes.
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Best Local S
Matches 73
                                                            Matches
                                                                            Best
                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0457; ANPEROXIDASE.
SMARR; SM00408; IGC2; 4.
SMARR; SM00082; LRRCT; 1.
SMARR; SM00013; LRRNT; 1.
SMARR; SM00369; LRR_TYP; 4.
SMARR; SM00369; LRR_TYP; 4.
SMARR; SM00214; VWC; 1.
PROSITE; PS01208; VWFC; UNKNOWN_1.
                                                                                                                                                  InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003000; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3
SMART; SM00408; IGc2; 2.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00093; vwc; 1.
PRINTS; PR00457; ANPER
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Q9P121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                         Li G., Jin J., Tan X., Hu S., Yuan J., Qiang B.; "Cloning and identification of human neurotrimin full length cDNA."; submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF120426; AAF37591.1; -
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                              Neurotrimin.
                                                                                                                     Immunoglobulin domain.
SEQUENCE 344 AA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 GSPARPTFVIQPQNTEVLVGESVTLECSATGHPPPRISWTRGDRTPLPVDPRVNITPS-- 411
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567
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 20 RLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGN
                                                                          Local
                            w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFSLP--TWGKVGLGL--AGTMLLTPTCTLTI-----RCCCCRRRCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGTLTCVATWKSLKARKSATVNLTV------IRCPQDT----GGGINIPGVLSSLPSL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVVAENEPCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNS--RLHGSAYLTVQVMGELFIPSVN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSGSGNEVIEGPQNATVLKGSQARFNCTVS-QGWKLIMWALSDMVVLSVRPMEPIITNDR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEPEPAITWNKDGVQVTESGKFHISPEGFLTINDVGPADAGRYECVARNTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVVIEGQTVDFQC-EAKGNPPPVIAWTKGGSQLSVDRRHLVLSSGTLR--ISGVALHDQ- 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GG-----LYIQNVVQGDSGEYACSATNNIDSVHATAFIIVQALPQFTVTPQD 458
                            RHLLTVPEAVGSGSGNEVI-EGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLS-- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GQYECQAV--NIIGSQKVVAHLTVQPRVTPVFASIPSDTTVEVGANVQLP-----CSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73;
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                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.5%;
25.0%;
                                                                                                                        37971 MW; DA4D12C295ABBE3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167209 MW; E9B9A7069BF1ABFF CRC64;
                                                                         6.4%; Score 133.5; DB 4; 24.5%; Pred. No. 0.00092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 135; DB 4; Length 1496; Pred. No. 0.0046;
                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                             Mismatches
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Q91562
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                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00060; FN3; 6.
SMART; SM00408; IGc2; 3.
SMART; SM00410; IG_like; 2.
Immunoglobulin domain; Repe
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00041; fn3; 6. Pfam; PF00047; 1g; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q91562;
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                       347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003961; FN_III.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U10986;
HSSP; P40189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-95113183; PubMed-7813784;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor suppressor
                                                                                                                                                                                                                243 LQRPSNVVAIEGQDAVLECAVS-GYPTPTIVWMQGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 SEDEYLE----IQGITREQSGDYECSAS-NDVAAPVVRRVKVTVNYPPYISEAKGTGVPV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 PEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCP-----QDTGGGI
                                                                                                                                                                                                                                               21 IEGPQNATVLKGSQARFNCTVSQGW--KLIMWALSDMVVLSVRPMEPIITNDRFTSQRYD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 NIPGVL----SSLPSLGFSLPTWGK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110
                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 DKWCLDPRVVLLSN---TQTQY-----SIEIQNVDVYDEGPYTCSVQTDNHPKTSRV
                                                                                                PCEVTCL----PSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGT 191
                                                                                                                                   VLGG--SNLLISNVTDDDAGAYTCVATYKNENTSFSADLTVMVPPQFLNHPANLYAYESM
                                                                                                                                                                        QGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENE 136
                                                               DIEFECAVSGKPS-----PTVKWTKNGEVVIPSDYFQIVDGSNLR----ILGLVKSDEGY 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQKGTLQCEASAVPSAEFQ---WYK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ession of a homologue of the deleted in colorectal cancer (DCC) in the nervous system of developing Xenopus embryos."; Biol. 166:654-665(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H----LIVOVSPKIVEISSDISINEGNNISLTCIATGRPE-PTVTWR----HISPKAVGFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRL 109
                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003006;
                                                                                                                                                                                                                                                                                                                                                                1427 AA;
                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA70168.1; -
                           --TWKSLKARKSATVNLTVI-RCPQDTGGGINIPGVLSS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                n; Repeat.
156533 MW;
                                                                                                                                                                                                                                                                                                      6.4%; Score 133; DB 1: 25.7%; Pred. No. 0.0065
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19,
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Last annotation updat
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                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                              61FEA12C8A674972 CRC64;
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                                                                                                                                                                                                                                                                                                                       DB 13;
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Q9DBP0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Arakawa T., Hara A., Shibata K., Yoshino M., Adachi J., Fukuda S., Ra Arakawa T., Hara A., Shibata K., Kiyosawa H., Kondo S., Yamanaka I., Ra Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ra Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochlwa H., Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J., Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J., Ra Kuehl R., Eurino, A., Aono H., Baldarelli R., Barsh G., Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Ra Sakai K., Oxido T., Furuno M., Aono H., Baldarelli R., Barsh G., Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ra Brownstein M.J., Mashima J., Mazzarelli J., Mombaerts P., Ra Kondone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Ra Myzshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Pan Hayashiyaki V., Noshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003841; Na_Pi_cotrans.
Pfam; PF02690; Na_Pi_cotrans; 1.
TIGRFAMs; TIGR01013; 2a58; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Solute carrier family 34 (sodium phosphate), member 2.
259 TCTLTIRCCCCRRRCCG-----CNC-CCRCCFCCRRKRGFRIQFOKKSEKEKINKETETE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1342284; S1c34a2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                   523
                                                                                                                                                                        155
                                                                                                                                                                                                             484
                                                                                                                                                                                                                                               103
                                                                                                                                                                                                                                                                          434 SVFTSAMTPLIGIGVISIERAYPLTLGSNI------GTTTTAILAALASPGNT--LRS 483
                                                                                                                                                                                                                                                                                                                                                380 LIMIVKLLGS-----VLRG-QVATVIKKTLNTDFPFPFAWLTGYLAILVGAGMTFIVQSS 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9DBP0
                                                                                                                                                                                                                                                                                                                       43
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 YQCIAENEAGNIQTYAQLIIPDPAVPSSSILPSAPRDV-----VPVLVSS 442
                                                                                                                                                                                                                                                                                                                                                                                         5 LLTVPEAVGSGSGNEVIEGPQNATVLK-----
                                                      LLLLVLCLRMLQFRCPR-----ILPLKLRDWNFLPLWMHSLKPWDNV-----ISLAT 611
                                                                                        LTVI-----RCPQDTGGGINIPGVL---SSLPSLGFSLPTWGKVGLGLAGTMLLTP
                                                                                                                               AKYRW---FAVFYLIFFFFVTP-----LTVFGLS-----
                                                                                                                                                                ----WELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVN 210
                                                                                                                                                                                                             SLQIALCH---
                                                                                                                                                                                                                                        SLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLP------DIS 154
                                                                                                                                                                                                                                                                                                                 QGWKLIMWALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AK004832; BAB23600.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 131; DB 1: Pred. No. 0.0039
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 124;
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Length 697;

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22;

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-LAGWPVLVGVGVPIIL 564

522

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Q9Z290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Type IIb Na/phosphate-cotransporter SLC34A2 OR NPT2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9Z290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          612 TC-FQRRCCCCCRVCCRVCCMVCGCKCCRCSKCCRD-----QGEEEEEKEQ------ 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02690; Na_Pi_cotrans; 1.
TIGRFAMS; TIGR01013; 2a58; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hilfiker H., Hattenhauer O., Traebert M., Forster I., Murer H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=NMRI; TISSUE=SMALL INTESTINE; MEDLINE=99045724; PubMed=9826740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterpro; IPR003841; Na_Pi_cotrans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 SLQIALCH-----FFFNISGI-----LLWYPIPFTRLPIRLAKGLGNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 SLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLP------DIS 154
                                                                                                                                                                                                                                                                                                                                                               211 LTVI-----RCPODTGGGINIPGVL---SSLPSLGFSLPTWGKVGLGLAGTMLLTP 258
                                                                                                                                                                                                                                                                                                       565 LLLLVLCLRMLQFRCPR-----ILPLKLRDWNFLPLWMHSLKPWDNV------ISLAT 611
                                                                                                                                                                                                                                                                                                                                                                                                                            523 AKYRW---FAVEYLIFFFFVTP-----LTVFGLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 ----WELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 QGWKLIMWALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGNENSGYNSDEOKTTETASLPPKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQASF 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVLSMKALSNTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVFTSAMTPLIGIGVISIERAYPLTLGSNI------GTTTTAILAALASPGNT--LRS 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIMIVKLLGS-----VLRG-QVATVIKKTLNTDFPFPFAWLTGYLAILVGAGMTFIVQSS 433
NLASPEKVSNTTV 385
                                                                                                                 SGNENSGYNSDEOKTTETASLPPKSCESSDPEORNSSCGPPHORADORPPRPASHPOASF 372
                                                                                                                                                                                  TC-FQRRCCCCCRVCCRVCCMVCGCKCCRCSKCCRD-----QGEEEEEKEQ------
                                                                                                                                                                                                                                             TCTLTIRCCCCRRRCCG-----CNC-CCRCCFCCRRKRGFRIQFQKKSEKEKTNKETETE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;
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(TremBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76286 MW; 839E5CCB0F565265 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
                                                                    ----DIPVKASGAFDNAAMSKEC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 131; DB 11
Pred. No. 0.0039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Musi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124; Indels 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 697;
                                                                                                                                                                                                                                                                                                                                                                                                                                         -LAGWPVLVGVGVPIIL 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cotransporter
                                                                       -QDEGKGQV 683
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RESULT 14
Q22048
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Q22048; Q1-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa, Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T01B7.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T01B7.8 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sims M.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR001271; Defensin_mammal.
InterPro; IPR000561; EGF-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z66499; CAA91301.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               none;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   684 EVLSMKALSNTTV 696
                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                              001761;
                                                                                                                                                                                          001761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of the nematode C.elegans:
             SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                    Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                157 LGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRC 216
 MEDLINE=99069613; PubMed=9851916
                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                          217 PQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCCRRRCCGC 276
                                                                                                                                                                                                                                                             102 CRTCCCTRCCTCCR 115
                                                                                                                                                                                                                                                                                       277 -- NCCC-RCCFCCR 287
                                                                                                                                                                                                                                                                                                                   58
                                                                                                                                                                                                                                                                                                                                                                      6 LAILLAIGTFIAV----SQVQSAV-----LPVSSTELATVGTDVSTASTAIDTLGNSSSRV 57
                                                                                                                      elegans UNC-89 protein (corresponding sequence C09D1.1).
                                                                                                                                                                                                                                                                                                                   KRQGGCGCCGCGC-
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00128; 4FE4S_FERREDOXIN; UNKNOWN_1.
PS00269; DEFENSIN; UNKNOWN_1.
PS000229; EGF_1; UNKNOWN_1.
PS01208; VAPC; UNKNOWN_1.
154 AA; 16499 MW; C002D48D36C9FCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000561; EGF-
IPR001007; VWF_
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                            6.2%; Score 129.5; DB 5 32.1%; Pred. No. 0.00081;
                                                                                   Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                     Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C002D48D36C9FCED CRC64;
                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                6632 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Search completed: April 28, 2003, 21:07:42 Job time: 41.1283 secs
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                                                                         2261 TVNGGNKKPEFVQAPQN 2277
                                                                                                                                   2202 -EVSWLLNGQPLTKSDTVQVVDHGDGTYHVTIAEAKPEMSGTLTAKAKNAAGECETSAKV 2260
                                                                                                                                                                                                           2144 TVKVTAQNSAGQDSKQADLKVEPNVKAPKFKSQLTDKVADEGEPLRWNLELDGPSPGT-- 2201
                                                                                                                                                                                                                                                                                   2098 IS-GFPAPTVKWTINEKIVEESRTITTIKTEDVYT-----LKISNAKIEQTG 2143
                                                                                                                                                                                                                                                                                                                                                       2038 LIIPNAQDSGKITVEASNEVGSSESSAQLTVNPPSTTPIVVDGPKSVTIKETETAEFKAT 2097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF003131; AAB54132.2; -. SEQUENCE 6632 AA; 731665 MW; 262D3EDD62960E89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Du Z., Le T.T., Wilson R.;
"The sequence of C. elegans cosmid C09D1.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                            210 NLT-----VIRCPQD 219
                                                                                                                                                             151 PDISWEL-GLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston R.; "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                            99 NIRCSLONSRLHGSAYLTVQVMGELFIPS-----VNLVVAENEPCEVTCL---PSHWTRL 150
                                                                                                                                                                                                                                                                                                                    41 VSQGW--KLIMWALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSG 98
                                                                                                                                                                                                                                                                                                                                                                                          6 LTVPEAVGSG-----SGNE------40
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GenCore version 5.1.4_{-p5\_4578} Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: April 28, 2003, 16:24:30 ; Search time 10.3692 Seconds (without alignments) 1543.990 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-729-264-6 2077 1 MERHLLTVPEAVGSGSGNEV......HPQASENLASPEKVSNTTVV 386

Scoring table:

Searched: 112892 seqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ν'n.	Result
133 133 130 130 129 129 128 128 128 128 128 128 128 129 129 120 130 14 15 110 100 100 100 100 100 100 100 100	13	Score
	7.3	% Query Match I
337 345 345 345 345 345 345 347 1010 4393 4493 1461 11070 4393 1461 11070 11463 1146	404	Length
		DB
G55A_CHICK DCC_MOUSE OPCM_HUMAN CPCM_BOVIN CEPU_CHICK OPCM_RAT DCC_HUMAN RMLS_HUMAN PTK7_HUMAN PTK7	RAGE_HUMAN	ID
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даккорддко со новор сок	Q15109 homo sapien	Description

4.5	44	43	42	41	40	39	38	37	36	ω 5	34
98.5	99	99	99	99	99.5	99.5	100	100	100	100.5	100.5
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NCA1_RAT	MPRI_BOVIN	LACH_DROME	LAMP_RAT	LAMP_HUMAN	CAML_MOUSE	TYO3_RAT	NPHN_HUMAN	CONT_CHICK	FAS2_DROME	UN52_CAEEL	KMLS_CHICK
P13596 rattus norv											P11799 gal·lus gall

ALIGNMENTS

; RRA	RESU RESU RAGE DT DT DT DT DT DT DT DT DT RR
MEDLINES FROM N.A. (ISOFORM 1). MEDLINES 5137587; pubMed-7838890; Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A., Inoko H., Ikemura T.; "Three genes in the human MHC class III region near the junction with the class II: gene for receptor of advanced glycosylation end products, PBX2 homeobox gene and a notch homolog, human counterpart of mouse mammary tumor gene int-3."; Genomics 23:408-419(1994). SEQUENCE FROM N.A. (ISOFORM 1). Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E., Banta A., Spies T., Hood L.; SUDMITTED FROM N.A. (ISOFORM 1). AND VARIANT ARG-100. Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y., Yamamoto H.; "Molecular heterogeneity of the receptor for advanced glycation endproducts."; SUDMITTED (JAN-2000) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. (ISOFORM 2). Malherbe P., Richards J., Gaillard H., Thompson A., Diener C., Schuler A., Huber G.; "CDNA cloning of a novel secreted isoform of the human Receptor for advanced Glycation End products (RAGE) and characterization of cells co-expressing cell-surface scavenger receptors and Swedish mutant Sumyloid precursor protein."; SEQUENCE FROM N.A. (ISOFORM 1).	LT 1 RAGE_HUMAN RAGE_HUMAN ST O1-NOV-1997 (Rel. O1-NOV-1997 (Rel. O1-NOV-1997 (rel. 15-JUN-2002 (Rel. 15-JUN-2002 (Rel. 15-JUN-2002 (Rel. HOW Sapiens (Hum Enkaryota; Metazo Mammalia; Eutheri NCBI_TaxID=9606; [1] SEQUENCE FROM N.A TISSUB-Lung; MEDLINE-9234054, Neeper M., Schmid Elliston K., Ster "Cloning and expr "Cloning and expr

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DOMAIN
DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-12 FROM N.A.
Hudson B.I., Futers T.S.;
"Novel polymorphisms in the receptor for advanced glycation
                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00410; IG_like; 1.
SMART; SM00408; IGC2; 1.
PROSITE; PS00290; IG_MHC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    end-products (RAGE) gene.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
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 CONFLICT
                         VARIANT
                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM;
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                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                         Immunoglobulin domain; Glycoprotein; Transmembrane;
Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: ENDOTRELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOWAIN.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secreted (isoform 2).
ALTERNATIVE PRODUCTS: 2 ISOFORMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARE PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RATE IN DIABETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M91211;
D28769;
                                                                                                                                                                                                                                                                                                                                                                                                            PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U89336; AMD4, 7.7.
AB036432; BAA89369.1; -.
AJ133822; CAB43108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC020669; AAH20669.1; AF208289; AAG35728.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U89336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:320; AGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003006; Ig_MHC.
IPR003598; Ig_c2.
IPR003600; Ig_like.
                          100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA03574.1; -.
BAA05958.1; -.
                                                                                                                                                                                                                                                                                                                                                                      IG_MHC; 1.
                                                                                                           342
363
404
106
215
208
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384
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                            100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENDOTHELIAL CELLS.
                                                    GVPLPLPPSPVLILPEIGPODQGTYSCVATHSSHGPQESRA
VSISIIEPGEEGPTAGSVGGSGLGTLALALGILGGLGTAGL
LIGVILWORRORRGEERKAPENOEEEEERAELNOSEEPEAG
ESSTGGP -> VSDLERGAGRTTRGGANCRLCGRIRAGNSS
PGPGDDGRPGDSRPAHWGHLVAKAATPRRGEEGPRKPGGRG
/FTId=VAR_011338.
M -> G (IN REF. ]
                          GACRTESVGGT
Q -> R.
                                                                                                                                                  N-LINKED (GLCNAC. . N-LINKED (GLCNAC. .
                                                                                                                                                                                                                   IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                   ADVANCED GLYCOSYLATION END SPECIFIC RECEPTOR.
                                                                                                                         MISSING (IN ISOFORM
                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (SHOWN HERE) AND 2/RAGESEC
                                        (IN ISOFORM
                                                                                                                         2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q62718;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seg
This SWISS-PROT entry is copyright. It is produce the European Bioinformatics Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us
                                                                                                                                               -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor trissue specificity: Central Nervous SYSTEM.
-!- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN SEVERAL DEVELOPING PROJECTION SYSTEMS: IN NEURONS OF THE THALAMUS, SUBPLATE, AND LOWER CORTICAL LAMINAE IN THE FOREBRAIN AND IN TRISSPACE, CEREBELLAR GRANULE CELLS, AND PURKINJE CELLS
                                                                                                                                                                                                                                          expressed neural cell adhesion molecules.";
J. Neurosci. 15:2141-2156(1995).
-!- FUNCTION: NEURAL CELL ADHESION MOLECULE.
                                                                                                                                                                                                                                                                                                                                      STRAIN-Sprague-Dawley;
MEDLINE-95198094; PubMed-7891157;
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Neurotrimin precursor (GP65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTRI_RAT
                                                                                                                                                                                                                                                                                                                   Struyk A.F.,
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                         "Cloning of neurotrimin defines a new subfamily of differentially
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 RRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEKT--NKETETESGNENSGYNSDEQKT 327
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                                                                                            SIMILARITY:
                                                                                                                         SIMILARITY:
                                                                                                          SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEIVDSAS--ELTAGVPN------KVGTCVSEGSYPAGTLSWHLDG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEAVGSGSGNEVIEGPQNATVLKGSQARFNCTVSQG----WKLIMWALSDMVVLSVRPMEP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGEEG - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT-----PTCTLTIRCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTVQVMGELFIP----SVNLVVAENEP-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
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                                                                                                                                      HINDBRAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISIIE-
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                                                                                                                         BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
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                                                                                                                                                                                                                                                                                                                                                                  AND SEQUENCE OF
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRRGEERKAPENQEEEEERAELN--
                                                                                                                                                                                                                                                                                                                      M.J., Rosen C.L., D'Eustachio
                                                              It is produced through
                                                                                                                                                                                                                                                                                                                                                                     217-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 AA
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                                  There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata;
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                    as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                 Muridae;
      Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                   Murinae; Rattus
                                                                                                                                                                                                                                  a GPI-anchor
       and
                                                  EMBL
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                                                     a collaboration
       for
                                                  outstation
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Best Local
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                                                               Gallus gallus (Chicken).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                              _CHICK
                                                                                                                      01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurite inhibitor 1555-A precursor (OBCAM protein
                                                                                                                                                                            Q98892;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID DISULFID
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   TISSUE=Brain;
                                                                                                                                                                                                             G55A_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                  SEQUENCE FROM N.A
                                                  NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00410; IG_like; 1.
SMART; SM00408; IGC2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U16845; AAA67445.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                   PEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCP-----QDTGGGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKWCLDPRVVLLSN---TQTQY-----SIEIQNVDVYDEGPYTCSVQTDNHPKTSRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----VRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGN 79
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24.9%;
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GPI-ANCHOR (POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 139.5; DB 1
Pred. No. 0.00049;
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                                                                                                                                                                                                            PRT;
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                                                                                                                             gamma isoform).
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                                                                              Phasianinae;
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CARBOHYD
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171
                              167
                                                             123
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143
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285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson D.J.A., Kim D.-S., Clarke G.A., Marshall-Clarke S., Woss D.J. "A family of glycoproteins (GP55), which inhibit neurite outgrowth, are members of the Ig sensity and are related to OBCAM, neurotrimin, LAMP and CEPU-1.";
J. Cell Sci. 109:3129-3138(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- TISSUE SPECIFICITY: RESTRICTED TO THE NERVOUS SYSTEM.
-!- DEVELOPMENTAL STAGE: INCREASES DURING DEVELOPMENT FROM VERY LOW
LEVELS AT EMBRYONIC DAY 10 AND IS MOST ABUNDANT AFTER HATCHING.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lodge A.P., Kim D.-S., Howard M.R., McNamee C.J., Smith N., "Cloning of CEPU-S, a secreted isoform of CEPU-1, and OBCAM chick: structural diversity of IgLON family proteins."; submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y08170; CAB41420.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97157768; PubMed=9004047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 64-337 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     5 LLTYPEAVGSGSGNEVI-EGPQNATYLKGSQARFNCTVSQGWKLIMWALSDMYVL----
GFVSEDEYLE----ITGITREQSGEYECSAV-NDVAVPDVRKVKVTVNYPPYISNAKNTG
                                                  YFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV-----IRCPQDTG
                                                                                                                                                 GSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHSSY
                                                                                                                                                                                                                                                                                                        LLFIP-GVPVRSGDATFPKAMDNVTVRQGESATLRCTVDDRVRRVAW-LNRSTILYAGND
                                                                                                    ----LIVQVPPQIVNISSDITVNEGSSVTLMCLAFGRPE-----PTVTWR----HLSGKGQ
                                                                                                                                                                                                   KWSIDNRVVILSN---TKTQY-----SIKIHNVDVYDEGPYTCSVQTDNHPKTSRVH
                                                                                                                                                                                                                                                   --SVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00410; IG_like; 1.
SM00408; IGC2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR003006; Ig_MHC.
IPR003598; Ig_c2.
IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317
317
337
115
201
201
201
201
208
1194
1133
1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36887 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                  6.4%;
25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell adhesion; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEURITE INHIBITOR GP55-A (
REMOVED IN MATURE FORM (PO'
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 133;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
BAE717551856651E CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
.0016;
                                                                                                                                                                                                                                                                                                                                                                                                       107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and OBCAM cDNAs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
V 1.
V 2.
V 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                       60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moss D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                    166
  225
                                                                                                                                                                                                                                                                                                     73
                                                                                                                                                                                                                                                                                                                                                       58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .J.;
                                                                                                                                                                                                                                                                                                                                                                                                    16;
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QΥ

222 GGINIPGVL----SSLPSLGFSLPTWGKVGLGLA

251

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RESULT 4
DCC_MOUSE
   P70211;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
        Pfam; PF00041; fn3; 6.
Pfam; PF00047; 1g; 4.
PRINTS; PR00014; FNTYPEIII.
SMART; SM00060; FN3; 6.
SMART; SM000410; IG_11ke; 2.
SMART; SM00408; IGc2; 3.
Glycoprotein; Immunoglobulin domain; Transmembrane; Signal; Glycoprotein; Immunoglobulin domain; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cooper H.M., Armes P., Britto J., Gad J., Wilks A.F.; "Cloning of the mouse homologue of the deleted in colorectal cancer gene (mDCC) and its expression in the developing mouse embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases -i- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
Repeat; Anti-
                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene 11:2243-2254(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/c; TISSUE=Brain; MEDLINE=96112625; PubMed=8570174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                    MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cooper H.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/c;
                                                                                                                                   InterPro;
                                                                                                                                                  InterPro;
                                                                                                                                                                   InterPro;
                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226
                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      produced by alternative initiation. A third isoform: C is produced by alternative splicing.
TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GE AND REMAIN AT THIS LEVEL IN THE ADULT.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS ISOFORM C IS EXPRESSED ONLY IN THE EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBFAMILY
                                                                                                                                                                                                                   MGI:94869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASVGQKGILQCEASAVPVAEFQ---WFKEDTRLA 256
                                                                                                                                                                                                                                    X85788; CAA59786.1;
P56276; 1TLK.
 Anti-oncogene; Alternative initiation; Alternative splicing.
                                                                                                                           IPR003006; Ig_MHC.
IPR003598; Ig_c2.
IPR003600; Ig_like.
                                                                                                                                                                                   IPR003961; FN_III.
IPR003962; FnIII_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Mouse).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; are
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                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                               Вþ
                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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INIT_MET
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Opioid binding protein/cell adhesion molecule
(Opioid-binding cell adhesion molecule) (OPCML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
"Cloning, sequencing and localization to chromosome 11 of a cDNA encoding a human opioid-binding cell adhesion molecule (OBCAM).";
                  MEDLINE=95237612; Pub
Shark K.B., Lee N.M.;
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                    Q14982;
                                                                                                                                                                                                OPCM_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                          SEQUENCE FROM N.A. TISSUE=Occipital c
                                                                                                         Homo sapiens (Human)
                                                                                                                      OPCML OR OBCAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                     380
                                                                                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                                                                                      111
                                                                                                                                                                                                                                                                                                                                            276
                                                                                                                                                                                                                                                                                                321
                                                                                                                                                                                                                                                                                                                                                                                     217 PASIRTGNEAEVRILSDPGLHRQLYFLQRPSNVIAIEGKDAVLECCVS-GYPPPSFTWLR 275
                                                                                                                                                                                                                                                                                                                                                                 53
                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                    GSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFV
                                                                                                                                                                                                                                                     VGGSNLR----ILGVVKSDEGFYQCVAENEAGNAQSSA 413
                                                                                                                                                                                                                                                                         PEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSA 207
                                                                                                                                                                                                                                                                                                ASAELTVLVPPWFLNHPSNLYAYESMDIEFECAVS-GKPVPTVNWMKNGDVVIPSDYFQI
                                                                                                                                                                                                                                                                                                                                            GEEVI ----
                                                                                                                                                                                                                                                                                                                                                                                                         PEAVGSGSGNEV------IEGPQNATVLKGSQARFNCTVSQGW--KLIMWAL 52
                                                                                                                                                                                                                                                                                                                                                                 SDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLH 110
                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      941
161
161
261
352
60
94
299
318
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                           -----QLRSKKYSLLGG--SNLLISNVTDDDSGTYTCVVTYKNENIS
                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                           cortex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1447
1447
1447
1097
1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1447
124
219
317
407
522
618
716
                                 PubMed=7721093;
                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                           6.3%;
25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158298
                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 131; DB
Pred. No. 0.01
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
MISSING (IN ISOFORM C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
TUMOR SUPPRESSOR PROTEIN
TUMOR SUPPRESSOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOR ISOFORM B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0D1F1097C22D5B9F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345
                                                                                                                               (OPCML)
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
.014;
                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                 90;
                                                                                                                                           precursor (OBCAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1447;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOFORM
ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                        169
                                                                                                                                                                                                                                                                                                                                            320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B ?
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9

Gene 155:213-217(1995).

P11834;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Opioid binding protein/cell adhesion molecule precursor (OBCAM)
(Opioid-binding cell adhesion molecule) (OPCML).

OPCM_BOVIN

STANDARD;

PRT;

ĄΑ

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos. NCBI_TaxID-9913;

Bos taurus (Bovine). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OPCML OR OBCAM OR OCAM.

protein with potential roles in opioid binding and cell EMBO J. 8:489-495(1989).

-i- FUNCTION: BINDS OPTOIDS IN THE PRESENCE OF ACIDIC L.

LIPIDS; PROBABLY contact.";

INVOLVED IN CELL CONTACT

Schofield P.R., McFarland K.C., Hayflick J.S., Wilcox J.N., Cho T.M., Roy S., Lee N.M., Loh H.H., Seeburg P.H.; "Molecular characterization of a new immunoglobulin superfamily

MEDLINE=89251576; TISSUE-Brain;

PubMed=2721489;

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

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SMART; SM00408; IGc2; 2.
                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                    TIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
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228 KAKNTGVSVGQKGILSCEASAVPMAEFQ---WFKEETRLATGLDG 269
                       216 CPQDTGGGINIPGVL----SSLPSLGFSLPTWGK----VGLGLAG 252
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SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
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                                                                    SYY----FVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV----IR 215
                                                                                                                LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHS 164
                                                                                                                                         NDKWSIDPRVIILVN---TPTQY-----SIMIQNVDVYDEGPYTCSVQTDNHPKTSR 127
                                             SVKEGQGFVSEDEYLE----ISDIKRDQSGEYECSAL-NDVAAPDVRKVKITVNYPPYIS
                                                                                              VH----LIVQVPPQIMNISSDITVNEGSSVTLLCLAIGRPE----PTVTWR--
                                                                                                                                                               ----SVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSR 108
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEBU-1 protein precursor.
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS: 2 ISOFORMS; A MAJOR FORM AND A MINOR FORM (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: FOUND ON THE DENDRITES, SOMATA AND AXONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor ALTERNATIVE PRODUCTS: 2 ISOFORMS; A MAJOR FORM AND A MINOR FORM
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                                                                 IPR003600; Ig_like.
                             ĬG_like; 1.
                                                                                                                                                   Ig_MHC
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SIGNAL
                                                                                                                                                                                                                 PPCM_RAT STANDARD; PRT; 345 AA. p3273E, Q01654; P3273E, Q01653; P3273E, Q01651; P3273E, Q01652; P3273E, Q01652; P3273E, Q01653; P3273E, Q01651EB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Q010101d binding protein/cell adhesion molecule propried binding cell adhesion molecule) (QPCML).
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MEDLINE=95198094;
Struyk A.F., Cano.
Salzer J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIPID
                                                                     "Opioid-binding cell adhesion molecule rat brain cDNA library.";
                                                                                                          MEDLINE=92347701; PubMed=1339369;
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                          OPCML OR OBCAM.
                         SEQUENCE OF 195-214, AND GPI-ANCHOR. MEDLINE=95198094; PubMed=7891157;
                                                           Gene 117:249-254(1992)
                                                                                               Lippman D.A., Lee
                                                                                                                       TISSUE-Brain;
                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                              226
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                                                                                                                                                                                                                                                                                                                                                      235 QKGILMCEASAVPSADFQ---WYK 255
                                                                                                                                                                                                                                                                                                                                                                                                                            171 EPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV-----IRCPQDTGGGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 DPRVVLLANTKTQYSIQ------IHDVDVYDEGPYTCSVQTDNHPKTSRVH-- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPD--ISWELGLLVSHSSYYFVP 170
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                                                                                                                                                                                                                                                                                                                                                                           IPGVL----SSLPSLGFSLPTWGK 245
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            Canoll P.D., Wolfgang M.J.,
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                                                                                              N.M., Loh H.H.;
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N-LINKED (GLCNAC. .
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MISSING (IN MAJOR ISOFORM).
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                                                                                                                                                                                                                                  precursor (OBCAM)
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                D'Eustachio
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SMART; SM00410; IG_like; 1.
SMART; SM00408; IGC2; 2.
Immunoglobulin domain; Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M88710; AAA40859.1; -.
EMBL; M88711; AAA40860.1; -.
EMBL; M88709; AAA40858.1; -.
PIR; JC1239; JC1239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annouentities requires re
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
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Neurosci. 15:2141-2156(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS
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SVKEGQGFVSEDEYLE - - - - ISDIKRDQSGEYECSAL - NDVAAPDVRKVKITVNYPPYIS
                                                                                                                                                               NDKWSIDPRVIILVN---TPTQY---
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                                                                                                                                                                                                                                                                                        RHLLTVPEAVGSGSGNEVI-EGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVL---
                                    SYY----FVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV----
                                                                             VH----LIVQVPPQIMNISSDITVNEISSVTLLCLAIGRPE----PTVTWR---
                                                                                                                    LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHS 164
                                                                                                                                                                                                    ----SVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSR
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                                                                                                                                                                                                                                                                                                                                                 6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                               38067 MW;
                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                                                   Score 128;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SATTALLFIP (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGVCGYLFLPWKCLVYVSLRLLFLVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC...)
GPI-ANCHOR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                      Length 345;
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(SHOWN
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HERE) AND 2
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RESULT 9
DCC_HUMAN
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P43146;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                            Cancer Res. 54:3007-3010(1994).

-i- EUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.

-i- SUBCELLULAR LOCATION: Type I membrane protein.

-i- TISSUE SPECIFICITY: FOUND IN AXONS OF THE CENTRAL AND PERIPHERAL NERVOUS SYSTEM AND IN DIFFERENTIATED CELL TYPES OF THE INTESTINE.

-i- DISEASE: COLORECTAL TUMORS THAT LOST THEIR CAPACITY TO DIFFERENTIATE INTO MUCUS PRODUCING CELLS UNIFORMLY LACK DCC EXPRESSION. INACTIVATION OF DCC DUE TO ALLELIC DELETION AND/OR POINT MUTATIONS MAY CAUSE BOTH LYMPHATIC AND HEMATOGENOUS METASTASIS OF OESOPHAGEAL SQUAMOUS CELL CARCINOMAS.

-i- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90100559; PubMed=2294591; Fearon E.R., Cho K.R., Nigro J.M., Kern Ruppert J.M., Hamilton S.R., Preisinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                    Miyake S., Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y "Point mutations and allelic deletion of tumor suppressor human esophageal squamous cell carcinomas and their relat:
                                                                                                                                                                                                                                                                         VARIANT CARCINOMA THR-168, AND VARIANT GLY-201 MEDLINE=94243823; PubMed=8187090;
                                                                                                                                                                                                                                                                                                                                   carcinomas."
                                                                                                                                                                                                                                                                                                                                                                        Cho K.R., Oliner J.D., Simons J.W., Hedrick L.,
                                                                                                                                                                                                                                                                                                                                                                                                        GENE STRUCTURE,
                                                                                                                                                                                                                                                                                                                                                                                                                                Cell 64:607-613(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Oliner J.D., Kinzler K.W., "Scrambled exons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nigro J.M., Cho K.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 107-472 FROM N.A. (SC MEDLINE-91121517; PubMed-1991322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 247:49-56(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a chromosome colorectal cancers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vogelstein B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-750 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vogelstein B.;
"The DCC gene product in cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCC_HUMAN
                                                                                                                                                                                                                                                                                                                      Genomics 19:525-531(1994).
                                                                                                                                                                                                                                                                                                                                                           Preisinger A.C., Hedge P.,
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94245241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                           -!- SIMILARITY:
                                                                                                                                                                                                                                 human esophageal squamous
                                                                                                                                                                                                                                                                                                                                                 "The DCC
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                                                      SUBFAMILY
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  SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dev. 8:1174-1183(1994)
                                                                                                                                                                                                                                                                                                                                                 gene: structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                           CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                      AND VARIANTS CARCINOMA HIS-1375
 entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8188295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fearon E.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DCC precursor (Colorectal
copyright.
                                                                                                                                                                                                                                                                                                                                                analysis
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                                                                                                                                                                                                                                                                                                                                                              Silverman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SCRAMBELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18q gene
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                                                                                                                                                                                                                                                                                                                                                an G.A., Vogelstein and mutations in co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wu T.-C.,
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  is
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  produced through a collaboration
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Thomas
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                                                                                                                                                                                                                                                                                                                                                                            Fearon
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                                                                                                                                                                                                                                                                  Yuasa Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                       relation
                                                                                                                                                                                                                                                                                                                                                  colorectal
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                                            DOMAINS
                                                                                                                                                                                                                                                                                                                                                                            E.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinzler
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use by non-profit institutions as long modified and this statement is not removed.

between the Swiss Institute of Bioinformatics

European Bioinformatics Institute.

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Query Match
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PRINTS; PR00014; FNTYPE:
SMART; SM00060; FN3; 6.
SMART; SM00410; IG_11ke.
SMART; SM00408; IGC2; 3
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DOMAIN
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                        CONFLICT
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Genew;
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A40098; A40098.
A38442; A38442.
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м63718;
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M63700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M32286;
M32288;
M32290;
                                                                                                                                                                                                                                                                                                                                                                                                                                 P56276;
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                                                                                                                                                                                                                                                                                                                                                                              IPR003962; I
IPR003006; I
IPR003598; I
                                                                                                                                                                                                                                                                                                                                                                                             IPR003961; FN_III.
IPR003962; FnIII_repeat.
                                                                                                                                                                                                                                                                                                                                                                      IPR003600;
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26
1098
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                                         138
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840
941
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161
161
261
352
94
299
318
478
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AAA52175.1; ALT_SEQ.
AAA52176.1; -.
AAA52177.1; -.
AAA52177.1; -.
AAA52178.1; -.
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AAA52180.1;
                                                                                                                                                                                                                                                                                                                Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA35751.1;
                                                                                                                                                                                                                                                                                                                       IG_like; 2.
IGc2; 3.
                 AA;
                                                                                                                                                                                                                                                                                                                                              FNTYPEIII.
                                                          1375
                                                                                                                 1042
117
212
310
400
94
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478
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Ig_c2.
Ig_like.
                 158456
6.2%;
                                                                                                                                                                                                                                                                                                        Disease
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IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 4.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 3.

FIBRONECTIN TYPE-III 4.

FIBRONECTIN TYPE-III 4.

FIBRONECTIN TYPE-III 6.

FIBRONECTIN TYPE-III 6.
                                                                                                               BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
Score
                                         /FTId=VAR_003911.
MISSING (IN REF.
                                                                                                                                                                                                                                                                                                               domain; Transmembrane;
                         MISSING
                                MISSING
                                                          /FTId=VAR_003910
P -> H (IN A COL
                                                                                                 N-LINKED
                                                                                                          N-LINKED
                                                                                 /FTId=VAR_003909
                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                        TUMOR SUPPRESSOR PROTEIN DCC
                                                                                                                                                                                                                                                                                                       mutation; Polymorphism
               SING (IN REF. 3).
SING (IN REF. 3).
SING (IN REF. 3).
4A8612766ED0471F CRC64;
128;
                                                                                         (IN OESOPHAGEAL
                                                                                                (GLCNAC.
DB
                                                        COLORECTAL CARCINOMA)
1;
Length 1447;
                                                                                                                       (POTENTIAL).
(POTENTIAL).
                                                                                                (POTENTIAL). (POTENTIAL). (POTENTIAL).
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            cloning,
                      "The human myosin light chain kinase
                                     Potier M.-C., Chelot E., Pekarsky Turnell W.G.;
                                                            TISSUE=Hippocampus;
MEDLINE=96121365; PubMed=8575746;
                                                                                    SEQUENCE OF 923-1914 FROM N.A.
                                                                                                               Submitted
                                                                                                                          REVISIONS (ISOFORM 2)
Birukov K.G., Garcia
                                                                                                                                                             Lazar V.L., Garcia J.G.N.;
"A single human myosin light chain
Genomics 57:256-267(1999).
                                                                                                                                                                                            TISSUE-Umbilical vein;
MEDLINE-99216419; PubMed-10198165;
                                                                                                                                                                                                                                                           REVISIONS.
Birukov K.G.,
                                                                                                                                                                                                                                                                                                               Verin A.D.; "Myosin light chain kinase in endothelium: molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Myosin light chain kinase, smooth muscle and non-muscle isozymes
(EC 2.7.1.117) (MLCK) [Contains: Telokin (Kinase related protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KMLS_HUMAN STANDARD;
Q15746; Q14844; Q16794;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                               Garcia J.G.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97304466; PubMed=9160829;
                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYLK OR MLCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q9uit9;
                                                                                                                                                                                                                                                                                                            regulation."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGSGNEV------IEGPQNATVLKGSQARFNCTVSQGW--KLIMWALSDM 55
                                                                                                                                                                                                                                                                                                Respir.
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sequencing, expression, 29:562-570(1995).
                                                                                                            .G., Garcia
(MAR-2000)
                                                                                                                                                                                                                                                 (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa; Chordata; C
Metazoa; Primates; C
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                                                                                                                                                                                                                                                            Garcia
                                                                                                                                                                                                                                                                                               Cell Mol. Biol. 16:489-494(1997)
                                                                                                                                                                                                                                                                                                                                               Lazar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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095796; 095797; 095798; 095799; Q9UBG5;
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                                                                                                             EMBL/GenBank/DDBJ
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Catarrhini;
                                                                                                                                                                                                                       3A;
           and
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                                               Υ.,
                                                                                                                                                                        kinase
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                         (MLCK) from hippocampus:
            localization to
                                                Gardiner K., Rossier J.,
                                                                                                                                                                                                                         AND 4)
                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata;
i; Hominidae;
                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99;
                                                                                                             databases.
                                                                                                                                                                        (MLCK; MYLK).";
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           3qcen-q21.";
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EMBL;
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-i- FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLAȚION OF A SPECIFIC SERINE IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC), AN EVENT THAT FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS. CENTRAL DETERMINANT IN THE DEVELOPMENT OF VASCULAR PERMEABILITY AND TISSUE EDEMA FORMATION. IN THE NERVOUS SYSTEM IT HAS BEEN SHOWN TO CONTROL THE GROWTH INITIATION OF ASTROCYTIC PROCESSES IN CULTURE AND TO PARTICIPATE IN TRANSMITTER RELEASE AT SYNAPSES FORMED BETWEEN CULTURED SYMPATHETIC CANGLION CELLS. CRITICAL PARTICIPANT IN SIGNALING SEQUENCES THAT RESULT IN FIBROBLAST APOPTOSIS.

-1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin light-chain]
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shrinsky V.P., Van Eldik L.J., Halecn J.;
Shrinsky V.P., Van Eldik L.J., Halecn J.;

"Analysis of the kinase-related protein gene found at human chromosome 3q21 in a multi-gene cluster: organization, expression, alternative
                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1456-1914 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watterson D.M., Schavocky J.P., Guo L., Weiss C., Chlenski A.,
Shrinsky V.P., Van Eldik L.J., Haiech J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Lung, and Placenta;
MEDLINE=20007838; PubMed=10536370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [6] SEQUENCE OF 1614-1914 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3B, 4 AND DEL-1790; ARE PRODUCED BY ALTERNATIVE SPLICING,
TISSUE SPECIFICITY: SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES ARE
EXPRESSED IN A WIDE VARIETY OF ADULT AND FETAL TISSUES AND IN
CULTURED ENDOTHELIUM WITH QUALITATIVE EXPRESSION APPEARING TO B
NEITHER TISSUE- NOR DEVELOPMENT-SPECIFIC, NON-MUSCLE ISOFORM 2
THE DOMINANT SPLICE VARIANT EXPRESSED IN VARIOUS TISSUES. TELOK
HAS BEEN FOUND IN A WIDE VARIETY OF ADULT AND FETAL TISSUES.
FYM: MICK IS PROBABLY DOWN-REGULATED BY PROSPENYLATION.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         light-chain] phosphate.
SUBUNIT: TELOXIN BINDS CALMODULIN.
ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; A NON-MUSCLE FORM (THE LONGEST FORM), A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH NO CATALYTIC ACTIVITY); ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; 1 (SHOWN HERE), 3B, 4 AND DEL-1790; ARE PRODUCED BY ALTERNATIVE SPLICING.
600922;
           X90870; CAA62378.1;
Q63450; 1A06.
; HGNC:7590; MYLK.
                                                                                                                                                                                                                                                                                                                        AF069602;
                                                                                                                                                                                                                                                                                                                                                              U48959; AAC18423.2;
                                                                                                                                                                                                                                                                  CAA59685
                                                                                                                                                                                                                    ; AAD15924.1; -
CAA59685.1; -
; AAD51380.1; -
; AAD51380.1; J
                                                                                                                                                                                                                                                                        ; AAD15921.2; -.
; AAD15922.1; -.
; AAD15923.1; -.
; AAD15924.1; -.
                                                                                                                             AAD51380
AAD51380
AAD54018
                                                                                                                                                                                    AAD51380.1;
AAD51380.1;
                                                                     AAD51381.1;
                                                                                                             AAD5138
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                                                                                                                                             JOINED.
JOINED.
JOINED.
JOINED.
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R SMART; SM00410; IG_Like; 1.

R SMART; SM00408; IGC2; 8.

R SMART; SM00220; S_TKC; 1.

R PROSITE; PS001107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS001107; PROTEIN_KINASE_DOM; 1.

R PROSITE: PS001108; PROTEIN_KINASE_DOM; 1.

R PROSITE: PS001109; PROTEIN_KINASE_CAlmodulin

R PROSITE: PS001109; PROTEIN_KINASE; Calmodulin

R PROSITE: PS001109; PROTEIN_KINASE; CHAIN KINASE;

CHAIN 1 1914
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                NP_BIND
BINDING
ACT_SITE
DOMAIN
                                                                                    CONFLICT
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VARSPLIC
                                      CONFLICT
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REPEAT
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REPEAT
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REPEAT
                                                 CONFLICT
                                                        CONFLICT
                                                                  CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                            INIT_MET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PD000001; Euk_pkinase; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRODO14; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000719;
                                                                                                                                                                      1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pkinase; 1.
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1413
1719
1774
1774
1891
1478
                                     1705
1790
933
963
1022
1050
1162
1210
1280
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923
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Ig_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euk_pkinase.
FN_III.
                                                  S -> A (1...

KPM -> EAH (I)

F -> L (IN RF

-> P (IN RF
4 T F
                                    P -> I
                                                                                           MISSING (IN ISOFORM 3A AND ISOFORM 3B)
MISSING (IN ISOFORM DEL-1790)
V -> M (IN REF. 5).
S -> P (IN REF. 3; AAD15922).
                           AAD15924).
                                                                                                                                                  ISOFORM 3B AND ISOFORM 4). GKFGQVFRLVEKKTRKVWAGKFFKAYSAKE%ENIRQEISIM
                                                                                                                                                                    VSGIPKPEVAMFLEGTPVRROEGSIPVYEDAGSHYLCLIKA
RTRDSGTYSCTASNAGGQVSCSWTLQVER -> G (IN
ISOFORM 2 AND ISOFORM 3B).
DEVEVSD -> MKWRCQT (IN ISOFORM 3A,
                                                                                                                                                                                                                                                     I-5 (INCOMPLETE)
6 X 12 AA APPROXIMATE TANDEM REPEATS.
II-1 (INCOMPLETE)
                                                                                                                                                                                                                                                                                                                                                         CALMODULIN-BINDING.
IG-LIKE C2-TYPE DOMAIN.
ATP (BY SIMILARITY).
                                                                                                                                          NCLHHPKLVQCVDAFEEKANIVMVLEIVSGGEL
                                                                                                                                                                                                                                                                                                                                                   ATP
                                                                                                                                                                                                                                                                                                                                                                                                        MUSCLE ISOZYME. FOR TELOKIN.
                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                               FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                           FOR MYOSIN LIGHT CHAIN KINASE, SMOOTH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
                                                                                                                                 (IN ISOFORM 4)
                                                                                                                                                                                                                                                                                                                       x 28
တ လ လ
                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
                                                                                 M (IN REF. 5).
P (IN REF. 3; AAD15922)
A (IN REF. 5).
                                                                                                                                                                                                                                                                                                                       AA APPROXIMATE TANDEM REPEATS
                                            H (IN REF. 5).
N REF. 3; AAD1
N REF. 5).
N REF. 3; AAD1
REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN KINASE, NON-MUSCLE
                                      5).
3; AAD15922/AAD15923)
                                                                 3; AAD15922/AAD15923).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calmodulin-binding;
                                     AAD15922/AAD15923/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
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RESULT
PTK7_HC
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTK7_HUMAN STANDARD,
Q13308; Q13417;
Q13308; Q13417;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-may-rootein kinase-like 7 precursor (Colon carcinoma kinase-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
CONFLICT
Mossie
"Colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                        TISSUE-Colon carcinoma, and Placenta
MEDLINE-96074849; PubMed-7478540;
Mossie K., Jallal B., Alves F., Sure
                                                                                                                                                                                                                                                                                                                                                                            PTK7 OR CCK4. (Human). Homo sapiens (Human). Euteryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                              tyrosine
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                DOMAIN
TRANSMEM
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                                            DOMAIN
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ProDom; PD000001; Euk_pkinase;
SMART; SM00410; IG_like; 2.
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TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, PANCREAS,
KINNEY, PLACENTA AND MELANOCYTES: WEAKLY EXPRESSED IN THYROID
GLAND, OVARY, BRAIN, HEART AND SKELETAL MUSCLE. ALSO EXPRESSED
ERYTHROLEUKEMIA CELLS. BUT NOT EXPRESSED IN COLON.
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSUI
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P08631; 12
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AF447167;
AF447170;
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AF447174;
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PF00069; pkinase; 1.
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AF447157;
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SM00219; TYIKC; 1.
E; PS00109; PROTEIN_KINASE_TYR; 1.
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IPR003598;
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IG-LIKE C2-TYPE I
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                                              C (POTENTIAL)
-TYPE DOMAIN
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SEQUENCE FROM N.A., AND REVISION TO 834.

Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

SIDDELL REPORTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABLY

THE CATALYTIC ACTIVITY OF TYROSINE KINASE. MAY BE CONNECTED TO THE

PATHOPHYSIOLOGY OF COLON CARCINOMAS AND/OR MAY REPRESENT A TUMOR
                                                                                                                                                                                                                                                                                                                                                                     receptor protein tyrosine kinase-like molecule closely related chick KLG.";
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted the companies of the companies of the contract of the companies o (See http://www.isb-sib.ch/announce/ There are no rest restrictions and EMBL outstation ST a for collaboration in in no way g

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Best Local (
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P98160; Q16287;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Basement membrane-specific heparan sulfate proteoglycan core
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DISULFID
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Mammalia; Eutheria;
                               molecules,
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                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=92112994; PubMed=1730768;
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                                                                                                         "Human
                                                                                                                           Kallunki P., Tryggvason K.
                                                                                                                                                                                                                                  NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
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  man basement membrane heparan sulfate proteoglycan core protein:
-kD protein containing multiple domains resembling elements of the density lipoprotein receptor, laminin, neural cell adhesion ecules, and epidermal growth factor.";
Cell Biol. 116:559-571(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATVFA------NGSLLLTQVRPRNAGIYRCIGQGQRGPPIILEATLHLAEIEDMPLF
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24.8%;
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BY SIMILARITY:
BY SIMILA
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AND 3).
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  TISSUE=Skin, and Colon;
TISSUE=Skin, and Colon;
MEDLINE=92235084; PubMed=1569102;
MEDLINE=92235084; PubMed=1., Tuan R.S., Iozzo R.V.;
Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;
Primary structure of the human heparan sulfate proteoglycan from Primary structure of the human heparan sulfate proteoglycan from Primary structure of the human heparan sulfate proteoglycan from Primary structure of the Low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, domains homologous to the low density lipoprotein receptor, laminin, 
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Cohen I.R., Graessel S., Murdoch A.D.,
"Structural characterization of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Fibrosarcoma;
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                                                                                                                                                                                                                                                                                                                                                         between
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Kallunki P., Eddy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91365376; PubMed=1679749;
Poddre G.R., Kovalszky I., Chu M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1018-1472 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Colon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND O-LINKED OLIGOSACCHARIDES.
SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV.
SIMILARITY: CONTAINS 22 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 3 LAMININ G-LIKE DO SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS SIMILARITY: CONTAINS 1 SEA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration
                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              properties. It serves as an attachment substrate for cells. SUBUNIT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane components such as laminin, prolargin and collagen type
                                            X62515;
M85289;
M64283;
S76436;
L22078;
P00740;
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                                                                                                                                                                                                                                                                            non-profit institutions as long and this statement is not removed.
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                                                                                                                                                                                                                               email to license@isb-sib.ch).
E; P98160;
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AAA52700.1;
AAA52699.1;
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R.L., Byers M.G.,
     HSPG2
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mplete human
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ProDom; PD003031; Laminin_B; 3.

SMART; SM00018); EGF_Lam; 6.

SMART; SM00018); EGF_Lia; 8.

SMART; SM00019; LDLa; 4.

SMART; SM00240; LamG; 3.

SMART; SM00282; LamG; 3.

SMART; SM00282; LamG; 3.

SMART; SM00282; EGF_1; 9.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01248; LAMININ_TYPE_EGF; 11

PROSITE; PS0125; LAM_G_DOMAIN; 3.

PROSITE; PS0125; LAM_G_DOMAIN; 3.

PROSITE; PS01209; LDLRA_1; 4.

PROSITE; PS01209; LDLRA_1; 4.

PROSITE; PS01204; EGF, 1:

PROSITE; PS0068; LDLRA_2; 4.

PROSITE; PS0024; SEA; 1.

PROSITE; PS0024; SEA; 1.
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rPro; IPR003906;
rPro; IPR003598;
rPro; IPR002172;
rPro; IPR002043;
rPro; IPR002049;
rPro; IPR000082;
rPro; IPR000082;
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rPro; IPR000083;
rPro; IPR000083;
rPro; IPR000083;
rPro; IPR000083;
rPr00053; laminit
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    matrix;
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19; 22.
1aminin_B; 3.
laminin_EGF; 7
laminin_G; 3.
ldl_recept_a;
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       EGF-like.
EGF_I.
EGF_I.
IJ_MHC.
IJ_C2.
LDL_recept_A.
Laminin_B.
Laminin_EGF.
Laminin_G.
SEA_domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 4.
IG-LIKE C2-TYPE DOMAIN 1
LAMININ BGF-LIKE 1 (N-TELL
LAMININ DOMAIN IV 1 (DOM.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.
  IG-LIKE
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POTENTIAL.

BASEMENT MEMBRANE-SDECIFIC HEDARAN

SULFATE PROTEOGLYCAN CORE PROTEIN.
IN EGF-LIKE 1 (N-TERMINAL).

IN EGF-LIKE 1 (C-TERMINAL).

IN EGF-LIKE 2 (INCOMPLETE).

IN EGF-LIKE 3 (INCOMPLETE).

IN EGF-LIKE 5 (N-TERMINAL).

IN EGF-LIKE 5 (N-TERMINAL).

IN EGF-LIKE 5 (N-TERMINAL).

IN EGF-LIKE 6.

IN EGF-LIKE 6.

IN EGF-LIKE 7.

IN EGF-LIKE 9 (N-TERMINAL).

IN EGF-LIKE 9 (N-TERMINAL).

IN EGF-LIKE 9 (N-TERMINAL).

IN EGF-LIKE 10.

IN EGF-LIKE 10.

IN EGF-LIKE 11.

RE C2-TYPE DOMAIN 2.

RE C2-TYPE DOMAIN 3.

RE C2-TYPE DOMAIN 5.

RE C2-TYPE DOMAIN 5.

RE C2-TYPE DOMAIN 6.

RE C2-TYPE DOMAIN 7.

RE C2-TYPE DOMAIN 9.

RE C2-TYPE DOMAIN 10.

RE C2-TYPE DOMAIN 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; Glycoprotein; Immunoglobulin domain;
SMP_COTJA
ID SMP_COTJA
AC Q92154;
DT 15-JUL-1998 (I
DT 15-JUL-1998 (I
DT 15-JUL-2002 (I
DT Schwann cell n
GN SMP.
OS Coturnix cotun
OC Eukaryota; Met
OC Archosauria; I
OC Coturnix.
OX NCBI_TaxID=938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
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                                                                                                                                                                                                                                                                                                      RESULT
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Best Local S
Matches 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3009
                                                                                               Coturnix coturnix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      φ
                                                                                                                                                                                                                                                                                                                                                                                                                    PODTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSRLHGSAYLTVQVMGELFI----PSVNL-VVAENEPCEVTCLPSHWTRLPDISWEL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --DTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGLMDSH-----TVLQISSAKPSDAGTYVCLAQNALGTAQKQVEVIV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLSVHGPPTVSVLPEGPVWVKVGKAVTLECVSAGEPRS----SARWTRISSTPAKLEQRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHIS--PNGSIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GLLVSHSSYYFVPEPSDLQSAVSTLALTPQSNGTLTCVATWKSLKARKSATVNLTVIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 25.3
52; Conservative
                                                                         Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                    221
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                                                                                                                                  (Rel. 36, Created)
(Rel. 36, Last sequence up
(Rel. 41, Last annotation
l myelin protein precursor.
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206
219
285
292
304
3325
                                                    Aves;
                                                                                                                                                                                                                                                            STANDARD;
                                                                       japonica (Japanese quail).
a; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212
225
234
297
310
319
337
                                                 Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG-LIKE C2-TYPE DOMAIN 12.
IG-LIKE C2-TYPE DOMAIN 13.
IG-LIKE C2-TYPE DOMAIN 14.
IG-LIKE C2-TYPE DOMAIN 15.
IG-LIKE C2-TYPE DOMAIN 16.
IG-LIKE C2-TYPE DOMAIN 17.
IG-LIKE C2-TYPE DOMAIN 19.
IG-LIKE C2-TYPE DOMAIN 20.
IG-LIKE C2-TYPE DOMAIN 21.
IG-LIKE C2-TYPE DOMAIN 21.
IG-LIKE C2-TYPE DOMAIN 21.
IG-LIKE C2-TYPE DOMAIN 22.
LAMININ G-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 3.
EGF-LIKE 3.
EGF-LIKE 3.
EGF-LIKE 4.
LAMININ G-LIKE 3.
LAMININ G-LIKE 4.
LAMININ G-LIKE 3.
HEPARAN SULFATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 122.5;
Pred. No. 0.26
98; Mismatches
                                                                                                                                                                                                                                                              PRT;
                                                    Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No. 0.2
                                                                                                                                                               update)
on update)
                                                                                                                                                                                                                                                            620
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A
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                                                    Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                         Euteleostomi;
                                                      Phasiahinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75;
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Best Local
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dulac C., Tropak M.B., Cameron-Curry P., Rossier J., Marshak D.F. Roder J., le Douarin N.M., "Molecular characterization of the Schwann cell myelin protein, structural similarities within the immunoglobulin superfamily.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00410; IG_like; 1.
SMART; SM00408; IGC2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S83711; AAB21466.1; -. HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Son send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myelin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92153423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 18-28; 120-132; 135-157 AND
                                                  280
                                                                                                                                        239
                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NONMYELINATING SCHWANN CELLS AND OLIGODENDROCYTES.

DEVELOPMENTAL STAGE: FIRST SYNTHESIZED AT EMBRYONIC DAY 5, :

REMAINS EXPRESSED BY CULTURED SCHWANN CELLS.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: EXCLUSIVELY EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         con 8:323-334(1992).
SUBCELLULAR LOCATION: Type I
VN--LVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAV---SIL
                                                                                                                                                                             PEAVGSGSGNEVIEGPQNATVLKGSQARFNCTV-SQGWKLIMWALSDMVVLSVRPMEPII 67
                                                                                     TNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPS
                                                                                                                                     PQVVGLWGPTEVVE---
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Cell adhesion; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003600;
                                                                                                                                                                                                                                                                                                              405
449
620
                                                                                                                                                                                                                             Conservative
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18
18
517
537
                                              REEPGRNL--RLLLSNVGPDDGGSFSCVAENRHGRHNRSLQLRVAYAPRAPV 329
                                                                                                                                                                                                                                                                                                                   ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Ig_c2.
: Ig_like.
                                                                                                                                                                                                                                                                                                                     66943 MW;
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                                                                                                                                                                                                                                                  5.7%;
21.5%;
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                                                                                                                                                                                                                                                                                                                                   IG-LIKE V-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN 1

IG-LIKE C2-TYPE DOMAIN 2

IG-LIKE C2-TYPE DOMAIN 3

IG-LIKE C2-TYPE DOMAIN 3

IG-LIKE C2-TYPE DOMAIN 4

BY SIMILARITY.

BY S
                                                                                                                                     GSDVELGCEAEGRPAPLISWFRGSEVL------
                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                  Score 118.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHWANN CELL MYELIN PROTEIN
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                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                  .049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rossier J., Marshak D.R.,
                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                             ;88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY MYELINATING
                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                    Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                           87;
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                                                                                                                                                                                                                         Gaps
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NEOL_CHICK
NEOL_CHICK
ACC POSSIBLE
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OC ENABLY
OC ENABLY
OC Archos
OC Gally
OC NCBL'
RR FENDER
RC STRAIL
RX MEDLI
R
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TRANSMEM
DOMAIN
DOMAIN
                                                                                 NON_TER
                                                                                                                                                               SMART; SM00060; FN3; 6.
SMART; SM00410; IG_like; 2.
SMART; SM00408; IGC2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vielmetter J., Roman J.M., Dreyer W.J.; "Neogenin, an avian cell surface protein expressed during neuronal differentiation, is closely related to the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q90610;
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 suppressor molecule deleted in colorectal cancer.";
J. Cell Biol. 127:2009-2020(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=White leghorn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neogenin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                      PRINTS; PRODO14;
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like
                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95105243; PubMed=7806578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEO1_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gell Biol. 127:2009-2020(1994).

FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION MOLECULE IN A BROAD SPECTRUM OF EMBRYONIC AND ADULT TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein.
DEVELOPMENTAL STAGE: IN RETINA, EXPRESSED ON GANGLION CELL FIBERS
AS SOON AS THEY BEGIN TO EXTEND THEIR AXONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GDGVRCVCMVNSIPDSSLVFELPT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGINIPGVLSSLP--SLGFSLPT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAIYEDHVTMEMRPARPEDGGTYSCVA--ENQHGASSTSFNISVEYPPLVLPASRCTAG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INGSLWVVSGDPVSVTCRAE----
                                                                                                                                                                                                                                                                                PF00041; fn3; 6
PF00047; ig; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P11276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U07644;
                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003961; FN_III.
IPR003962; FnIII_repeat.
                                                                                                                                                                                                                                                                                                                                                                                              IPR003006;
1091
1112
33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC59662:1; -.
                                                                                                                                        Immunoglobulin domain; Glycoprotein; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                         FNTYPEIII.
  1090
1111
1443
142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Embryonic brain;
                            CYTOPLASMIC (POTENTIAL)
                                                         POTENTIAL.
                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and for
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                          Neogenin precursor.
NEOL OR NGN.
HOMO Saplens (Human).
Eukaryota; Metazoa; Chordata; Ci
Mammalia; Eutheria; Primates; Cc
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID DISULFID DISULFID
                 TISSUE-Fetal brain;
MEDLINE-97312699; PubMed-9169140;
Wielmetter J., Chen X.-N., Miskevich F., Lane R.P., Yamakawa K.,
Korenberg J.R., Dreyer W.J.;
"Molecular characterization of human neogenin, a DCC-related pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          092859; 000340;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                         TISSUE=Fetal brain;
MEDLINE=97236653; PubMed=9121761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                              gene."
                                                                                                                                                                                                                                                                            Meyerhardt J.A., Look A.T., Bigner S.H.,
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                  Oncogene
                                                                                                                                                                                                                                                     "Identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEO1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 GFYQCIA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 LRAGGS----LLISDVTEEDVGTYTCIADNENETIEAQAELAVQVPPEFLKRPANIYAHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 -DQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSAYLTVQVMGELFIPSVNLVVAE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 IEGPQNATVLKGSQARFNCTVSQGW--KLIMWALSDMVVLSVRPMEPIITNDRFTSQRY- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRQPSSLTKVTGQNAVFPC-VAGGFPTPYVRWTKNG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTLTCVA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMDIVFECEVTGKPT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NE----PCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
49; Conser
       mapping
                                                                                                                                                                                                     14:1129-1136(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
       of its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,
                                                                                                                                                 (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%;
26.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158050
     gene (NEO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - PTVKWVKNGDVVIPSDYFKIVKEHNLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG-LIKE C2-TYPE DOMAIN 2
IG-LIKE C2-TYPE DOMAIN 3
IG-LIKE C2-TYPE DOMAIN 4
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 2
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 6
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 117.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             558C6795579C0E26
     to chromosomal position 15q22.3-
                                                                                                                                                                                                                                                   of neogenin, a DCC-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .17;
                                                                                                                                                                                                                                                                          Fearon E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73;
                         a DCC-related protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EELITED - - - SERFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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     InterPro; IPR003600; Ig_like Pfam; PF00041; fn3; 6. Pfam; PF00047; ig; 4. PRINTS; PR00014; FNTYPEIII. SMART; SM00060; FN3; 6. SMART; SM00410; IG_like; 1.
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EMBL; U72391; AAC51287.1;
HSSP; P02751; lTTF.
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밁 Qy

Que Mat	Query Match 5.5%; Score 114.5; DB 1; Length 1461; Best Local Similarity 24.4%; Pred. No. 0.3; Matches 68; Conservative 31; Mismatches 107; Indels 73; Gaps 1:
Qy	16 SGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITN 69
₽	203 SGMLVISNATEGDGGLYRCVVESGGPPKYSDEVELKVLPDPEVISDLVFLKQ 254
Qy	70QGGNFTSEMIHNV 92
뮹	255 PSPLVRVIGQDVVLPCVASGLPTPTIKWMKNEEALDTESSERLVLLAGGSLEISDV 310
Qy	LFIPSVNLVVAENEI
뮹	311 TEDDAGTYFCIADNGNETIEAQAELTVQAQPEFLKQPTNIYAHESMDIVFECEVTGKPT- 369
Qy	147 WTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARK 205
В	370PTVKMVKNGDMVIPSDYFKIVKEHNLQVLGLVKSDEGFYQCIAENDVGNAQA 421
Qy	206 SATVNLTVIRCPQDTGGGINIP-GVLSSLPSLGFSLPTW 243
рь	422 GAQL-IILEHAPATTGPLPSAPRDVVASLVSTRFIKLTW 459
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

April 28, 2003, 18:09:54; Search time 19.0659 Seconds

(without alignments) 1946.300 Million cell updates/sec

Title: Perfect score: US-09-729-264-6 2077

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

DB seq length: 0
DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match Match 100% first 45 summaries

Listing

Database :

score is derived No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

. 29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	о.	ഗ	4	ω	2	_	No.	Result
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	50K glycoprotein p	JC5519	2	338	4.9	101	45
-	killer cell inhibi	JC5894	N	841	4.9	101.5	44
	hypothetical prote	T46266	N	421	4.9	101.5	43
	T-cell surface gly '	RWRTC2	ب	344	4.9	101.5	42
	CD22 homolog/B lym	A46512	N	868	4.9	102	41
	hypothetical prote	T41530	N	721	4.9	102	40
	sax-3 protein'- Ca	T42405	N	1273	5.0	103	39
	coxsackie- and ade	JC7780	N	365	5.0	103	38
	connectin 3B - chi	PN0568	N	1323	5.0	103.5	37
	hypothetical prote	T29549	N	423	5.0	103.5	36
	sdk protein – frui,	T13924	N	2222	5.0	104	<u>3</u> 5
	polyprotein - fava	T12117	N	5825	5.1	105	34
	hypothetical prote	T16525	N	662	5.1	105	ω ω
	heparan sulfate pr	S18252	N	3707	5.1	105.5	32
	receptor tyrosine	I38912	Ν	882	5.1	105.5	<u>3</u>
	differentiation an	149583	Ν	862	5.1	105.5	30

ALIGNMENTS

advanced glycosylation end-products receptor precursor - human N;Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprot C;Species: Homo sapiens (man) C;Date: 24-May-1996 #Sequence_revision 07-Feb-1997 #text_change 16-Jul-1999 C;Date: 44-May-1996 #Sequence_revision 07-Feb-1997 #text_change 16-Jul-1999 C;Accession: I61596; B42879; S27968 R;Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, R;Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko,

Genomics 23, 408-419, 1994
A;Title: Three genes in the human MHC class III region near the junction with the clanterpart of mouse mammary tumor gene int-3.
A;Reference number: A55562; MUID:95137587; PMID:7835890
A;Accession: I61596

A; Molecule A; Status: nucleic acid sequence not shown; translation not shown; translated type: DNA from GB/

A; Residues: 1-404 < RES>

A;Cross-references: GB:D28769; NID:g561657; PIDN:BAA05958.1; PID:g561659 R;Neeper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan. Y.C.; Elliston, K.; J. Biol. Chem. 267, 14998-15004, 1992 A;Title: Cloning and expression of a cell surface receptor for advanced glycosylation A;Reference number: A42879; MUID:92340547; PMID:1378843 A;Accession: B42879.

A;Molecule type: mRNA
A;Residues: 'C',2-99,'R',101-404 <NEE>
A;Cross-references: EMBL:M91211; NID:g190845; PIDN:AAA03574.1; P[D:g190846

A; Note: sequence extracted from NCBI backbone (NCBIP:109438) A; Experimental source: lung

C;Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycellular function, thus contributing to tissue lesions in diabetes. C;Comment: This receptor appears also to mediate the effects of amyloid beta peptide ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.

A; Gene: GDB: AGER

A;Cross-references: GDB:306354; OMIM:600214 A;Map position: 6p21.3-6p21.3 A;Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2

C; Function:

A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG> F;23-404/Product: advanced glycosylation end products receptor #status predicted F;23-344/Domain: extracellular #status predicted <EXT> F;31-101/Domain: immunoglobulin homology <IM1>

F;137-210/Domain: immunoglobulin homology <IM2> F;252-303/Domain: immunoglobulin homology <IM3>

F;345-362/Domain: transmembrane #status predicted <TMM>F;345-362/Domain: intracellular #status predicted <TMT>F;25-81/Binding site: carbohydrate (Asn) (covalent) #status F;38-99,144-208,259-301/Disulfide bonds: #status predicted (covalent) #status predicted

Query Match

Score 151; DB 1;

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A;Title: Cloning of neurotrimin defines a new subfamily of differentially expressed A;Reference number: 156551; MUID:95198094; PMID:7891157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C;Accession: I56551
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues: 1-344 <RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                         181
                                                                                                                                                    129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 LTVQVMGELFIP----SVNLVVAENEP------
                                                                                                                                                                                                                               80
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GQKGTLQCEASAVPSAEFQ---WFK
                                 NIPGVL----SSLPSLGFSLPTWGK 245
                                                                                                            PEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCP-----QDTGGGI 224
                                                                                                                                                    H----LIVQVSPKIVEISSDISINEGNNISLTCIATGRPE-PTVTWR---HISPKAVGFV
                                                                                                                                                                                       HGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFV 169
                                                                                                                                                                                                                             DKWCLDPRVVLLSN---TQTQY---
                                                                                                                                                                                                                                                                  ----VRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSRL 109
                                                                                                                                                                                                                                                                                                                                          RHLLTVPEAVGSGSGNEVI-EGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLS-- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVPNEKGVSVKEQTRRHPETGLFTLQSELM---VTPARGGDPRPTFSCSFSPGLPRHRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IITNDRFTS-----QRYDQGGNFT--SEMIIHNVEPSD$GNIR----CSLQNSRLHGSAY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEDEYLE----IQGITREQSGEYECSAS-NDVAAPVVRRVNVTVNYPPYISEAKGTGVPV 235
                                                                                                                                                                                                                                                                                                        RLLFLYPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT-----PTCTLTIRCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTAPIQPRVWEPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIHWM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-344 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
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                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISIIE- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QSEEPEAGESSTGGP
                                                                                                                                                                                                                                                                                                                                                                                                     24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                   6.7%; Score 139.5;
24.9%; Pred. No. 0.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- PTAGSVGGSGLGTLALALGILGGLGTAALLIGVILW
                                                                                                                                                                                                                                                                                                                                                                                               Pred.
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8; Mismatches 1
                                                                                                                                                                                                                             ----SIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404
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                                                                                                                                                                                                                                                                                                                                                                                                     0.0062;
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                                                                                                                                                                                                                                                                                                                                                                                   110;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 344;
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                                                                                                                                                                                                                                                                                                                                                                                   49;
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Gene 155, 213-317, 1995
A;Title: Cloning, sequencing
A;Reference number: JC4025; N
                                                                                                                                                                                                                               A;Gene: GDB:OPCML; OBCAM; OPCM
A;Cross-references: GDB:251677; OMIM:600632
A;Map position: llpter-llqter
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-ter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51669
                                QΥ
                                                                           В
                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          opioid-binding cell adhesion protein - human C;Species: Homo sapiens (man) C;Date: 13-Jun-1995 #sequence_revision 14-Ju
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151669
밁
                                                                                                                                                                                                                                                                                                                                    A; Experimental source: brain C; Comment: This protein binds opioid alkaloids
                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-345 < SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Shark, K.B.; Lee, N.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: JC4025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                      C; Genetics
                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:L34774; NID:g514373; PIDN:AAA36387.1; PID:g514374
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: JC4025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U10986; NID:g606873; PIDN:AAA70168.1; PID:g606874
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A; Residues: 1-1427
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                                                                                                                                                                            Query Match
Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 LQRPSNVVAIEGQDAVLECAVS-GYPTPTIVWMQGD-----
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79
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                                                                           RLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAW-LNRSTILYAG
                                                                                                                RHLLTVPEAVGSGSGNEVI-EGPONATVLKGSQARFNCTVSQGWKLIMWALSDMVVL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCEVTCL----PSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGT 191
NDKWSIDPRVIILVN---TPTQY----
                                    ----SVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIEFECAVSGKPS-----PTVKWTKNGEVVIPSDYFQIVDGSNLR----ILGLVKSDEGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENE 136
                                                                                                                                                          l Similarity
73; Conserv
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25.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           g and localization to chromosome MUID:95237612; PMID:7721093
                                                                                                                                                            34;
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                                                                                                                                                                          Score 130; DB 2
Pred. No. 0.031;
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Pred. No. 0.
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---SIMIQNVDVYDEGPYTCSVQTDNHPKTSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-Jul-1995 #text_change
                                                                                                                                                                                              DB 2;
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                                                                                                                                                            108;
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                                                                                                                                                                                            Length 345
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127
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP:T01B7.8
A; Map position: 2
A; Introns: 20/3; 90/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z19867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: clone T01B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL: 266499; PIDN: CAA91301.1; GSPDB: GN00020; CESP: T0187.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      opioid-binding protein OPCAM precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 17-Mar-2000
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R;Schofield, P.R.; McFarland, K.C.; Hayflick, J.S.; Wilcox, J.N.; Cho, T.M.; Roy, S.; Le EMBO J. 8, 489-495, 1989

BMBO J. 8, 489-495, 1989

A;Title: Mclecular characterization of a new immunoglobulin superfamily protein with pot A;Title: Mclecular characterization of a new immunoglobulin superfamily protein with pot A;Reference number: S03199; MUID:89251576; PMID:2721489
                                                                                                            C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: transmembrane protein
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-345/product: opioid-binding protein OPCAM #status predicted <MAT>
                                                                                                                                                                                                                  A;Cross-references: EMBL:X12672; NID:9585; PIDN:CAA31192.1; PID:9586
                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-345 <SCH>
                                                                                                                                                                                                                                                                                                     A; Accession:
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                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 KAKNTGVSVGQKGILSCEASAVPMAEFQ---WFKEETRLATGLDG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 CPQDTGGGINIPGVL----SSLPSLGFSLPTWGK----VGLGLAG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 SVKEGQGFVSEDEYLE----ISDIKRDQSGEYECSAL-NDVAAPDVRKVKITVNYPPYIS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 SYY----FVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV-----IR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 LGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 PQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCCRRRCCGC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 CRTCCCTRCCTCCR 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 KRQGGCGCCGCGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LAILLAIGTEIAV----SQVQSAV-----LPVSSTELATVGTDVSTASTAIDTLGNSSSRV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
Local Similar - ... hes 72; Conservative
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                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.2%; Score 129.5; DB 32.1%; Pred. No. 0.015;
                        6.2%; Score 129; DB 2; Length 345
25.7%; Pred. No. 0.037;
ative 33; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                DB 2; Length 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        k:Du, Z.; Le, T.T.; Wilson, R. submitted to the EMBL Data Library, May 1997 A; Description: The sequence of C. elegans cosmid C09D1. A; Reference number: Z20679 A; Recession: T29757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999 C;Accession: T29757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein UNC-89 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Map position: 1
A:Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2: 454/1; 500/1; 537/1
/3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-6642 <DUZ>
A;Cross-references: EMBL:AF003131; PIDN:AAB54132.1; GSPDB:GN00019; CESP:unc-89
A;Experimental source: strain Bristol N2; clone C09D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 SVKEGQGFVSEDEYLE----ISDIKRDQSGEYECSAL-NDVAAPDVRKVKITVNYPPYIS 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 CPQDTGGGINIPGVL----SSLPSLGFSLPTWGKVGLGLA 251
                                                                                                                                                                                                                                                                                                                                                                                2038 LIIPNAQDSGKITVEASNEVGSSESSAQLTVNPPSTTPIVVDGPKSVTIKETETAEFKAT 2097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 NDKWSIDPRVIILVN---TPTQY------SIMIQNVDVYDEGPYTCSVQTDNHPKTSR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 RLLFLYPTGYPYRSGDATFPKAMDNYTYRQGESATLRCTIDDRYTRYAW-LNRSTILYAG 78
                                                                                                                                                                                        2144 TVKVTAQNSAGQDSKQADLKVEPNVKAPKFKSQLTDKVADEGEPLRWNLELDGPSPGT-- 2201
                                                                                                                                                                                                                                                                                    2098 IS-GFPAPTVKWTINEKIVEESRTITTIKTEDVYT-----LKISNAKIEQTG 2143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 ----SVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 RHLLTVPEAVGSGSGNEVI-EGPQNATVLKGSQARFNCTVSQGWKLIMWALSDNVVL---
                                                                                         2202 -EVSWLLNGQPLTKSDTVQVVDHGDGTYHVTIAEAKPEMSGTLTAKAKNAAGECETSAKV 2260
2261 TVNGGNKKPEFVQAPQN 2277
                                                                                                                                                                                                                                                                                                                                                                                                                               6 LTVPEAVGSG-----SGNE-------------------------VIEGPQNATVLKGSQARFNCT 40
                                                                                                                                       151 PDISWEL-GLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watch 6.2%; Score 129; DB Local Similarity 23.0%; Pred. No. 0.89;
                                                210 NLT-----VIRCPQD 219
                                                                                                                                                                                                                                                                                                                                  41 VSQGW--KLIMWALSDMVVLSVRPMEPIITNDRETSQRYDQGGNFTSEMIIHNVEPSDSG 98
                                                                                                                                                                                                                                    99 NIRCSLONSRLHGSAYLTVQVMGELFIPS----VNLVVAENEPCEVTCL---PSHWTRL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 6642:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97; Indels 60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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opioid-binding protein (clones SG8 and SG13) - rat C;Species: Rattus norvegicus (Norway rat)

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C;Keywords: transmembrane protein; tumor suppressor
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-1447/Product: tumor suppressor protein DCC #status predicted <MAT>
                                                                                                                                                               A;Cross-references: GDB:119838; OMIM:120470
A;Map position: 18q21.1-18q21.1
                                                                                                                                                                                                                                     A;Cross-references: GB:M32292; NID:g181492; PIDN:AAA35751.1; PID:g181493
                                                                                                                                                                                                                 A; Gene: GDB: DCC
                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-750 <FEA>
                                                                                                                                                                                                                                                                                                                                       A; Title: Identification of a chromosome 18g gene that is altered in colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                              A;Residues: Ī-1447 <HED>
A;Cross-references: EMBL:X76132; NID:g453209; PIDN:CAA53735.1; PID:g453210
R;Fearon, E.R.; Cho, K.R.; Nigro, J.M.; Kern, S.E.; Simons, J.W.; Ruppert, J.M.; Hamilto
                                                                                                                                                                                                                                                                                                                          A; Accession: A40098
                                                                                                                                                                                                                                                                                                                                 A; Reference number: A40098; MUID:90100559; PMID:2294591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The DCC gene product in cellular differentiation and colorectal tumorigenesis. A;Reference number: A54100; MUID:95011532; PMID:7926722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hedrick, L.; Cho, K.R.; Fearon, E.R.; Wu, T.C.; Kinzler, K.W.; Vogelstein, Genes Dev. 8, 1174-1183, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 05-Nov-1999
C;Accession: A5410; A40098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor suppressor protein DCC precursor - human N;Alternate names: colorectal cancer suppressor DCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Lippman, D.A.; Lee, N.M.; Loh, H.H.
Gene 117, 249-254, 1992
A;Title: Opicid-binding cell adhesion molecule (OBCAM)-related clones from a rat brain A;Reference number: JC1238; MUID:92347701; PMID:1339369
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C;Accession: JC1239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 SYY----FVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV----IR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 VH----LIVQVPPQIMNISSDITVNEISSVTLLCLAIGRPE-----PTVTWR------HL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 NDKWSIDPRVIILVN---TPTQY------SIMIQNVDVYDEGPYTCSVQTDNHPKTSR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 ----SVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQ-----NSR 108
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                                        Similarity
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                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                    24.8%;
                             6.2%; Score 128; DB 24.8%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.2%; Score 128; DB 2; Length 345; 25.3%; Pred. No. 0.044;
         33; Mismatches
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                                           DB 2; Length 1447;
      99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110; Indels
      50;
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Gaps
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  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-871 <GAN1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S60738
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                                                                                                                                                                                 Local Similarity
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                                                                                                                                                          Conservative
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C;Superfamily: mouse ror-related receptor; immunoglobulin homology; protein kinase ho C;Keywords: ATP; glycoprotein; phosphotransferase; receptor; transmembrane protein; t F;2-21/Domain: signal sequence #status predicted <SIG> F;2-871/product: protein-tyrosine kinase nskz, splice form 2 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice form 4 #status predicted <MAT2 F;22-456,'A',466-871/product: protein-tyrosine kinase nskz, splice f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;222,462/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;575-865/Domain: protein kinase homology <KIN>F;583-591/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;42-101/Domain: immunoglobulin homology <IMM1>F;135-192/Domain: immunoglobulin homology <IMM2>F;226-284/Domain: immunoglobulin homology <IMM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;498-518/Domain: transmembrane #status predicted <TRM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: X86444; NID: g929723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;CICOSS-references: EMBL:X86444; NID:g929723; PIDN:CAA60165.1; PID:g929724
A;Experimental source: splice form 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Ganju, P.; Walls, E.; Brennan, J.; Reith, A.D.
Oncogene 11, 281-290, 1995
A;Title: Cloning and developmental expression of Nsk2, a novel receptor tyrosine kina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000 C;Accession: I48696; S60738 R;Ganju, P.; Walls, E.; Brennan, J.; Reith, A.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: nucleic acid sequence not shown; translated from GB/ENBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-tyrosine kinase (EC 2.7.1.112) nsk2 precursor, splice form 2 - mouse
N;Alternate names: receptor-type tyrosine kinase
N;Contains: protein-tyrosine kinase nsk2 precursor, splice form 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comment: For alternate splice forms see PIR:148697
172 -----SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKLVKLEVEVLGRILRAPESHNV 223
                                                                                                                                                                                                             122 KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD-----NALRENSRIAALE- 171
                                                                                                      78 DQGCNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY----LTVQVMGELFIPSVNLVV 132
                                                                                                                                                                                                                                                                                                         19 EVIEGPQNATYLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRPMEPIITNDRFTSQRY 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 SNLR----ILGVVKSDEGFYQCVAENEAGNAQTSAQLIVPKPAIPSSS------VLPS 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 SDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 ELTVLVPPWFLNHPSNLYAYESMDIEFECTVS-GKPVPTVNWMKNGDVVIPSDYFQIVGG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 YLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 VI-----QLRSKKYSLLGG--SNLLISNVTDDDSGMYTCVVTYKNENISASA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 SRTGNEAEVRILSDPGLHRQLYFLQRPSNVVAIEGKDAVLECCVS-GYPPPSFTWLRGEE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 VVLSVRÞMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSGNEV------IEGPQNATVLKGSQARFNCTVSQGW--KLIMWALSDM 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-456, 'A', 466-871 <GAN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source: splice form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.1%; Score 127.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                           125; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X86445; NID:g929725
A;Experimental source: splice form 3
C;Comment: For alternate splice forms see PIR:I48696.
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A; Residues: 1-456,'A',466-881 <GAN2>
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A;Title: Cloning and developmental expression of Nsk2, a novel receptor tyrosine kinase A;Reference number: I48696; MUID:95349951; PMID:7624144
A;Accession: I48697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein-tyrosine kinase (EC 2.7.1.112) nsk2 precursor, splice form 1 -
N;Alternate names: receptor-type tyrosine kinase
N;Contains: protein-tyrosine kinase nsk2 precursor, splice form 3
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C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;498-518/Domain:
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A;Experimental source: splice form 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Ganju, P.; Walls, E.; Brennan, J.; Reith, A.D.
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                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                         133 AENEPCEVTC----LPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQ 187
                                                                                                                                                                                                                                        122 KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD-----NALRENSRIAALE- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 AENEPCEVTC----LPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQ 187
224 TFGSFVTLRCTEIGIP-----VPTISWIENGNAVSSGSIQESVKDRVIDSRLQLFITKP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 TFGSFVTLRCTEIGIP-----VPTISWIENGNAVSSGSIQESVKDRVIDSRLQLFITKP-
                                                                                                                                                                        78 DQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY----LTVQVMGELFIPSVNLVV 132
                                                                                                                                                                                                                                                                                           19 EVIEGPQNATVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRPMEPIITNDRFTSQRY 77
                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                     -----SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKLVKLEVEVLGRILRAPESHNV 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNGTLTCVAT - - - - WKSLKARKSATVNLTVIR - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GLYTCIATNKHGEKFSTAKAAATVSIAEWSKSQKDSQGYCAQYRGEGVLMQGPGEKML 335
                                                                                                                                                                                                                                                                                                                                                             70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-881 <GAN1>
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148697; S60740
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein kinase homology <KIN>
protein kinase ATP-binding motif
site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane #status predicted <TRM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   splice form
                                                                                                                                                                                                                                                                                                                                                                               6.18;
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                                                                                                                                                                                                                                                                                                                                                       41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Score 127.5; DB 1; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                       125;
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                                                                                                                                                                                                                                                                                                                                                       87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1070 <PAR>
A;Cross-references: GB:U40271; NID:g1322231; PIDN:AAC50484.1; PID:g1322232
C;Comment: This protein is a member of receptor protein tyrosine kinase far
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;726-1070/Domain: intracellular *status predicted <INC>
F;794-1065/Domain: protein kinase homology <KIN>
F;116,175,184,214,268,283,405,463,567,646/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:134760; OMIM:601890
A;Map position: 6p21.1-6p12.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: JC4593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 16-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein-tyrosine kinase-related receptor PTK7 precursor - human
N;Alternate names: receptor protein tyrosine kinase-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JC4593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: PTK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Characterization of the human full-length PTK7 A; Reference number: JC4593; MUID:97037064; PMID:8882711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Park, S.K.; Lee, H.S.; I Biochem. 119, 235-239,
379 ANIAESDAGVYTCHAA--NLAGQRRQDVNITVATVPSWLKKPQDSQLEEGKPGYLDCL 434
                                                        183 ALTPQSN-GTLTCVATWKSLKARKSATVNLTV-----IRCPQDTGGGINIPGVLSSL
                                                                                                                329 EPRVFTAGSEE---RVTCLPPKGLPEPSVWWEHAGVRLPTHGRVY-----QKGHELVL 378
                                                                                                                                                                     125 IPSVNLVVAENEPCEVTCLPSHWTRLPDISWE-LGL-LVSHSSYYFVPEPSDLQSAVSIL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 LVFLPTTSHRDPEDAQELLIHTAWNEL----
                                                                                                                                                                                                                                278 ATVFA-
                                                                                                                                                                                                                                                                                                                                       218 SIADESFARVVLAPQDVVVARYEEAMFHCQFSAQPPPSLQWLFEDETPITNRSRPPHLRR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389 VVPTPMPICREYCLAVKELFCAK 411
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                                                                                                                                                                                                                                                                                  70 DRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSR-----LHGSAYLTVQVMGELF 124
                                                                                                                                                                                                                                                                                                                                                                                               11 AVGSGSGNEVIEGPQNATVLKGSQARFNCTVS-QGWKLIMWALSDMVVLSVRPMEPIITN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JC4593
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19, 235-239, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                             ---NGSLLLTQVRPRNAGIYRCIGQGQRGPPIILEATLHLAEIEDMPLF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                     6.0%; Sur
24.8%; Preč
34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 125; DB 2
Pred. No. 0.25;
34; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 1070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          109;
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submitted to the EMBL Data Library, May 1996 A; Description: The sequence of C. elegans cosmid C27A2 $\,$

R;Nhan,

C;Species:

hypothetical protein C27A2.5 - Caenorhabditis elegans

Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15651

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Submitted to the EMBL Data Library, October 1991

A; Reference number: $77946

A; A; Reference number: $77946

A; A; Cession: $77946

A; A; Cession: $77946

A; Molecule type: mRNA

A; Residues: 1-57, 'D', 59-434, 'A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R'
71-2979, 'H', 2981-2994, 'G', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-4
A; Cross: references: EMBL:X65215; NID:g39469; PIDN:CAA44373.1; PID:g329470

R; Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K.
Genomics 11, 389-396, 1991

A; Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the A; Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the A; Reference number: A41059; MUID:92120660; PMID:1685141

A; Accession: A41059
A; Molecule type: mRNA
A; Cross-references: GB:S76436; NID:g243370; PIDN:AAB21121.1; PID:g243371
R; Dodge, G.R.; Kovalszky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Tozzo, Genomics 10, 673-680, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 07-Apr-1994 *tesquence_revision 07-Apr-1994 *text_change 05-Nov-1999 C;Date: 07-Apr-1996; S19256; S77946; A41059; A40306; B33625; A43625; A41736 R;Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
J. Biol. Chem. 267, 8544-8557, 1992
J. Biol. Chem. 267, 8544-8557, 1992
A;Title: Primary structure of the human heparan sulfate proteoglycan from basement membrator, laminin, neural cell adhesion molecules, and epidermal growth factor.
A;Reference number: A38096; MUID:92235084; PMID:1869102
A;Accession: A38096
A;Molecule type: mRNA
A;Residues: 1-4391 cMUR>
A;Cross-references: GB:M85289; NID:g184426; PIDN:AAA52700.1; PID:g184427
R;Kallunki, P.; Trygqvason, K.
J. Cell Biol. 116, 559-571, 1992
A;Reference number: A41736; MUID:92112994; PMID:1730768
A;Molecule type: mRNA
A;Residues: 1-57;D; 59-434, 'A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R', 71-2979, 'H', 2981-2994, 'G', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-3
A;Title: Heparan sulfate proteoglycan of human colon: partial molecular (A;Reference number: A40306; MUID:91365376; PMID:1679749
A;Accession: A40306
A;Molecule type: mRNA
A;Residues: 1018-1405, 'G', 1407-1409, 'G', 1411-1465 < DOD>
A;Residues: 1018-1405, 'G', 1407-1409, 'G', 1411-1465 < DOD>
A;Cross-references: GB:M64283; NID:9184424; PIDN:AAA52699.1; PID:9184425
R;Heremans, A; van der Schueren, B; De Cock, B.; Paulsson, M.; Cassimar J. Cell Biol. 109, 3199-3211, 1989
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A;Accession: T15651
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-188 <NHA>
A;Cessidues: 1-188 <NHA>
A;Cessidues: EMBL:U58760; NID:g1330384; PID:g1330389; PIDN:AAB00710.1; GSPDB:GN00A;Cross-references: EMBL:U58760; NID:g1330384; PID:g1330389; P
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A; Map position: 2
A; Introns: 19/3; 91/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X62515 R; Tryggvason, K.
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Best Local
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                                                                 J.J.;
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opioid-binding protein (clone DUZ1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03
C;Accession: JC1238
R;Lippman, D.A.; Lee, N.M.; Loh, H.H.
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F;4149-4151/Region: motor neuron attachment (L-R-E) motif F;4299-4301/Region: motor neuron attachment (L-R-D) motif F;4299-4301/Region: motor neuron attachment (L-R-D) motif F;629-53-71,76/Binding site: heparan sulfate (Ser) (covalent) #status predicted F;89,554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate F;2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1677-3686/Domain:
F;2007-2034/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: LDL receptor ligand-binding repeat homology; C;Keywords: chondroltin sulfate proteoglycan; glycoprotein; F;1-21/Domain: signal sequence #status predicted <SIG>F;22-4391/Product: perlecan #status predicted <MAT>F;22-193/Domain: I <DOM1>F;22-193/Domain: I <DOM1>
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F;1563-1610/Domain:
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F;531-1676/Domain:
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A; Residues: 1379-1384,'X',1386-1388,'X',1390-1398
JC1238
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F;4147-4175/Domain:
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                    RESULT 15
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                                                                                                                                                                                                                                                                                                                                                              VVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC------
                                                                                                                                                                                                   -GLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRC 216
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EGF homology <EGF>
laminin G repeat homology
EGF homology <EGF2>
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laminin-type EGF-like
laminin-type EGF-like
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                                                                                                                                                              -AVLQISSAKPSDAGTYVCLAQNALGTAQKQVEVIV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
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Pred. No. 1.7
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03-May-1994 #text_change

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A;Molecule type: mRNA
A;Residues: 1-338 <LIPY
A;Residues: 1-338 <LIPY
A;Cross-references: GB:M88709; NID:g203245; PIDN:AAA40858.1; PID:g203246
A;Experimental source: brain
C;Genetics:
A;Gene: OBCAM
A;Gene: OBCAM
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
Search completed: April 28, 2003, 21:09:17 Job time: 27.0659 secs
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A;Title: Opioid-binding cell adhesion molecule (OBCAM)-related clones from a rat brain A;Reference number: JC1238; MUID:92347701; PMID:1339369
A;Accession: JC1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.7%; Score 118.5; DB 2; Length 338; Best Local Similarity 25.2%; Pred. No. 0.22; Matches 72; Conservative 36; Mismatches 107; Indels 71;
                                                                                                        223 KNTGVSVGQKGILSCEASAVPMAEFQ---WFKEDTRLATGLDGVRI 265
                                                                                                                                       168 KEGQGFVSEDEYLE----ISDIKRDQSGEYECSAL-NDVAAPDVRKVKITVNYPPYISKA 222
                                                                                                                                                                                                                                                             167 Y----FVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTV-----IRCP 217
                                                                                                                                                                                                                                                                                                                   123 ----LIVQVPPQIMNISSDITVNEISSVTLLCLAIGRPE-----PTVTWR------HLSV 167
                                                                                                                                                                                                                                                                                                                                                                   111 GSAYLTVQVMGELFIPSVNLVVAENEPCEVTCL----PSHWTRLPDISWELGLLVSHSSY 166
                                                                                                                                                                                                                                                                                                                                                                                                                           74 KWSIDPRVIILVN---TPTQY------SIMIQNVDVYDEGPYTCSVQTDNHPKTSRVH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 --SVRPMEPIITNDRETSQRYDQGGNETSEMIIHNVEPSDSGNIRCSLQ-----NSRLH 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 LLFIP-GVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAW-LNRSTILYAGND 73
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Total number of hits satisfying chosen parameters:
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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2077
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                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

SUMMARIES

Result

esult No.	Score	Query Match 1	Length	₽ .	ID	Description
1	145.5	7.0	405	- ;	US-08-755-235-4	Sequence 4, Appli
N	138.5	6.7	2473	9	US-10-184-644-559	559,
ω	138.5	6.7	2473	9	US-10-184-634-559	Sequence 559, App
4	134	б. 5	708	9	US-10-174-590-584	Sequence 584, App
ഗ	134	6.5	708	9	US-10-176-758-584	Sequence 584, App
6	134	6.5	708	9	US-10-175-737-584	Sequence 584, App
7	134	6.5	708	9	US-10-173-706-584	Sequence 584, App
80	134	6.5	708	9	US-10-175-738-584	Sequence 584, App
9	134	6.5	708	9	US-10-175-752-584	Sequence 584, App
10	134	6.5	708	9	US-10-176-482-584	Sequence 584, App
11	134	6.5	708	9	US-10-176-757-584	Sequence 584, App
12	134	6.5	708	9	US-10-176-913-584	Sequence 584, App
13	134	6.5	708	9	US-10-180-552-584	•
14	134	6.5	708	9	US-10-180-557-584	Sequence 584, App
15	134	6.5	708	9	US-10-173-700-584	•
16	134	6.5	708	9	US-10-174-572-584	Sequence 584, App
17	134	6.5	708	9	US-10-174-579-584	`
18	134	ი. 5	708	9	US-10-174-582-584	Sequence 584, App
19	134	6.5	708	9	US-10-174-588-584	Sequence 584, App

45	44	43	42	41	40	39	38	37	36	35	34	သ	32	31	30	29	28	27	26	25	24	23	22	21	20	
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Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Seguence 584,	Sequence 584,	Seguence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,	Sequence 584,					
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ALIGNMENTS

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US-08-755-235-4
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Publication No. US20030059423A1

GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Schmidt, Ann Marie
APPLICANT: Wu, Jun
TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
FILE REFERENCE: 0575/50159
CURRENT APPLICANTION UMBER: US/08/755,235
CURRENT FILING DATE: 1996-11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.0%; Score 145.5; DB 1; Best Local Similarity 23.5%; Pred. No. 0.0034; Matches 91; Conservative 38; Mismatches 111;
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 405
TYPE: PRT
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216 CPODTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT------PTCTLTIRCCC 268
                                                                                                                                                                        221 RTAPIQPRVWEPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIHWM 272
                                                                                                                                                                                                        115 LTVQVMGELFIP----SVNLVVAENEP-------CEVTCLPSHWTRLPDISWE 156
                                                                                                                                                                                                                                                                            164 LYPNEKGYSYKEQTRRHPETGLFTLQSELM----VTPARGGDPRPTFSCSFSPGLPRHRAL 220
                                                                                                                                                                                                                                                                                                         9 PEAVGSGSGNEVIEGPQNATVLKGSQARFNCTVSQG---WKLIMWALSDMVVLSVRPMEP 65
                                                                            KD------GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVVSISIIE 323
                                                                                                                         LGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKS-ATVNLTVIR 215
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LENGTH: 2473
TYPE: DNA
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           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C217
   CURRENT APPLICATION
                                                                           APPLICANT:
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CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                                  2308 -----ATTCCTCATCGCCCACCCCACCCCGCCCCCACCACC 2344
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                                                                                                                                                                                                                                                                                                                                                                                                                                    243 WGKVGLGLAGTMLLTPTCTLTIRCCCCR-RRCCGCNCCCRCCFCC 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                      559, Application US/10184634
                                                                                                                                                                                                                                                     Baker, Kevin P.
                                                                                    Smith, Victoria Watanabe, Colin K. Wood, William I.
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                                                                     Zhang, Zemin
                                                                                                                                           Pan, James
                                                                                                                                                              Gurney, Austin L.
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o. US20030044930A1
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NUMBER: US/10/184,634
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; ORGANISM: Homo Sapien
US-10-184-634-559
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 584
LENGTH: 708
TYPE: PRT
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/174,590 CURRENT FILING DATE: 2002-06-18
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187 STLTLTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVT 230
                                  177 SAVSILALTPOSNGTLTCVATWKSLKARKSATVNLTVIRCPODT 220
                                                                            132 ---PSVSLVA--GVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEGTPGSVE 186
                                                                                                                   123 LFIPSVNLVVAENEPCEVTCLPSHWTR-LPDISW-ELGLLVSHSSYY--FVPE--PSDLQ 176
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                                                                                                                                                          72 WSRYWISGNAANGQHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVLVPPEAPQVLGG 131
                                                                                                                                                                                               74 SQRYDQGGNFTS---EMIIHNVEPSDSGNIRCSLQNSRLHG-SAYLTV-----QVMGE 122
                                                                                                                                                                                                                                        20 AGPSPHFLQQPEDLVVLLGEEARLPCALGAYWGLVQWTKSGLALGGQR------DLPG 71
                                                                                                                                                                                                                                                                           14 SGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRFT 73
                                                                                                                                                                                                                                                                                                                                      Match 6.5%; Local Similarity 23.7%;
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Godowski, Paul J.
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 584
LENGTH: 708
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION
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CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker, Kevin P.
                                                    CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C50
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Goddard, Audrey
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                                                                                                                                                                  Wood, William I.
                                                                                                                                                                                      Smith, Victoria Watanabe, Colin K.
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Pred. No. 0.045;
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-584
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Best Local Similarity 23.7%;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT FILING DATE: 2002-06-17
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177 SAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDT 220
                                                          132 ---PSVSLVA--GVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEGTPGSVE 186
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                                                                                                123 LFIPSVNLVVAENEPCEVTCLPSHWTR-LPDISW-ELGLLVSHSSYY--FVPE--PSDLQ 176
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                                                                                                                                         72 WSRYWISGNAANGQHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVLVPPEAPQVLGG 131
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Godowski, Paul
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Pred. No. 0.045;
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                                                                                                                                                                                                                                                                                                                                     Publication No.
                                                                                                                                                                                                                                                                                                                                                          Sequence 584,
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LENGTH: 708
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CURRENT APPLICATION NUMBER: US/10/175,752
                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C60
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 584
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Best Local Similarity
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CURRENT FILING DATE: 2002-06-20
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NUMBER OF SEQ ID NOS: 612
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                                                            72 WSRYWISGNAANGQHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVLVPPEAPQVLGG 131
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US-10-176-757-584
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CURRENT FILING DATE: 2002-06-20
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Godowski, Paul
Watanabe, Colin K. Wood, William I.
                                                                              Gurney, Austin L.
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23.7%;
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Pred. No. 0.045;
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NUMBER OF SEO ID NOS: 612
SEO ID NO 584
LENGTH: 708
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Best Local :
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LENGTH: 708
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/180,552
CURRENT FILING DATE: 2002-06-25
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CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                         Prior Application removed NUMBER OF SEQ ID NOS: 612
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                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapien
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74 SQRYDQGGNFTS---EMIIHNVEPSDSGNIRCSLQNSRLHG-SAYLTV-----
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; TYPE: PRT; ORGANISM: Homo Sapien US-10-180-557-584
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                                                                                                                                                                                                                                  RESULT 15
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 584
LENGTH: 708
                                                                                                                                               GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/180,557
CURRENT FILING DATE: 2002-06-25
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                                                                                                      APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                   Godowski, Paul J. Gurney, Austin L.
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Goddard, Audrey
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LENGTH: 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/173,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
187
                                       177
                                                                              132 --- PSVSLVA--GVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEGTPGSVE 186
                                                                                                                                                                                                                                                20
                                                                                                                                                                                                       74 SQRYDQGGNFTS---EMIIHNVEPSDSGNIRCSLQNSRLHG-SAYLTV-----QVMGE 122
                                                                                                                                                                                                                                                                                        14 SGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRFT 73
                                                                                                                                                                                                                                                                                                                                                     Local Similarity
STLTLTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVT 230
                                       SAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDT 220
                                                                                                                      LFIPSVNLVVAENEPCEVTCLPSHWTR-LPDISW-ELGLLVSHSSYY--FVPE--PSDLQ 176
                                                                                                                                                               WSRYWISGNAANGQHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVLVPPEAPQVLGG 131
                                                                                                                                                                                                                                                   AGPSPHFLQQPEDLVVLLGEEARLPCALGAYWGLVQWTKSGLALGGQR-----
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                                                                                                                                                                                                                                                                                                                                    Conservative
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23.7%;
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Pred. No. 0.045;
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10;

Search completed: April 29, 2003, 20:17:34 Job time: 27.0659 secs

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Result
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Maximum DB
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    Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/backfiles1.pep:*
     Length
    DВ
 US-08-977-767-3
US-09-041-886-25
PCT US94-05277-2
US-08-374-334-16
US-08-644-271-29
US-08-644-271-29
US-09-651-200-2
US-09-651-200-2
US-09-651-200-24
US-09-651-200-24
US-09-651-200-24
US-08-633-148-2
US-08-633-148-2
US-08-634-271-1
US-09-077-955-1
US-09-077-955-1
US-09-079-954-15
US-09-79-424-3
US-08-95-084-93-15
PCT-US95-08493-19
PCT-US95-08493-21
US-08-445-640-2
US-08-445-640-2
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808.430 Million cell updates/sec
Sequence 3, Appli
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Sequence 3, Appli
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Query Match

6.2%;

Score 128.5;

DB 2;

Length 1345;

RESULT 1 US-08-977-767-3 US-08-977-767-3 J Sequence 3, Application US/ Patent No. 5972684 GENERAL INFORMATION: APPLICANT: Bendman, Olg. APPLICANT: Wile, Henry APPLICANT: Corley, Weil TITLE OF INVENTION: CAR APPLICANT: Greenwald, S. APPLICANT: Greenwald, S. APPLICANT: Greenwald, S. APPLICANT: CORLEY, Weil TITLE OF INVENTION: CAR RESEE: Incyte Pha STREET: 3174 POTTER COUNTRY: USA ZIP: 94304 COUNTRY: USA ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compati OPERATION SYSTEM: DOS SOFTWARE: FASTSEQ for CURRENT APPLICATION UMBER: USA APPLICATION NUMBER: USA APPLICATION NUMBER: HILING DATE: FILING DATE: Herewith CLASSIFICATION NUMBER: USA APPLICATION NUMBER: USA APPLICATION NUMBER: USA APPLICATION NUMBER: REFERENCE/DOCKET NUMBER: FELETAX: 650-845-4166 TELEEYA: 650-845-4166 TELEX: REFERENCE/DOCKET NUMBER: REFER		28 109.5 5.3 30 109.5 5.3 31 109.5 5.3 32 109.5 5.3 33 107.5 5.3 34 106.5 5.1 35 106.5 5.1 36 106 5.1 37 105 5.1 38 105 5.1 40 105 5.1 41 105 5.1 42 105 5.1 43 105 5.1 44 105 5.1 45 104.5 5.0
ON: ON: ON: ON: ON: ON: ON: ON: OHAN; Sara Tley, Neil C. Tley, Neil C. Tley, Neil C. Ton: CARBONIC ANHYDRASE VIII NCES: NCYE Pharmaceuticals, Inc. Porter Drive Lite Diskette M Compatible	ALIGNMENTS	890 3 US-08-445-461-2 911 1 US-08-286-305A-1 911 2 US-08-441-104A-1 911 2 US-08-441-381A-1 911 4 US-09-417-381A-1 912 1 US-08-415-751-6 946 5 PCT-US95-08493-1 801 1 US-07-906-349A-6 319 1 US-08-597-495B-22 319 4 US-09-368-051A-22 319 4 US-09-365-3656-6 319 4 US-09-354-465A-6 319 4 US-09-254-465A-6 319 4 US-09-254-465A-6 319 4 US-09-353-132-2 690 4 US-09-553-132-2 690 4 US-09-553-132-2 1297 4 US-09-540-245A-17 1381 4 US-09-540-245A-17 1381 4 US-09-540-245A-17
		Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 22, Appl Sequence 22, Appli Sequence 6, Appli Sequence 2, Appli Sequence 17, Appli Sequence 17, Appli

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Best Local Similarity
                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILLING CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

NAME: Campbell, Cathryn A.

1.815
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
 383 SNLR----ILGVVKSDEGFYQCVAENEAGNAQTSAQLIVPKPAIPSSS-----VLPS 430
                                    173 SDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSS
                                                                                                      114 YLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                        324 ELTVLVPPWFLNHPSNLYAYESMDIEFECTVS-GKPVPTVNWMKNGDVVIPSDYFQIVGG 382
                                                                                                                                                   279 VI-----
                                                                                                                                                                                                                    220 SRTGNEAEVRILSDPGLHRQLYFLQRPSNVVAIEGKDAVLECCVS-GYPPPSFTWLRGEE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                456 CGTGAAGAGGGTCCTCTATGACCCCTTTCCTGCCCCCTCTGAGACTCAGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 GTCTCTGT----
                                                                                                                                                                                56 VVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSA 113
                                                                                                                                                                                                                                                            14 SGSGNEV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 GTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGI----NIPGVLSSLPSLGFSLPTWGK 245
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                        1447 amino acids
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                                                                                                                                                                                                                                                      -------IEGPQNATVLKGSQARFNCTVSQGW--KLIMWALSDM 55
                                                                                                                                              -QLRSKKYSLLGG--SNLLISNVTDDDSGMYTCVVTYKNENISASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proapoptotic Peptides, Dependence Polypeptides and Methods of Use : 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          6.2%; Score 128; DB 4; Length 1447; 24.8%; Pred. No. 0.012; tive 33; Mismatches 99; Indels 5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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APPLICANT:
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431 AP 432
                                                                                                    173 SDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                  233 LP 234
                                                                  383 SNLR----ILGVVKSDEGFYQCVAENEAGNAQTSAQLIVPKPAIPSSS---
                                                                                                                                        324 ELTVLVPPWFLNHPSNLYAYESMDIEFECTVS-GKPVPTVNWMKNGDVVIPSDYFQIVGG 382
                                                                                                                                                                              114 YLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEP 172
                                                                                                                                                                                                                279 VI-----QLRSKKYSLLGG--SNLLISNVTDDDSGMYTCVVTYKNENISASA 323
                                                                                                                                                                                                                                                                                      220 SRTGNEAEVRILSDPGLHRQLYFLQRPSNVVAIEGKDAVLECCVS-GYPPPSFTWLRGEE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FITLE OF INVENTION:
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                                                                                                                                                                                                                                                  56 VVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSRLHGSA 113
                                                                                                                                                                                                                                                                                                                        14 SGSGNEV-------IEGPQNATVLKGSQARFNCTVSQGW--KLIMWALSDM 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1001 G Street: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202.508.9299
TELEX: 197430 BBMB UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1447 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                              Conservative
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Zabrecky, James R.
VENTION: Antibodies Specific for DCC Gene Product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinzler, Kenneth W.
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Jarosz, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Pred. No. 0.012;
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RESULT 4
US-08-374-834-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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APPLICANT: Valenz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: REFERENCE/DOCKET NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: //.
STREET: //.
CITY: Tarrytown
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 01
FILING DATE: 21-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD-----SPLRENSRIAVLE- 171
    328 TETASLPPKSCESSDPEQRNSSCGPPHQRADQRP----PRPASHPQASFNLA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 P-----CEVTCLPSHWTRLPDISW-ELGLLVSHSSYYFVPEPSDLQSAVSILALTPQ 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 -----SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKVVKLEVEVFARILRAPESHNV 223
                                                                               389 TPIPICREYCLAVKELFCAKE----WLVMEEKTHRGLYRSEMHLLSVPECSKLPSMHWDP 444
                                                                                                                                                                                                                                          336 FLNTSYADPEEAQELLVHTAWNEL-----KVVSPVCRPAAEALLCNHIFQECSPGVVP 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 TFGSFVTLHCTATGIP-----VPTITWIENGNAVSSGSIQESVKDRVIDSRLQLFITKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Cobert, Robert J. REGISTRATION NUMBER: 36,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 DQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMGELFIPSVNLVVAENE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 EVIEGPQNATVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRPMEPIITNDRFTSQRY 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNGTLTCVAT----WKSLKARKSATVNLTVIRCPQDTGGG------INIPGVLSSLP 234
                                                                                                                                                      ----CCCRCC-----FCCRRKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKT 327
                                                                                                                                                                                                                                                                                                                                                                                                     --GLYTCIATNKHGEKFSTAKAAATISIAEWSKPQKDNKGYCAQYRGEVCNAVLAKDALV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
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amino acid
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                                                                                                                                                                                                                                                                                                                     ----PTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 127.5; DB Pred. No. 0.0065;
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Patent No. 5814478
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                      Matches
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TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
TITLE OF INVENTION: AND LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/008,657
FILING DATE: 15-DEC-1995
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: |
                                                                                                                                                                                                                                                                                                        122 KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD-----SPLRENSRIAVLE- 171
336 FLNTSYADPEEAQELLVHTAWNEL------KVVSPVCRPAAEALLCNHIFQECSPGVVP 388
                                                                                                                                                                                                                             172 -----SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKVVKLEVEVFARILRAPESHNV 223
                                                                                                              188 SNGTLTCVAT----WKSLKARKSATVNLTVIRCPQDTGGG------INIPGVLSSLP 234
                                                                                                                                                     224 TFGSFVTLHCTATGIP-----VPTITWIENGNAVSSGSIQESVKDRVIDSRLQLFITKP- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Regemeto... - street: 777 Old Saw Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 10-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Tarrytown
                                                                                                                                                                                                                                                                    78 DQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMGELFIPSVNLVVAENE 136
                                                                                                                                                                                                                                                                                                                                              19 EVIEGPQNATVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRPMEPIITNDRFTSQRY 77
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                                    ----PTWGKVGLGLAGTMLLTPTCTLTTRCCCCRRRCCGCN-----
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; Pred. No. 0.0065;
51; Mismatches 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 869;
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                                                                      Sequence 1, Application US/09062365 Patent No. 6465422
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SEQ ID NO 33
LENGTH: 869
APPLICANT: Stern, David
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Best Local :
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                    APPLICANT: Schmidt, Ann Marie
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NUMBER OF SEQ ID NOS: 36
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CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PC/US96/20696
EARLIER FILING DATE: 1996-12-13
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TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
FILE REFERENCE: REG195-B-PCT-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/008,657
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                                                                                                                                                                                                                    445 TACARLP-----HLDYNKENLKTFPP--MTSSKPSVDIPNLPSSSSSSFSVS
                                                                                                                                                                                                                                                                                                                                                          278 ----CCCRCC-----FCCRRKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKT
                                                                                                                                                                                                                                                                  328 TETASLPPKSCESSDPEQRNSSCGPPHQRADQRP----PRPASHPQASFNLA 375
                                                                                                                                                                                                                                                                                                               389 TPIPICREYCLAVKELFCAKE----WLVMEEKTHRGLYRSEMHLLSVPECSKLPSMHWDP 444
                                                                                                                                                                                                                                                                                                                                                                                                             336 FLNTSYADPEEAQELLVHTAWNEL------KVVSPVCRPAAEALLCNHIFQECSPGVVP 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 SNGTLTCVAT----WKSLKARKSATVNLTVIRCPQDTGGG-----INIPGVLSSLP 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 TFGSFVTLHCTATGIP-----VPTITWIENGNAVSSGSIQESVKDRVIDSRLQLFITKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 -----SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKVVKLEVEVFARILRAPESHNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD-----SPLRENSRIAVLE- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 SLGFSL-----PTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 DQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMGELFIPSVNLVVAENE 136
                                             INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GLYTCIATNKHGEKFSTAKAAATISIAEWSKPQKDNKGYCAQYRGEVCNAVLAKDALV 335
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US-09-062-365-1
                                                                                                                                       Matches 77;
                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                    SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09651200 Patent No. 6429303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Green et al
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
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Best Local
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-0
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PRIOR FILING DATE: 1999-(
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
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CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                 LENGTH: 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 LVPNEKGVSVKEQTRRHPETGLFTLQSELM---VTPARGGDPRPTFSCSFSPGLPRHRAL 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 PEIVDSAS--ELTAGVPN------KVGTCVSEGSYPAGTLSWHLDG------KP 141
       67
                                               48
                                                                                     14 SGSGNEVIEGPQNATV-LKGSQARFNCTVS--QGWKL----IMWALSDMVVLSVRPMEPI 66
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                                          SPTGAVEVQVPEDPVVALVGTDATLHCSFSPEPGFSLTQLNLIWQLTDTKQLV----- 100
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                                                                                                                                    Conservative
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                                                                                                                                                       6.0%; Score 124.5; DB 21.2%; Pred. No. 0.0033;
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                                                                                                                                  51; Mismatches
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                                                                                                                                                                          DB 4; Length 340;
                                                                                                                                127; Indels 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Green et al
APPLICANT: Green et al
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
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PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
PRIOR FILING DATE: 2000-02-18
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Homo sapiens
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HGSVTITGQPMTFPPEAL---
                                     GGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCCRRCCGCNCCC 280
                                                                                VTTSQMANEQGLFDVHSVLRVVLGANGTYSC-----
                                                                                                                                                                                                       AYLTVQVMGELFIPSVNLV----VAENEPCEVTCLPSHWTRLP--DISWELGL---LVSH 163
                                                                                                                                                                                                                                                ---HSFTEGR-DQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV-SIRDFGS 256
                                                                                                                                                                                                                                                                                          ITNDRFTSQRYDQGGNF------TSEMIIHNVEPSDSGNIRCSLQNSRLHGS 112
                                                                                                                                                                                                                                                                                                                                 SPTGAVEVQVPEDPVVALVGTDATLHCSFSPEPGFSLTQLNLIWQLTDTKQLV-----
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                                                                                                                                                               AAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITC--SSYRGYPEAEVFWQDGQGVPLTGN 314
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                                                                                                                                                                                                                                                                                                                                                                                                                    1. Similarity 21.2%; Pred. No. 0.0047; 77; Conservative 51. Winner-1.0047;
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                                                                                                                                                                                                                                                                                                                                                                                                                    51; Mismatches 127; Indels 109;
-WVTVGLSVCLIALLV--
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; SOFTWARE: PatentIn Ver.

; SEQ ID NO 6

; LENGTH: 534

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-651-200-6
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Best Local
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CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/153383
PRIOR FILING DATE: 1999-09-03
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PRIOR FILING DATE: 2000-02-18
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                                                                                                                                                     ALAFVCWRK-----IKQSCEEENAGAEDQDG----
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US-09-651-200-24

Sequence 24, Application US/09651200 Patent No. 6429303

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SEQ ID NO 24
LENGTH: 534
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                                                                                                                                                                                                          Sequence 4, Application US/08633148 Patent No. 5864018
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PRIOR APPLICATION NUMBER: 60/172909
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-02-18
                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                          APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIHODLES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND
                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                      APPLICANT:
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   TWO EMBARCADERO CENTER,
                                                                                                                                                                      MORSER, MICHAEL J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.9%;
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                     8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LVRNPVLQQDA 449
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                                                                                              AND USES THEREFOR
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US-08-633-148-2
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Best Local
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                   APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARKO
APPLICANT: HOLLANDER, DORIS &
TITLE OF INVENTION: ANTIBODII
TITLE OF INVENTION: END-PRODI
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                               NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
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                                                                                            STREET: TWO EMBARCADERO CENTER, 8TH FLOOR CITY: SAN FRANCISCO
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                                                    COUNTRY:
                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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                                                                             CALIFORNIA
                                                      U.S.A.
                                                                                                                                                                                                                                                                MORSER, MICHAEL J.
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Sequence 2, Application US/08633148 Patent No. 5864018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 PQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGT 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 16-APR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 PEAVGSGSGNEVIEGPONATVLKGSQARFNCTVSQG----WKLIMWALSDMVVLSVRPMEP 65
                                                                                                                                                                                                                                                                                             LGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRC 216
                                                                                                                                                                                                                                                                                                                                          RTAPIQPRVWEPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIHWM 250
                                                                                                                                                                                                                                                                                                                                                                                             LTVQVMGELFIP----SVNLVVAENEP------CEVTCLPSHWTRLPDISWE 156
                                                                                                                                                                                                                                               KD-----GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISIIE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IITNDRFTS-----QRYDQGGNFT--SEMIIHNVEPSDSGNIR----CSLQNSRLHGSAY 114
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SYSTEM: PC-DOS/MS-DOS
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24.9%; Pred. No. 0.005;
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END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

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US-08-374-834-1
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TELEPHONE: (415) 326-2400
TELEPHANE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                            STREET: Tarrytown CITY: Tarrytown STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                      SOFTWARE: PatentIn Rel. CURRENT APPLICATION DATA:
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                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 LVPNEKGVSVKEQTRRHPETGLFTLQSELM---VTPARGGDPRPTFSCSFSPGLPRHRAL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 PEIVDSAS--ELTAGVPN------KVGTCVSEGSYPAGTLSWHLDG-------KP 163
                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 IITNDRFTS-----QRYDQGGNFT--SEMIIHNVEPSDSGNIR----CSLQNSRLHGSAY 114
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                    CLASSIFICATION:
                                        FILING DATE:
                                                      APPLICATION NUMBER: US/08/374,834
                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 PEAVGSGSGNEVIEGPQNATVLKGSQARFNCTVSQG---WKLIMWALSDMVVLSVRPMEP 65
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SYSTEM: PC-DOS/MS-DOS
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linear
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US-08-644-271-1
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                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08644271 Patent No. 5814478
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APPLICANT: Valenz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                               TITLE OF INVENTION: TITLE OF INVENTION:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
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                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                                                                                                                              COUNTRY:
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VENTION: NOVEL TYROSINE KINASE RECEPTORS
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                 FastSEQ Version 2.0
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Search completed: April 28, 2003, 21:12:23 Job time : 18.0485 secs
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SEQUENCE CHARACTERISTICS:
SEQUENCE: 868 amino acids
TYPE: amino acid
                                                                                                           328 TETASLP-----PKSC 338
                                                                         432 PECSKLPSMHQDPTAC 447
                                                                                                                                                389 TPMPICREYCLAVKELFCA---
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TOPOLOGY: unknown
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                                                                                                                                                                                                                                                            ----TWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCN----- 277
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Total number of hits satisfying chosen parameters:
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score greater than or equal to the score or the result well and is derived by analysis of the total score distribution. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

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Extracorporeal cir	Mouse B7-like prot	Mouse B7-like prot	Rat B7-like protei	Mouse B7-like prot	Novel human diagno	Human B7-like prot	Human B7-like prot	Human B7-like prot	Human B7-like prot	Description

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ABG61942	AAW08747	AAB68421	AAG77856	78	7	AAY52130	CD.	AAR84091,	AAW62573	AAR84092	AAW62568		AAW26506	AAW26611	AAW62583	AAW62569	AAR94982	AAW62575	AAU84351	AAR13144	AAB50693	AAY33498	AAR68553	AAM38713	575	AAU29315	ABB75753	ABB75751	ABB11587	AAY70469	AAW81030	AAM48745	775	AAE23219
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ALIGNMENTS

ğ	7 1 542 AAU/5542 standard; Protein; 386 AA.
	ein; 3

Human; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirelumatic; antiinflammatory; dermatological; antipscriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder.

Homo sapiens.

WO200200710-A2

03-JAN-2002

28-JUN-2000; 2000US-214512P. 28-NOV-2000; 2000US-0729264. 28-JUN-2001; 2001WO-US20719

(AMGE-) AMGEN INC.

Welcher AA, Sarmiento UM, Schultz HJ, Chute HT;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the amino acid sequence of human B7-L_h3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Fig 3; 135pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for enhancing the immune response to tumours. (I) plays \mathfrak g growth and maintenance of cancer cells based on the observation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
241 PTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKS
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                                                                                                                                                                                                                                                                                                                      RPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVM
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                                                                                                                                               ILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSL
                                                                                                                                                                                                  GELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVS
                                                                                                                                                                                                                                             GELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVS
                                                                                                                                                                                                                                                                                               RPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVM
                                                                                                                                                                                                                                                                                                                                                                                          MERHLLTYPEAVGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSV
                                                                                               ILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                 testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L
                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and proliferating disorders.
                                                                                                                                                                              seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian,
                                                                                                                                                                                                                                              proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and afterlosclerosis -
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                   autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic
                                                             molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat
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28-NOV-2000;
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and psoriasis, chronic
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2000US-0729264.
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Best Local
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                             Homo sapiens
                                                                                          antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease;
                                                                                                                                           Human; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirheantiinflammatory; dermatological; antipsoriatic; neuroprotective;
                                                                                                                                                                                                            Human B7-like protein, B7-L_h2.
                                                                                                                                                                                                                                                 23-APR-2002
                                                                                                                                                                                                                                                                                  AAU75541;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shock syndrome
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                                                             shock syndrome; allergy; nephropathy; skin disorder;
rinopathy; lymphoproliferative disorder.
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                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SNTTVV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergy, asthma and hypersensitivity reactions,
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Pred. No. 3.3e-159;
1; Mismatches 0;
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autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They
                                                                                                                                                                                                                                                                                                       are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polypeptide, polypucleotide encoding it and antibody against (i useful for treating B7-like polypeptide-related disease, disorders conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and
                                        treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the amino acid sequence of human B7-L_h2.
                                                                                                                                                                                                                         proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat
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Sequence 38E

Query Match Best Local : Matches Local 371; Similarity Conservative 96.3%; Score 2000; DB 23; Pred. No. 4.8e-158; Mismatches DB 23; Indels Length 386; 0; Gaps

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AENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTL 192

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                            The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) a useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive, antiarthritic; antitutemat antiinflammatory; dermatological; antipscriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       for diagnosing, preventing and treating reproductive, immune proliferative disorders, e.g. cancer and arteriosclerosis
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N-PSDB; ABK13031.
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                                                                                                                                                                                                                                                                                                                                                                                          Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the amino acid sequence of human B7-L_h4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat
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                                                                                                                TMLLTPTCTLTIRCCCCRRRCCGCUCCCRCCFCCRRKRGFRIQFQKKSEKEKTNKETETE 312
                                                                                                                                                                                                    TCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAG
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T---PATIQMNKRPQTPLLSLP
                                        SGNENSGYNSDEQKTTETASLP 334
                                                                                        TMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRG---NLKKRRQTKKLRQKVEMK
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ABG28169
                                    Novel human diagnostic protein #28160
                                                 18-FEB-2002
                                                                         ABG28169 standard; Protein;
                                                 (first entry
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

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Best Local Similarity
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23-AUG-2000;
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                                                                                                                                                                 VPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPG
                                                                                                                                                                                                                                                                                                                MWALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSR 108
                                  KRG
                                                                                                                                                                                                                                                          LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYF 168
                                                                                                                                                                                                                                                                                             MWALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSR
KRG
                                                                                                        VLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRR
                                                                                                                                             VPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPG
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                                                                       VLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRR
                                                                                                                                                                                                                                                                                                                                                                        243;
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                                  291
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2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                      Score 1326; DB 22; pred. No. 7.3e-102;
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                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                       Length 463;
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antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse B7-like protein,
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                                                                                                                                                                                                                                                                                                                                                                                     WO200200710-A2
                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B7-L_m1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              antirheumatic;
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Welcher AA, (AMGE-) AMGEN INC Sarmiento UM, Schultz HJ, Chute HT;

2002-130881/17.

28-JUN-2000; 2000US-214512P 28-NOV-2000; 2000US-0729264

28-JUN-2001; 2001WO-US20719

03-JAN-2002

New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis

Claim 13; Fig 5; 135pp; English.

seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarrian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune disease. B7-L molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, imune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also The polypeptide, polynucleotide encoding it and antibody aga useful for treating B7-like polypeptide-related disease, disconditions including reproductive disorders (e.g. infertilismissarriage, preterm labour and delivery and endometriosis) proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role growth and maintenance of cancer cells based on the observation of nephropathies (e.g. treatment of allergy, asthma and hypersensitivity reactions invention relates to an isolated B7-like (B7-L) polypeptide (I). polypeptide, polynucleotide encoding it and antibody against (I) for treating B7-like polypeptide-related disease, disorders o for diagnosis and treatment of diseases involving abnormal cell glomerulonephritis), skin disorders (pemphigus and intertility or S are in

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiucer; antiallergic;
                                                                              28-JUN-2000; 2000US-214512P
28-NOV-2000; 2000US-0729264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU75547 standard; Protein; 631
                      (AMGE-) AMGEN INC
                                                                                                                                                           28-JUN-2001; 2001WO-US20719
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                                                                                                                                                                                                                                                                                                                                                                                    endocrinopathy; lymphoproliferative disorder
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CC polypeptide. Hence modulators of (1) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, cc testicular cancer and cancers of heaematopoietic system. B7-L polypeptide cc pathway can be manipulated to regulate cytotoxic T-lymphocyte response ci nallograft transplantation, graft versus host diseases, T-cell concluding chronic immune call dysfunction or to treat cautoimmune diseases such as systemic lupus erythematosus, rheumatoid carthritis, multiple sclerosis, diabetes, immune thrombocytopenic inflammatory bowel disease (Crohn's disease and ulcerative colitis), crave's disease, Hashimoto's thyroiditis and diabetes mellitus. They care also useful as immunosuppressive agents for bone marrow and organ cransplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of disease involving abnormal cell consideration, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions, conspirative (e.g. glomerulonephritis), skin disorders (pemphigus and conspirative disorders such as multiple myeloma. The present to sequence represents the amino acid sequence of rat B7-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for enhancing the immune response to tumours. (I) plays a regrowth and maintenance of cancer cells based on the observation of seminal vesicle hyperplasia in transgenic mice overexpressing B7-L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New B7-like polypeptides, polynucleotides and their modulators, for diagnosing, preventing and treating reproductive, immune any proliferative disorders, e.g. cancer and arteriosclerosis
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Sequence
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  ΑĄ,
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Query Match

Similarity

28.3%;

Score 587.5; DB Pred. No. 3e-40;

DB 23;

Length 631;

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The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and
                                                                                                                              New B7-like polypeptides, polynucleotides and their modulators, of diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective;
                                                                                                 Claim 13; Fig 6; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                   Welcher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse B7-like protein, B7-L_m2.
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                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC.
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28-NOV-2000;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restensis.
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KHQPGPATHPRVSFDIASPQKVRNVTLV 270
                                               QRPPRPASHPQASFNLASPEKVSNTTVV 386
                                                                                                NMRTNKADPETKLKSGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSSL--PYQELN
                                                                                                                          KEKTNK---ETETESGNENSGYNSDEQKTTETASLPPKSCESSDPEQRNSSCGPPHQRAD 358
                                                                                                                                                                                                    IILLAVAFSLLLILIIVLIIIFCCC-----
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                                                                                                                                                                                                                                                KVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQ---KKSE
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23-APR-2002

(first entry)

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dependent B-cell mediated diseases and autoimmune diseases. B7-L molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are
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                                                                                      treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (cave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia,
                                                                                                                                                                                     useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for
                                                                                                                                                                                                                                                                                           are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also
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(extrinsts alveolitis), vasculopathies, coefficient uses and thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present lymphoproliferative disorders such as multiple myeloma. The present lymphoproliferative disorders such as multiple myeloma. The present lymphoproliferative disorders such as multiple myeloma.
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                                                      Material for extracorporeal circulation, applicable in selective elimination of diabetic complication factors such as carbonyl stress products caused by abnormally promoted carbonyl stress from excretor
                                                                                                                                                                                                                                                                                Unidentified.
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                                                                                                                                  Shimizu
                                                                                                                                                                                 08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                  AAB81925 standard; protein; 404
                                                                                                          WPI; 2001-290314/30.
                                                                                                                                                         (TORA ) TORAY IND INC
                                                                                                                                                                                                        08-SEP-2000; 2000WO-JP06172
                                                                                                                                                                                                                                                         WO200118060-A1
                                                                                                                                                                                                                                                                                                        diabetes; vascular
                                                                                                                                                                                                                                                                                                                    Extracorporeal circulation;
                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                           AAB81925
                                                                                                                                                                                                                                 15-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPSVNLVVAENEPCEVTCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILAL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYILAQLTASGSSYQIIEGPQNVTVLKDSEAHFNCTVTHGWKLLMWTLNQMVVLSLTTQG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLTVPEAVGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPME 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THKADPETKLKSGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSSL--PYQELNKHQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 AA;
                                              in vascular
                                                                                                                                  Kubota M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                  99JP-0254463
                                                                                                                                                                                                                                                                                                                                            circulation
                                                                                                                                                                                                                                                                                                         lesion;
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31.2%;
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                                                                                                                                  Akiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                       ; carbonyl stress product; receptor;
excretory dysfunction.
                                                                                                                                                                                                                                                                                                                                            material receptor protein
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Pred. No. 2.2e-33;
                                                                                                                                   Ξ
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                                                          excretory
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Claim 1; Page 31-32;

36pp; Japanese.

describes a material for extracorporeal circulation

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RESULT 11
AAE23219
ID AAE23
XX AAE23
XX AAE23
XX Human
XX Human
XX Human
XX Homo
KW Tissu
KW Myocoa
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WPI; 2002-426260/45
                                                              Stern DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Receptor for advanced glycosylation end product; RAGE; cardiant; tissue growth; neointimal formation; blood vessel; restenosis; diabetes; myocardial infarction; angioplasty; peripheral vascular surgery; angina; transgenic animal; acute thrombotic stroke; venous thrombosis.
                                                                                                                             (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                               13-OCT-2000; 2000US-0687528
                                                                                                                                                                                                                                                      12-OCT-2001; 2001WO-US32036
                                                                                                                                                                                                                                                                                                                                   18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                     WO200230889-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human receptor for advanced glycosylation end product (RAGE) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE23219 standard; Protein; 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which is made from a water:insoluble carrier immobilized with a protein having the sequence shown here. The materials of the invention, including adsorbents, are for extracorporeal circulation, which are applicable in the selective elimination of diabetic complication factors from a body fluid, and are therefore useful in treating vascular lesions like arteriosclerosis due to carbonyl stress products caused by abnormally promoted carbonyl stress from excretory dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 LVPNEKGVSVKEQTRRHPETGLFTLQSELM---VTPARGGDPRPTFSCSFSPGLPRHRAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 PEAVGSGSGNEVIEGPQNATYLKGSQARFNCTVSQG---WKLIMWALSDMYVLSVRPMEP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                           Schmidt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404 AA;
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                                                           Marso S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PTAGSVGGSGLGTLALALGILGGLGTAALLIGVILW
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                                                           Topol E,
                                                       Lincoff AM;
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RESULT 12
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Receptor for advanced glycation end product; RAGE; receptor; amyloid beta peptide; blood-brain barrier; neurovascular str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for inhibiting new tissue growth or neointimal formation in blood vessels in a subject that has experienced blood vessel injury and preventing exaggerated restenosis in a diabetic subject. The method comprises administering an inhibitor of receptor for advanced glycation/glycosylation end product (RAGE), so as to inhibit new tissue growth or neointimal formation in subject's blood vessels and preventing restenosis in the subject. The method is useful for inhibiting new tissue growth or neointimal formation in blood vessels in a subject that the subject is a subject to the subject that the subject is a subject to the subject that the subject is a subject that has subject that the subject is a subject that has experienced blood vessels in a subject t
                                                                                                 Human receptor for advanced glycosylation end product (RAGE).
                                                                                                                                                                             05-JUN-2002
                                                                                                                                                                                                                                            AAU77543;
                                                                                                                                                                                                                                                                                                       AAU77543 standard; Protein; 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 PEIVDSAS--ELTAGVPN------KVGTCVSEGSYPAGTLSWHLDG------KP 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTAPIQPRVWEPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIHWM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 151; DB 23; Pred. No. 0.00035;
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Best Local
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(I) inhibits transcytosis of amyloid beta peptides across blood-brain barrier, thus decreasing cerebral vasoconstriction and increasing cerebral blood flow. (I) is useful for treating amyloid angiopathy in a subject, decreasing cerebral vasoconstriction in a transgenic non-human animal (preferably, transgenic mouse overexpressing mutant human amyloid beta precursor protein) or a human, suffering from chronic or acute cerebral amyloid angiopathy, preferably, Alzheimer's disease, and for ameliorating heurovascular stress comprising cerebral amyloid angiopathy in a subject, where the neurovascular stress is caused by Alzheimer's disease, aging, Down's syndrome, head trauma or stroke. This is the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ameliorating neurovascular stress and decreasing cerebral vasoconstriction in subject suffering from chronic/acute cerebral amyloid angiopathy, by administering inhibitor of receptor for advanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerebral vasoconstriction suppressor; cerebral blood flow enhancer; cerebral amyloid angiopathy; transgenic animal; amyloid beta precursor; Alzheimer's disease; Down's syndrome; head trauma; stroke; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 16; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chronic or acute cerebral amyloid angiopathy, comprising administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product (RAGE)
                                                                                                                                                                                                                                                                                                                                                                 124
                  270
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                                                                                                                                                                                                                                                                                      164 LVPNEKGVSVKEQTRRHPETGLFTLQSELM~--VTPARGGDPRPTFSCSFSPGLPRHRAL
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                                                                                                                                                                                                                                                                                                                                                                                                     PEAVGSGSGNEVIEGPQNATVLKGSQARFNCTVSQG---WKLIMWALSDMVVLSVRPMEP 65
                                                                                                                                                                                                                                                                                                                         IITNDRFTS-----QRYDQGGNFT--SEMIIHNVEPSDSGNIR----CSLQNSRLHGSAY 114
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                                                                                            PQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT-----PTCTLTIRCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       se, aging, Down's syndrome, head trauma or stroke. This is acid sequence of human receptor for advanced glycation end ct (RAGE) described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404 AA;
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CCRCCFCCRKKRGFRIQFQKKSEKEKT--NKETETESGNENSGYNSDEQKT
                                                                                                                                  -GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVSISIIE-
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                                                          --PTAGSVGGSGLGTLALALGILGGLGTAALLIGVILW
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RESULT 13
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nephrotropic; dermatological; antiarteriosclerotic; nootropic; diabetes; alzheimer's disease; cancer; inflammation; kidney failure; systemic lupus; nephritis; erectile dysfunction; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 2; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting a receptor for advanced glycated endproducts (RAGE) modulators, for treating e.g., cancer, diabetes or inflammation, comprises measuring the amount of bound anti-RAGE antibody -
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05-MAR-2001; 2001US-0799152.
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LTVQVMGELFIP----SVNLVVAENEP--
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                                             LVPNEKGVSVKEQTRRHPETGLFTLQSELM---VTPARGGDPRPTFSCSFSPGLPRHRAL
                                                                                                            PEIVDSAS--ELTAGVPN------KVGTCVSEGSYPAGTLSWHLDG------KP 163
                                                                                                                                       PEAVGSGSGNEVIEGPQNATVLKGSQARFNCTVSQG---WKLIMWALSDMVVLSVRPMEP 65
                                                                           IITNDRFTS-----QRYDQGGNFT--SEMIIHNVEPSDSGNIR----CSLQNSRLHGSAY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAGE; receptor for advanced glycated endproduct; receptor;
                                                                                                                                                                          90;
                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                       404 AA;
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Pred. No. 0.00035;
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                  CEVICLPSHWIRLPDISWE 156
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AAW81030
            This polypeptide comprises a portion of a new human melanoma associated antigen, designated MG50. The amino acid sequence was deduced from a cDNA clone (see AAV9922) isolated from melanoma cell line MSM M-1 cDNA by subtractive hybridisation. The 5' region of MG50 cDNA was not obtained. MG50 mRNA has been detected in melanoma, lung carcinoma and rhabdomyosarcoma cells, foetal brain, foetal heart and human placenta. The invention also provides T cell epitopes (see AAW81031-54) from MG50, including cytotoxic and celle pitopes, antibodies that specifically bind to MG50 ran MG50 T cell epitope, recombinant vectors, and antigen melanoma associated antigen in an individual and for identifying an melanoma associated antigen in an individual and for identifying an entined in the models of stimulating T lymphocytes that are reactive melanoma associated antigen as methods of stimulating T lymphocytes that are reactive argainst an MG50 and for treating as individual and for identifying and the models of stimulating T lymphocytes that are reactive argainst an MG50 and for treating as individual and for identifying and the models of stimulating T lymphocytes that are reactive argainst an MG50 and for treating as individual and for identifying and models are models as methods of stimulating T lymphocytes that are reactive argainst an MG50 and for treating as individual and for identifying and models are methods of stimulating T lymphocytes that are reactive.
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                                                                                                                                                                                                                                                                                                                       Claim 1; Page 45-49; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                 rhabdomyosarcoma
                                                                                                                                                                                                                                                                                                                                                                                      MG50-expressing cancers,
                                                                                                                                                                                                                                                                                                                                                                                               New MG50 melanoma associated antigen fragments - used to develop products for the detection, treatment and prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deans RJ, Kap-Mitchell J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW81030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MG50; melanoma gene-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Melanoma associated antigen MG50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 RTAPIQPRVWEPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIHWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-080820/07.
DB; AAV99922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRR-----QRRGEERKAPENQEEEEERAELN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGEEG-----PTAGSVGGSGLGTLALALGILGGLGTAALLIGVILW 363
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          cancer
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        cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer;
      expressing MG50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              melanoma associated antigen; human;
                                                                                                                                                                                                                                                                                                                                                                              e.g. melanoma, lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minev BR,
and for treating an individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rhabdomyosarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRG2; p53 target; human; modulate; cell proliferation; immunomodulatory; chromosome 2p24.3; cytostatic; gene therapy; tumour cell; inducer; diagnosis; therapeutic; proliferative disease; cell cycle arrest; cancer; treatment; apoptosis; knockout animal; cancer susceptibility; dPxn; hPxn; peroxidasin; redox-regulation; reactive oxygen species; ROS.
                                                N-PSDB; AAZ51671.
                                                                                                                                    Horikoshi N,
                                                                                                                                                                                           (UYPR-) UNIV PRINCETON
                                                                                                                                                                                                                                                    28-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human p53 target molecule, PRG2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rhabdomyosarcoma.
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                                                                              2000-246724/21.
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Pred. No. 0.041;
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New p53-inducible isolated nucleic acid molecule including open

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC upregulated in response to induction of p53 activity in human colon CC cancer EB1 cells. This sequence is the human homologue (hPxn) of CC Drosophila peroxidasin gene dPxn, that is expressed in heart, placenta, CC spleen, ovary and intestines. PRG2 is involved in p53-mediated growth CC suppression pathways and plays a role in redox regulation. It is a CC tharm peroxidase that increases the intracellular content of reactive CC oxygen species (ROS). They are potential targets of p53 regulatory CC exitivity and are useful for modulation of cellular proliferation. PRG2 Gene is localised to human chromosome 2p24.3. The PRG target molecules CC proteins and antibodies are useful as diagnostic and therapeutic agents CC for detection and treatment of cancer and other proliferative diseases. CC the gene/cDNA may be used for gene therapy, to restore a gene function CC downstream of p53, that cannot be activated in the p53-deficient tumour CC cell. Antibodies can be used as inducers of cell cycle arrest and/or CC as a model of cancer susceptibility.
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Search completed: April 28, 2003, 18:14:34 Job time : 41.4662 secs
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                                                                                                                                            237 GFSLP--TWGKVGLGL--AGTMLLTPTCTLTI------RCCCCRRRCCG
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                                                                                               567 GEPEPAITWNKDGVQVTESGKFHISPEGFLTINDVGPADAGRYECVARNTIG 618
                                                                                                                                                                                                                                                                                                 459 RVVIEGQTVDFQC-EAKGNPPPVIAWTKGGSQLSVDRRHLVLSSGTLR--ISGVALHDQ-
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                                                                                                                                                                                                                                                                                                                                                                                                      412 -----GG-----LYIQNVVQGDSGEYACSATNNIDSVHATAFIIVQALPQFTVTPQD 458
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. BG863468 602796941 BF784177 602108039 BG740428 602633817 BB663870 BB663870 BE032610 132035 MA BE476432 159670 BA Description REFERENCE AUTHORS TITLE VERSION KEYWORDS BG863468 LOCUS FEATURES COMMENT SOURCE DEFINITION ACCESSION RESULT 000 ORGANISM JOURNAL found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10830 row: b column: 12 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., High quality sequence stop: 768. Location/Qualifiers Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 784)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Mus musculus mRNA sequence. BG863468 602796941F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE: 4917803 BG863468.1 GI:14214006 cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can house mouse ALIGNMENTS 784 bp mRNA

EST 29-MAY-2001

Result No.

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Match Query

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SUMMARIES

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/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:4917803"
/clone_ibb="NCI_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 794)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9844 row: n column: 10
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 694.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Strain="FVB/N"
/db_xref="Taxon:10090"
/clone="IMAGE:4236489"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pcMV-SPORT6; Site_1: l
Site_2: Sall; Cloned unidirectionally. Primer: Olic
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
86 a 214 c 215 g 179 t
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iner: Oligo dT
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                                    1086 GATCAACGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTAATCTGGCCAGTCCT 1145
557 GATCAACGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCCT
                                                                                                                                                                        437
                                                                                                                                                                                                                                                                                      906 AAGAAATCTGAAAAAGAGAAGACAAACAAAGAAACTGAGACAGAAAGTGGAAATGAAAAC 965
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                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                             TGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCTCCTCACCAGCGGGCT
                                                                                                   TGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCCTCCTCACCAGCGGGCT 1085
                                                                                                                                                               TCCGGCTACAATTCAGATGAACAAAAGACCACAGACACCGCTTCTCTCCCCCAAATCC
                                                                                                                                                                                     AGGAAATCTGAAAAAGAGAAGACAAACAAAGAAACTGAGACAGAAAGTGGAAATGAAAAC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCAGTCT 728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGAGTTACAATTCCTTTCTGGAGCC--GGGCACTTTATGAGGGTCTGAGTGTCCTGGAA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 725.
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Plate: LLAM10635 row: b column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HG/40428 725 bp mRNA linear EST 15-MAY-2001 602633817F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778789 5',
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/db_xref="taxon:9606"
/clone="IMAGE:4778789"
/clone_lib="NCI_CGAP_Skn3"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 163 c 159 g 176 t
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URL:http://genome.gsc.riken.go.jp/
Carninci,P, Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
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Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
                                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                            e mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer-based methods for the mouse full-length cDNA
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/tissue_type="lung"
/dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                                                      /clone_lib="RIKEN full-length enriched, 0 day neonate
                                                                                                                                                                              /clone="E030016M12"
                                                                                                                                                                                                                  /db_xref="taxon:10090"
                                                                                                                                                                                                                                               organism="Mus musculus"
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Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia

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RESULT 5
BE032610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 GAGATGGGGCTTGTGATTTTCCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACATTCCTAGCAACAACCTTATAGTCACTGAGGGTGAACCCTGTAATGTGACTTGCTAT 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCCCATCATCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCAGAATGTAACAGTCCTAAAGGACTCAGAGGCTCACTTCAACTGCACCGTGACTCAC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGCTGGTCATCCTGGCTCAGCTGACAGCTTCCGGATCCAGTTATCAGATCATAGAAGGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAAGCTATTATT 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCTCACACTGGACCCGGCTCCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCAT 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCATTCCCAGTGTTAATCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTA 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCAGAACAGCCATGGGTTTGGATCTGCCTTCCTCTCAGTGCAAGTCATGGGGACCCTG 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTCGGAGTTGATCATCCATGATGTGCAGCCCAGTGACTCGGGATCCGTGCAATGCAGC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGGGGGAACATCAGATGCAGC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGACCCATCATCACCAACAACCGCTTCACCTATGCCAGTTACAACAGCACTGACAGCTTC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTGGAAGCTTCTCATGTGGACTCTTAACCAAATGGTGGTGCTGAGTCTCACCACCCAA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCCATG 203
                                                                                                                                                                                                                                                                                                                                                                                                                      TCGAGTTACAATT 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347;
                                                                                                                                                                                                                                                        132035 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BE032610
                                                                                                                                                                                                                                     BE032610.1 GI:8327619
Design and use of two pooled tissue normalized
                            and Keele, J.W.
                                                 Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A.,
                                                                    1 (bases 1 to 527)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                Sus scrota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cap-trapper. Second strand cDNA was prepared with the
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         cDNA libraries for
                                                    Laegreid, W.W.
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Best Local Similarity
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                                 ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                           264 ACCTCGGAGATGATCCACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGCTGGTCGTTCTGGCTGGGCTGGCAGCTTGTGGATCCGGCAATGAAATCTTAGAGGGT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGGTGCTAAGCGTCAGG;CCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCCAGAATGCAACAGTCCTGAAGGGCTCCCCAGGCTCCGCTTCAACTGCACCGTCTCCCAG
                                                                                                                                                                                                                        CTCATTCCCGGAGGCAGCCTCGTAGTCCTTGCGGA
                                                                                                                                                                                                                                                         TTCATTCCCAGTGTTAATCTTGTAGTCGCTGAGAA 418
                                                                                                                                                                                                                                                                                         GAGCCCATCATCACCAACGACCGATTCACGTCTGCAAGTTATGAAGAGGGCGGTAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCCCATCATCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTGGAAGCTCATCATGTGGGCTCTGAAAGGCACGGTGGTTCTGAGCGTCACGCCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAGGAACGTCACGGCGGTGAAGGGCTCGGAGGCTCAACTGCACCATCTCCCAG
                                                                                                                                                                                                                                                                                                                                                          ATCTCTGAGATGATCATCCATGACGTGCAGCTCAGTGATGCCGGGCAGGTCAAAIGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACKWARD: GTTTTCCCAGTCACGACG
Plate: 63 row: E_column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single pass sequencing. Bases call v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
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                                                                    EST
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                   Bos taurus
                                                  COW
                                                                                  BE476432.1 GI:9595965
                                                                                                     BE476432
                                                                                                                   159670 BARC 5BOV Bos taurus cDNA
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/tlssue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
/note="Vector: pCMV SPORT6; Site_1end and 11. 13, 15, 20
and 30 embryos."
147 c 176 g 99 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9823"
/clone_lib="MARC lPIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Sus scrofa"
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76.7%;
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Pred. No. 3.1e-47;
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                                                                                                                  5', mRNA sequence
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                                                                                                                                                                                 CTTCAGAACAGCAATCGGGATGGAGCCGCCTTCCTTTCTGTTC
                                                                                                                                                                                                                           ATCTCTGAGATGATTAATTCATGACGTGCAACTGAGCGATGCCGGGCAAGTCAAATGCAGC
                                                                                                                                                                                                                                                                                                                      GAGCCCATCATCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTC 263
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                                                                                                                                                                                                                                                                                                                                                                                                                     CCCAAGAATGTCACAGCCCTGAAGGGCTCGGAGGCTCGCTTCAACTGCACCATCTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGCTGGTGGTCCTGGCCGTGCTGGCAGCCTGTGGATCCAGCAGTGAAATCATAGAGGGT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGATGGGGCTTGTGATTTTCCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGC 83
                                                                                                                                                                                                                                                         ACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGGGGGAACATCAGATGCAGC 323
                                                                                                                                                                                                                                                                                        GAGACCATCATCACCAGTGACCGCTTCACTTCGGCAAGCTACCAAGAGGGCGGGAACTTC
                                                                                                                                                                                                                                                                                                                                                      GGCTGGAAGCTCGTCATGTGGGCTCTGAGAGGCACAGTGGTGCTGAGCATGACACCTAAT 354
                                                    AV601192
5', mRNA
 AV601192
AV601192.1 GI:9723510
EST.
                                                                                  AV601192
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Plate: 27 row: H column: 19
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mapping of Expressed Sequence Tags from a normalized bovine mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sonstegard, T.S., Capuco, A.V., Van Tassell, C.P., Ashwell, M.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Bovinae;
                                                    mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 517)
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301 504 8414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tads@anri.barc.usda.gov
                                                                 Bos taurus kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

a 133 c 165 g 102 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 199;
Pred. No. 7.
                                                                                 524 bp
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                                                                 tetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       called and alt_trimmed with phred d by cross_match with the -minscore
                                                                 Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
7.1e-36;
                                                                                 mRNA
                                                              taurus cDNA clone E1KI002H04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 517;
                                                                                 linear
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                                                                               EST
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                                                                               27-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 GAGATGGGCCTTGTGATTTTCCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGC 83
                                                                                                                                                                                                                                                                                                                                                      ACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCCCATCATCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTC
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                                                                                                                                                                     CTTCANAACAGCAATCGGGATGGAGCCGC 524
                                                                                                                                                                                                                                                                                                              ATCTNTGAGATGATAATTCATGACGTGCAACTCAGCGATGCCGGGCAAGTNAAATGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGACCATCATCACCAGTGACCGCTTCACTTCGGCAAGCTACCAAGAGGGCGGGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTGGAAGCTCGTCATGTGGGCTCTGAGAGGCACAGTGGTGCTGAGCATGACACCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCAAGAATGTCACAGCCCTGAAGGGCTCGGAGGCTCGCTTCAACTGCACCATCTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGCTGGTGGTCCTGGCCGTGCTGGCAGCCTGTGGATCCAGCAGTGAAATCATAGAGGGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single pass sequencing. This clone was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 29 (22), E108 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Establishment of a high throughput EST sequencing system using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takasuga, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Animal Genetics Division
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 524)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tail-removed cDNA libraries and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Gev_susy.
/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1;
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1;
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1;
/note="Vector: pXL1; Site_1: Sal1; Site_1: Not1;
/note="Vector: pXL1; Site_1: Sal1; Site_1: Not1;
/note="Vector: pXL1; Site_1: Sal1; Site_1: Not1;
/note="Vector: pXL1; Site_1: Sal1; Site
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/clone_lib="Bos taurus kidney fetus"
/tlssue_type="kidney"
/dev_stage="fetus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.3%;
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Pred. No. 3.7e-34;
0; Mismatches 87;
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AG069679 AG069679.1 GSS.

GI:16621481

troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male Library clone:PTB-060r12.F.

AG069679 62: Pan troglodytes DNA, clone:

622

2 bp DNA PTB-060F12.F,

linear GSS (

GSS 03-NOV-2001

sequence

Yada, T.,

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                                                                                                     ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                           192
                                                                                                                                                                                                                                                                                                                                                                                                                                                              594 TGCGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTG 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 GACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGACTTTGACT 191
                                                                                                                                                                                                                                                                                                                                                         252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 GACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGACTTTGACT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 TCCGCGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGTTCCGGAGCCCAGC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                         ATTCGGCGTCCCCAAGGTAAGTGAAGATGT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCGTGGCTACCTGGAAGAGCCTGAAGGCCCACAAGTCTGCAACTGTAAATCTCACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, 'Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes
                                                                                                                                                                          677 bp DNA linear GSS 03-NOV-200 AG107877 GI:16728395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujiyama, A., Hattori, M., Toyoda, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                             BAC
                                                                                                                                                Pan
Totoki,Y., Watanabe,H. and Sakaki,Y
                     Fujiyama,A.,
                                                                                                       Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165
                                                                                                                      troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male Library clone:PTB-112N07.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Site 1 : SacI
R.Site 2 : SacI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="1ymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
153 c 128 g 176 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="PTB-060F12.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                  Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.2%;
94.3%;
                       Hattori, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : pKS145
                                                                Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 190.8; DB 1
Pred. No. 5.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                         Toyoda, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taylor, T.D., Yada, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17;
                         Taylor, T.D., Yada, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                        GSS 03-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 TGCGTGGCTACCTGGAAGAGCCTGAAGGCCCACAAGTCTGCAACTGTAAATCTCACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 GACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGACTTTGACT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 TCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGTTCCGGAGCCCAGC 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534 GACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGACTTTGACT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             654 ATTCGGTGTCCCCAAGACACTGGAGGTGGT 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 TCCGCGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGTTCCGGAGCCCAGC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTCGGCGTCCCCAAGGTAAGTGAAGATGT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 677)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                        mx91d09.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:6937135', mRNA sequence.
        Unpublished (1996)
Contact: Marra M/M
                                                 The WashU-HHMI Mouse EST Project
                                                                                    Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 471)
                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                     AA265274.1 GI:1901370
                                                                                                                                                                                                                                                                                                                         AA265274
                                                                                                                                                                                                                                                                                                                                                                                     AA265274
                                                                         Waterston, R.
                                                                                                                                                                                                                                                            house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168
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R.Site 2 : SacI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
159 c 143 g 207 t
          Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-112N07.F"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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: SacI

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                     471 bp
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EST 20-MAR-1997

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RESULT 11
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                                                 ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                264 ACCTCGGAGATGATCCACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGC 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 GAGATGGGGCTTGTGATTTTCCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                       CTGCAGAACAGCCATGGGTTTGGATCTGCCTTCCTCTCAGTGCAAG 435
                                                                                                                                                                                                                                                                                                                             GGACCCATCATCACCAACAACCGCTTCACCTATGCCAGTTACAACAGCACTGACAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCCCATCATCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTGGAAGCTTCTCATGTGGACTCTTAACCAAATGGTGGTGCTGAGTCTCACCACCCAA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTGGAAGCTCATGTGGGCCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCAGAATGTAACAGTCCTAAAGGACTCAGAGGCTCACTTCAACTGCACCGTGACTCAC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGCTGGTCATCCTGGCTCAGCTGACAGCTTCCGGATCCAGTTATCAGATCATAGAAGGT 149
                                                                                                                                                                                                                                                                                                                                                              ATCTCGGAGTTGATCATCCATGATGTGCAGCCCAGTGACTCGGGATCCGTGCAATGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246;
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                     uf37d05.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1513545 5' similar to TR:060962 060962 L549.1.;, mRNA
                                                                                                                                                                                                   AW990468
                                                                  house mouse
                                                                                                          AW990468.1 GI:8186027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: ~28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of MedicineP
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares mouse NML"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:693713"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Liver"
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Pred. No. 7.4e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 GGCTGGAAGCTTCTCATGTGGACTCTTAACCAAATGGTGGTGCTGAGTCTCACCACCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 GAGATGGGGCTTGTGATTTTCCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                        CTGCAGAACAGCCATGGGTTTGGATCTGCCTTCCTCTCAGTGCAAG 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGCTGGTCATCCTGGCTCAGCTGACAGCTTCCGGATCCAGTTATCAGATCATAGAAGGT 158
  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                         Mus musculus
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                                                                                                                             BG173684
                                                                                                                                              mRNA sequence.
                                                                                                                                                             BG173684 931 k
602336823F1 NCI_CGAP_Mam1 Mus
                                                                  house mouse.
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This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 611)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:940397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMAGE Consortium (info@image.llnl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sits of the modified pT7T3 vector. Library is normalized. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was constructed by Bento Soares and M. Fatima Bonaldo. _{\rm 1} _{\rm 155} c _{\rm 156} g _{\rm 148} t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polylinker; 1st strand cDNA was prepared from mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1513545"
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Pred. No. 7.6e-33;
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                 musculus cDNA clone IMAGE:4459973 5',
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                                                                                                                                                                                                                                                                                                                   CTGCAGAACAGCCATGGGTTTGGATCTGCCTTCCTCTCAGTGCAAG 476
                                                                                                                                                                                                                                                                                                                                                           ATCTCGGAGTTGATCATCCATGATGTGCAGCCCAGTGACTCGGGATCCGTGCAATGCAGC 430
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Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 628.
                                                                                                            Mus musculus adult male small intestine cDNA, RIKEN enriched library, clone:201003D20:homolog to IGSF5 (FRAGMENT), full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
clone:2010003D20
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                  Mus musculus (strain:C57BL/6J) adult male small intestine cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                       AK008060.1 GI:12842009
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Library constructed by Life Technologies. Investigator 
providing samples: Gilbert Smith, NIH" 
a 277 c 242 g 179 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="10 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:4459973"
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Pred. No. 7.9e-33;
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                                                                                                                                                                                Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adachi, J., Aizawa, K., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hori, F., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Ainayawa, A., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Ainayawa, A., Sano, H., Sasaki, D., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Physical and Chemical Research (RIKEN), Laboratory for Gen Exploration Research Group, RIKEN Gemomic Sciences Center
                                                    Direct Submission
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of RTKEN), Laboratory for Genome
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                        (GSC)
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BASE COUNT
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264 ACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGC 323
                                                                                                               204 GAGCCCATCATCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTC 263
                                                                                                                                                                                                                               144 GGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATG 203
                                                                                                                                                                                                                                                                                            163 CCTCAGAATGTAACAGTCCTAAAGGACTCAGAGGCTCACTTCAACTGCACCGTGACTCAC 222
                                                                                                                                                                                                                                                                                                                                                                                                               103 GTGCTGGTCATCCTGGCTCAGCTGACAGCTTCCGGATCCAGTTATCAGATCATAGAAGGT 162
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                                                                              283
                                                                                                                                                                                                                                                                                                                                                  84 CCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 GAGATGGGGCTTGTGATTTTCCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                         GGACCCATCATCACCAACAACCGCTTCACCTATGCCAGTTACAACAGCACTGACAGCTTC
                                                                                                                                                                            GGCTGGAAGCTTCTCATGTGGACTCTTAACCAAATGGTGGTGCTGAGTCTCACCACCCAA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3,], cDNA was prepared by using trehalose thermo-activated reverse transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of normalization to Rot = 5.0 and subtraction to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          further details.
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/db_xref="GI:12842010"
/db_xref="GI:12842010"
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DSGSYQCSLQNSHGFGSAFLSVQDSIGEEGPALPTWAIILLAVAFSLLLILIIVLIII
FCCCCASRREKEESTTQNEIRKSANNRTNKADPETKLKSGKENYGYSSDEAKAAQTAS
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homolog to IGSF5 PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="small intestine"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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/db_xref="MGD:MGI:1904786"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.8%; Score 186; DB 11; 71.1%; Pred. No. 8.4e-33;
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AI425363
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               84 CCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAG 143
                                                               90
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                                                                                                                                                          Local
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                                                                                             GAGATGGGGCTTGTGATTTTCCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGC 83
245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:427273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   correct orientation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mx91d09.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:693713
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                                                                                                                                                                                                                                                                     constructed and normalized by Bento Soares and M. Fatima
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/clone="IMAGE:693713"
/clone_lib="Soares mouse NML"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCAGAACAGTCGCCTGCATGGATCTGCTTACCGTTACCGTCCAAG 369
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                  CCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAG 143
                                                        GTGCTGGTCATCCTGGCTCAGCTGACAGCTTCCGGATCCAGTTATCAGATCATAGAAGGT 124
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BE376590
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                    143
                                                                                                                                       Conservative
                                                                                                                                                                                                                                  providing samples: Gilbert Smith, NIH"
193 c 170 g 157 t
                                                                                                                                                                                                                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:3584645"
/clone_lib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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70.8%;
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Pred. No. 1.8e-32;
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                                                                      CTGCAGAACAGCCATGGGTTCGGATCTGCCTTCCTCTCAGTGCAAG
                                                                                                       GAGCCCATCATCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTC
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                                                                                                                                                                        ACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGGGGGAACATCAGATGCAGC 323
                                                                                                                                                                                                            GGACCCATCATCACCAACAACCGCTTCACCTATGCCAGTTACAACAGCACTGACAGCTTC
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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Mismatches 5; GACAAACAAAGAAACTGA	Score 269; DB 9; Le pred. No. 1.9e-72; 0; Mismatches 5; Agaacacaaacaaacaaacaaacaaacaaacaaacaaaca	ACID SEQUENCES CDNA LIBRARIES /918,995 35,076 sion 3.0	ALIGNMENTS	US-09-811-469-3 US-10-007-557-8 US-09-918-995-19918	US-09-919-580-574 US-09-919-580-570 US-09-918-8428-1399 US-09-938-8428-1399	US-09-918-995-11012 US-10-078-090-83 US-10-003-295-1 US-09-728-444-25 US-09-728-444-25	US-09-476-242-26 US-09-822-846-129 US-09-916-145-1 US-09-917-8008-1546	US-09-864-761-7357 US-09-735-367B-5 US-09-735-367B-1 US-09-969-347-171 US-09-735-367B-1 US-09-735-367B-1 US-09-735-367B-1 US-09-925-300-486 US-09-918-95-10212 US-09-919-580-878 US-09-919-580-878	US-09-864-761-24079
CGCTTCTCTCCCTCC 1018	Iength 474; Indels 0; Gaps 0; GAGACAGAAAGTGGAAA 958	OBTAINED		Sequence 3, Appli Sequence 8, Appli Sequence 19918, A	Sequence 371, App Sequence 475, App Sequence 570, App Sequence 1399, App	Sequence 11012, A Sequence 83, Appl Sequence 1, Appli Sequence 25, Appl Sequence 371 Appl	Sequence 129, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1546, Ap	Sequence 7357, Appli Sequence 5, Appli Sequence 171, App Sequence 9, Appli Sequence 1, Appli Sequence 486, App Sequence 10212, A Sequence 878, App Sequence 16, Appl	Sequence 24079, A

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; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = US-09-864-761-16305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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IOR APPLICATION NUMBER: PCT/USO1/00666
IOR FILING DATE: 2001-01-30
IOR APPLICATION NUMBER: PCT/USO1/00667
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                                                                                                     Sequence 1, Application US/10008739A Patent No. US20020161194A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4945
LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1998-12-17
NUMBER: OF SEQ ID NOS: 5912
                       APPLICANT: Pfizer Inc.
APPLICANT: Castleberry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Warren,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: 26-LIB34-017-Q1-E1-G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 CTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCCAGGGCTGGAAGCTCATCATG
                                                                                                                                                                                                                                                                                                                                                                              341 GAGACCATCATCACCAGTGACCGCTTCACTTCGGCAAGCTACCAAGAGGGCCGGAACT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 GACCGCTTCACCTCTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                204 GAGCCCATCATCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 CCCAAGAATGTCACAGCCCTGAAGGGCTCGGAGGCTCGCTTCAACTGCACCATCTCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 GTGCTGGTGGTCCTGGCCGTGCTGGCAGCCTGTGGATCCAGCAGTGAAATCATAGAGGGT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 TACCTTCCAGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATGCAAGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 12.18;
Local Similarity 74.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 GAGATGGGGCTTGTGATTTTCCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACCGCTTCACCTCTCAGAG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTGGAAGCTCGTCATGTGGGCTCTGAGAGGCACAGTGGTGCTGAGCATGACACCTAAT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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Mathialagan, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tao, Nengbing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
Bihong
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                                   Tessa

 Mismatches

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Pred. No. 2.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
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; LENGTH: 3577
; TYPE: DNA
; ORGANISM: Canine
US-10-008-739A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/09849243 Patent No. US20020157127A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.9%;
Best Local Similarity 65.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO
                                                                                                                                                     INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1310 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/008,739A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: The Canine Androgen Receptor FILE REFERENCE: PC10893AGPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    573 TTGCTGCTGCTGCTGCTGCTGCCGCTGCTGCTGAAGGAG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          836 TGGCTGCAACTGCTGCTGCCGTTGTTGTTTCTGCTGTAGAAG 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                633 GCTGCTGCTACCTTCTGATACTACCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     776 GCTTCTGACGCCGACGTGTACTCTTACAATACGCTGCTGCTGCTGCCGCCGTCGTTGTTG 835
                                                                                                                                                                                                            NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REPERENCE/DOCKET NUMBER: 38005-0148
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)912-2000
TELEFAX: (202)912-2020
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/849,243 FILING DATE: 07-May-2001 ATTORNEY/AGENT INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                            MOLECULE TYPE: cDNA
                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: HELLER, EHRMAN, WHITE & MCAULIFFE STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PURIFICATION OF HIGHER ORDER TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kirschbaum, Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                   NAME/KEY: exon LOCATION: 1..1
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Owen, Thomas A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smock, Steven L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berglund, Erick
                     1..1310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 0.0036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM TRANSGENIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Sequence 15, Application US/09849243; Patent No. US20020157127A1 GENERAL INFORMATION:
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                                                                                   US-09-849-243-15/c
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                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-09-822-846-491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-09-822-846-491/c
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                                                                                                                                                                                                                                                                                     Query Match 3.8%;
Best Local Similarity 76.4%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 491
LENGTH: 2614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa
APPLICANT: Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 491, Application US/09822846 Publication No. US20030027139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-04-06 NUMBER OF SEQ ID NOS: 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/195,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                  2119 GCTGCTGCCGCA 2108
                                                                                                                                                                                                                  868 GCTGTAGAAGAA 879
                                                                                                                                                                                                                                                   808 GCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTGTTTCT 867
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                APPLICANT:
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Similarity 81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graham, James R.
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Howes, Steven H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wong, Gordon G.
Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merberg, David
Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Resnick, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steininger II, Robert J. Bowman, Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agostino, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spaulding, Vikki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
          Kirschbaum, Bernd
Berglund,
                                                                                                                                                                                                                                                                                                                                                                                                                                               2.0
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                                                                                                                                                                                                                                                                                                     Score 44.8; DB 9; Length 2614; Pred. No. 0.0068;
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Pred. No. 0.0043;
0; Mismatches 12; Indels 0
                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                         Indels
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RESULT 8
US-09-949-243-14/c
; Sequence 14, Application US/09849243
; Patent No. US20020157127A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 38005-0148
REFERENCE/DOCKET NUMBER: 38005-0148
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)912-2000
TELEFAC: (202)912-2020
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1370 GCTG 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          808 GCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTTTTT 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          868 GCTG 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          match 3.8%;
Local Similarity 81.2%;
es 52; Conservative 0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,243
FILING DATE: 07-May-2001
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PURIFICATION OF HIGHER ORDER TRANSCRIPTION COMPLEXES FROM TRANSGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: EHRMAN, WHITE & MCAULIFFE ADDRESSEE HELLER, EHRMAN, WHITE & MCAULIFFE STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 1..3263
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linea MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3263 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                       NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: HELLER, EHRMAN, WHITE & MCAULIFFE STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                              POLITES, Greg
TITLE OF INVENTION: PURIFICATION OF HIGHER ORDER TRANSCRIPTION
                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                    CITY: Washington STATE: D.C.
COUNTRY: USA
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Polites, Greg
                                                                                                                                                                                                                                       Meisterernst, Michael
                                                                                                                                                                                                                                                              Berglund, Erick
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                                                                                                                                  NON-HUMAN ANIMALS: 17
                                                                                                                                                                           COMPLEXES FROM TRANSGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
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US-09-880-107-1748/C
Sequence 1748, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
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                                                                           , OTHER INFORMATION: Genbank Accession No. US20020142981A1 D83783 US-09-880-107-1748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1748
        Query Match 3.8%; Score 44.8; DB 10; Best Local Similarity 76.4%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
Matches
                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEO ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 6604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.8%;
Local Similarity 81.2%;
les 52; Conservat;...
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)912-2000
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NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 38005-0148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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55; Conservative
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LOCATION: 1..4286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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 Mismatches

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Pred. No. 0.0095;
  0; Mismatches
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                                           Length 6604;
    Indels
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172 PSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDT 220

PGSVESTLTLTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVT 230

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US-10-176-913-584
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                                                                                                                                                                                                                                                                                                                                      US-10-180-552-584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.1%; Score 128; DB 9; Length 708; Best Local Similarity 23.1%; Pred. No. 0.095; Matches 53; Conservative 41; Mismatches 95; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Publication No. US20
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             Sequence 584, Application US/10180552 Publication No. US20030022300A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 584,
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APPLICANT:
APPLICANT:
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                                                                                 APPLICANT:
                                                                                                                                                                                      APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prior Application removed - See file Wrapper or Palm NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: P3430R1C66
CURRENT APPLICATION NUMBER: US/10/176,913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                             APPLICANT:
                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo Sapien
                                           PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 708
                                                                                                                                                                                                                                                                                                                                                                                                                          182 PGSVESTLTLTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 PSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 ---PSVSLVA--GVPANLTCRSRGDARPT-----PELLWFRDGVLLDGATFHQTLLKEGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 LFIPSVNLVVAENEPCEVTC-----LPSHWTWLPDISW-ELGLLVSHSSYY--FVPE-- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 WSRYWISGNAANGQHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVLVPPEAPQVLGG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 SORYDOGGNETS---EMITHNVEPSDSGNIRCSLQNSRLHG-SAYLTV-----QVMGE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 SGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITNDRFT 73
  <sub></sub>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGPSPHFLQQPEDLVVLLGEEARLPCALGAYWGLVQWTKSGLALGGQR------DLPG 71
INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baker, Kevin P.
                                                      Smith, Victoria Watanabe, Colin K. Wood, William I.
                                       Zhang, Zemin
                                                                                                                                            Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                      Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard, Audrey
Godowski, Paul J.
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                                                                                                                             Pan, James
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o. US20030022298A1
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LENGTH: 708
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.1%; Score 128; DB 9; Length 708; Best Local Similarity 23.1%; Pred. No. 0.095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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CURRENT APPLICATION NUMBER: US/10/180,552
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrap;
NUMBER OF SEQ ID NOS: 612
                                                                                                                                          172
                                                                                            182 PGSYESTLTLTPFSHDDGATFYCRARSQALPTGRDTAITLSLQYPPEYT 230
                                                                                                                                                                                        132 ---PSVSLVA--GVPANLTCRSRGDARPT----PELLWFRDGVLLDGATFHQTLLKEGT 181
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                                                                                                                                       PSDLQSAVSILALTPOSNGTLTCVATWKSLKARKSATVNLTVIRCPQDT 220
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RESULT 11 US-10-175-752-584

Application US/10175752

US20030022295A1

Sequence 584, Applic Publication No. US20 GENERAL INFORMATION:

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US-10-176-482-584
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US-10-175-752-584
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LENGTH: 708
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                        CURRENT APPLICATION NUMBER: US/10/176,482
CURRENT FILING DATE: 2002-06-20
                                                                                 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                  FILE REFERENCE: P3430R1C70
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CURRENT FILING DATE: 2002-06-19
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NUMBER OF SEQ ID NOS: 612
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      Application
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Godowski, Paul
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Pred. No. 0.095;
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Matches 53;
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SEQ ID NO 584
LENGTH: 708
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LENGTH: 708
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CURRENT APPLICATION NUMBER: US/10/176,757
CURRENT FILING DATE: 2002-06-20
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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ORGANISM: Homo Sapien
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132 ---PSYSLVA--GVPANLTCRSRGDARPT----PELLWFRDGVLLDGATFHQTLLKEGT 181
                                  123 LFIPSVNLVVAENEPCEVTC-----LPSHWTWLPDISW-ELGLLVSHSSYY--FVPE--
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                                                                           72 WSRYWISGNAANGQHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVLVPPEAPQVLGG 131
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Godowski, Paul
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Watanabe, Colin K.
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US-10-173-706-584
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LENGTH: 708
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                SEQ ID NO 584
LENGTH: 708
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CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 612
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                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C7
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                                                                                            CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
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LENGTH: 7
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 584
LENGTH: 708
TYPE: PRT
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Best Local Similarity
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C45
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                                     172 PSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDT 220
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PGSVESTLTLTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVT 230
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Godowski, Paul
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Pred. No. 0.095;
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Pred. No. 0.095;
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; ORGANISM: Homo US-10-174-590-584
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    Query Match
                                                                                              SEQ ID NO 584
LENGTH: 708
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APPLICANT: No. US20020150876Alartis AG
TITLE OF INVENTION: Selectable Marker Genes
FILE REFERENCE: 4-31193A
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                                                                                                                                      Prior application removed NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/174,590
                                                                                                                                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                               CURRENT FILING DATE:
                                                                                                                                                                                                                        FILE REFERENCE: P3430R1C42
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                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 MEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMG 121
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                                                                                                                                                                                                                                                                                Zhang, Zemin
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    6.18;
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DB
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RESULT 8
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LENGTH: 708
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CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
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                                                                                                                  PSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDT 220
                                                                                                                                                                                                                                   WSRYWISGNAANGQHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVLVPPEAPQVLGG 131
                                                                              PGSVESTLTLTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVT 230
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Godowski, Paul
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23.1%; Pred. No. 0.095;
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US-10-184-644-559
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US-10-184-644-559
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SEQ ID NO 559
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SEQ ID NO 559
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                Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
                                          CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
                                                                       APPLICANT: Zhang Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin P.
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CURRENT FILING DATE: 2002-06-28
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Similarity 29.5%;
            SEQ ID NOS:
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Godowski, Paul J.
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Godowski, Paul J.
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o. US20030068684A1
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o. US20030044930A1
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RESULT 4
US-10-016-283-33
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CURRENT FILING DATE: 2001-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1996-12-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/09/077,955A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS FILE REFERENCE: REG195-B-PCT-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Valenzuela et al.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 WGKVGLGLAGTMLLTPTCTLTIRCCCCR-RRCCGCNCCCRCCFCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 ALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 -SPLRENSRIAVLE------SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKVVKLEV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 MEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRP 62
                                                                                                                                                                                                                                                                                                                 RVIDSRLQLFITKP---GLYTCIATNKHGEKFSTAKAAATISIAEWSKPQKDNKGYCAQY 320
QASFNLA 375
                                                                                                                                     LCNHIFQECSPGVVPTPIPICREYCLAVKELFCAKE----WLVMEEKTHRGLYRSEMHLL 429
                                                                                                                                                                                                                           RGEVCNAVLAKDALVFLNTSYADPEEAQELLVHTAWNEL------KVVSPVCRPAAEAL 373
                                                                                                                                                                                                                                                                                                                                                           SDLQSAVSILALTPQSNGTLTCVAT----WKSLKARKSATVNLTVIRCPQDTGGG-----
                                                                                                                                                                                                                                                                                                                                                                                                          EVFARILRAPESHNVTFGSFVTLHCTATGIP-----VPTITWIENGNAVSSGSIQESVKD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELFIPSVNLVVAENEP-----CEVTCLPSHWTWLPDISW-ELGLLVSHSSYYFVPEP 172
                                              SVPECSKLPSMHWDPTACARLP-----HLDYNKENLKTFPP--MTSSKPSVDIPNLPSSS 482
                                                                                      SGNENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSCGPPHQRADQRP----PRPASHP 368
                                                                                                                                                                               CCRRRCCGCN------CCCRCC-----FCCRRKRGFRIQFQKKSEKEKTNKETETE 312
                                                                                                                                                                                                                                                                     ----INIPGVLSSLPSLGFSL-----
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US-10-173-706-584

US-10-175-738-584

US-10-175-738-584

US-10-176-482-584

US-10-176-482-584

US-10-176-757-584

US-10-176-757-584

US-10-180-552-584

US-10-180-552-584

US-10-174-572-584

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US-08-755-235-4
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Matches
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Publication No. US20030059423A1

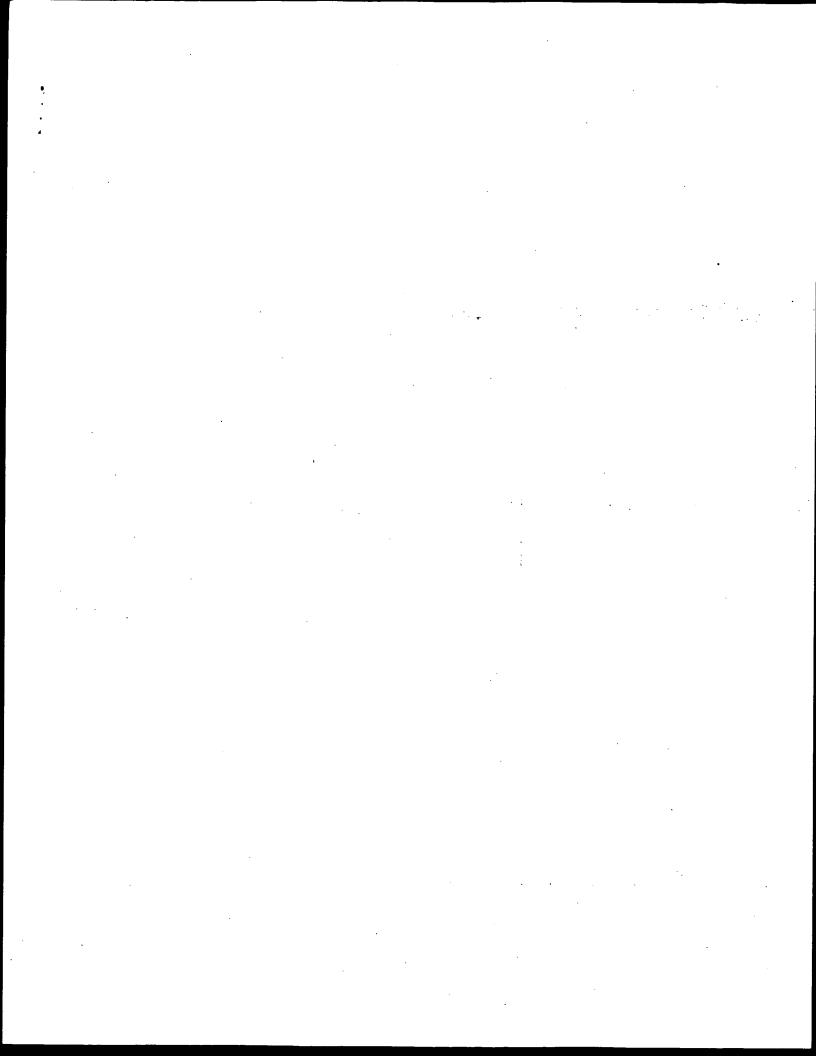
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Schmidt, Ann Marie
APPLICANT: Wu, Jun Marie
APPLICANT: Wu, Jun MeTHOD FOR TREATING SYMPTOMS
TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS
FILE REFERENCE: 0575/50159
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version
SEQ ID NO 4
LENGTH: 405
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/08/755,235
CURRENT FILING DATE: 1996-11-22
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                                                                                                                                                                                                                                                                   162 KPLVPNEKGVSVKEQTRRHPETGLFTLQSELM----VTPARGGDPRPTFSCSFSPGLPRHR 218
                         267
                                                                                                                             271
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                                                                                                                                                                                                                                                                                       64 EPIITNDRETS-----QRYDQGGNFT--SEMIIHNVEPSDSGNIR----CSLQNSRLHGS 112 : | : | : | : | : | | | | | |
                                                                                                                                                                                                                                                                                                                                     Local Similarity 23.7 les 78; Conservative
                       CCCRRRCCGCNCCCRCCFCCRRKRGFRIQFQKKSEKEKT - - NKETETESGNENSGYNSDE 324
                                                                                                                                                                                               ALRTAPIQPRVWEPVPLEEVQLVV---EPEGGAVAPGGTVTLTCEVPAQPS-----PQIH
                                                                                                                                                                                                                                 AYLTVQVMGELFIP----SVNLVVAENEP------
                                                                                                                                               WELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKS-ATVNLTV 213
                                                                                         IRCPODTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLT-----PTCTLTIRC
                                                                                                                             WMKD------GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRAVVSISI
                                                           IE-PGEEG-----
                                                                                                                                                                                                                                                                                                                                    6.7%; Score 140; DB 1
23.7%; Pred. No. 0.006;
Live 34; Mismatches
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Result No.

Score

Gaps

16;



당 C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; pro C;Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; glycq γQ B Qγ structural protein
F;24752-25008/Domain: protein kinase homology <KIN>
F;24752-25008/Domain: protein kinase homology <KIN>
F;84,177,905,2276,2378,2459,2481,2563,2669,2763,2896,3088,3179,3384,3432,3628,3772,4068
F;84,177,905,2276,2378,2459,2481,2563,2669,2763,2896,3088,3179,3384,3432,3628,3772,4068
98,11066,11488,11515,11635,11949,12170,12478,12526,12645,12875,13001,13036,13295,13540,: Search completed: April 28, 2003, 21:09:09
Job time: 40.0659 secs 밁 Query Match 5.5%; Score 114.5; DB 1; Length 26926; Best Local Similarity 22.1%; Pred. No. 45; Matches 62; Conservative 31; Mismatches 87; Indels 101; 16477 VKWGKVDGEIRDAAIIDVT-----16422 AGVGEHADVPGPIIVEEKLEAPDIDLDLELRKIINIRAGGSLRLFVPIKGRP-----TPE 16476 16571 YIVEKREATRKSYAAVVTNCHKNSWKIDQLQEGCSYYFRVTAENEYGIGLPAQTADPIKV 16630 16517 TLENSSGTKSAFVTVRVL-DTPSPPVNLKVTEITKDSVSI----TWEPPLLDGGSKIKN 16570 103 SLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTWLPDI------ 153 182 LALTPQSNGTLTCVATWKSLKARKSATVNLTVIRCPQDTGG 154 ------VPEPSDLQSAVSI 181 43 QGWKLIMWALSDMYVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC 102 3 AGAMENRDPPGSGSGNEVIEGPQ------NARV-----LKGSQARFNCTVS 42 ----SSFTS-LVLDNVNRYDSGKYTL 16516 87; Indels 101; Gaps 12;

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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I49583
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A; Residues: 1-862 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                707
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                                                                                                                                                                                                                                                                                                                                                                                                                                      139 EVTCLP-----SHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTP---QSN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  520 PRDVKVLKVSPASEIRAGQRVLLQCDFAESNPAEVRFFWKKNGSLVQEGRYLSFGSVSPE 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 NPQGSGS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 LSDMVVLSVRPMEPIITNDRFTSQ------RYDQGGNFTSE---MIIHNVEPS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 DPPGSGSGNEVIEGPQNARVLKGSQARFN-----CTVSQGWKL-----IMWA 51
   cardiac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTNCHKNSWKIDQLQEGCSYYF-RVTAENEYGIGLAARTADPIKVAEVPQPPGKITVDDV 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VMGELFIPSVNLVVAENEPCEVTCLPSHWTWLPDI----
                                                                                                                                                                                                                                                                                                                                                              GTLTCVATWKSLKARKSATVNLTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSGNYNCMVNNS------IGETLSQAWNLQVLYAPRRLRVSISPGDHVMEGKKA 627
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                                                                                               QAPPPNNSDSVTYSVIQKRPMGDYENVNPSC 829
                                                                                                                                                                                                                                                                                   LAGIMLLIPICILIIRCCCCRRRCCGCNCCCRCCFCCRRKRGFRIQ-----
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                                                                                                                                                                        NSSGQSFFVRNKKARRTPLSEGPQSQGCYNPAMDDTVSYAILRFPESDMHNAGDAGTPAT
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Pred. No. 1.1
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A;Molecule type: mRNA
A;Residues: 'P',22278-22431,'R',22433-22448,'G',22450-22453,'Q',22455-22480,'TR',2248
A;Residues: 'P',22278-22431,'R',22433-22448,'G',22450-22453,'Q',22455-22480,'TR',2248
A;Residues: 'P',22278-22431,'R',22433-22448,'G',22450-22453,'PID:937195
A;Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labeit, S.
J. MOl. Biol. 256,566,563, 1996
A;Title: Genomic organization of M line titin and its tissue-specific expression in t
A;Reference number: S63665; MUID:96177761; PMID:8604138
A;Accession: S63665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X90568; NID:g1017424; PID:g1017425
R;Musco, G.; Tzlatzios, C.; Schuck, P.; Pastore, A.
Biochemistry 34, 553-561, 1995
A;Title: Dissecting titin into its structural motifs: identification of A;Reference number: 138345; MUID:95119041; PMID:7819249
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C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Sep-2000
C;Accession: 138344; 138345; S20898; S20897; S20899; S63665; S37393
                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Improta, S.; Politou, A.S.; Pastore, A. submitted to the Brookhaven Protein Data Bank, February 1996 A; Reference number: A66736; PDB: 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Phosphorylation of KSP motifs in the C-terminal region of titin in different A;Reference number: S37393; MUID:94008990; PMID:8404852 A;Accession: S37393
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A;Residues: 15330-16382,'S',16384-16756,'E',16758-16860 <LAB3>
A;Cross-references: EMBL:X64699; NID:g37190; PIDN:CAA45940.1; PID:g37191
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Science 270, 293-296,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Gautel, M.; Leonard, K.; Labeit, EMBO J. 12, 3827-3834, 1993
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A; Residues: 13597-14200,'I',14202-14696 <LAB2>
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A; Residues: 1977-2014 <MUS>
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A; Residues: 1-26926 <
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                                                                                                                                                                                                                                                                                                                          submitted to the Brookhaven Protein Data Bank, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                   A; Contents: annotation; conformation by (1)H-NMR, residues 5253-5341
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A; Description: structural protein forming filaments in striated muscle
                                                                            A; Map position: 2q31-2q32
                                                                                                                       A;Cross-references: GDB:127867; OMIM:188840
                                                                                                                                                                                                                                         A; Contents: annotation; conformation by (1)H-NMR, residues 'S', 26059-26155
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A; Residues: 26831-26926 <GAU>
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A;Cross-references: EMBL:X92412; NID:g1236761
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Kolmerer, L.
1995
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Proc. Natl. Acad. Ster. U.S.A. 90, 2899, 1993
A;Title: Muscle-specific trk-related receptor with a kringle
A;Reference number: A47299; MUID:93219391; PMID:8385349
                                                                                                                                                                                                                                                                                                                                                                                                    F;572-588/Domain: transmembrane #status predicted <TMN>
                                                                                                                                                                                                                                                                                                                                                                                                                           F;464-542/Domain: kringle homology <KR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                            F;137-195/Domain: immunoglobulin homology <IM2>F;229-287/Domain: immunoglobulin homology <IM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: electric organ
A; Note: sequence extracted from NCBI backbone (NCBIN:128724, NCBIP:128726)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L11311; NID:g290857; PIDN:AAA49285.1; PID:g290858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-946 < JEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A47299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Date: 10-Sep-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ror-related receptor RTK - Pacific electric ray N;Contains: protein-tyrosine kinase (EC 2.7.1.112) C;Species: Torpedo californica (Pacific electric r.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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F;726-1070/Domain: intracellular #status predicted <INC>
F;794-1065/Domain: protein kinase homology <KIN>
F;116,175,184,214,268,283,405,463,567,646/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Keywords: cell adhesion; extracellular protein; glycoprotein; phosphotransferase;
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-1070/Product: protein-tyrosine kinase 7 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                    58-666/Region: protein kinase ATP-binding 225,340,477,544/Binding site: carbohydrate
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                           650-940/Domain: protein kinase homology <KIN>658-666/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
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;31-703/Domain: extracellular #status predicted <EXC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 VYTCHAA--NLAGQRRQDVNITVATVPSWLKKPQDSQLEEGKPGYLDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 TLTCVATWKSLKARKSATVNLTV-----IRCPQDTGGGINIPGVLSSL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 ENEPCEVTCLPSHWTWLPDISWE-LGL-LVSHSSYYFVPEPSDLQSAVSILALTPQSN-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 ----NGSLLLTQVRPRNAGIYRCIGQGQRGPPIILEATLHLAEIEDMPLFEPRVFTAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 VVLAPQDVVVARYEEAMFHCQFSAQPPPSLQWLFEDETPITNRSRPPHLRRATVFA---- 282
                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 QGGNFTSEMIIHNVEPSDSGNIRCSLQNSR-----LHGSAYLTVQVMGELFIPSVNLVVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 VIEGPQNARVLKGSQARFNCTVS-QGWKLIMWALSDMVVLSVRPMEPIIINDRFTSQRYD 78
                                                                                                                                                                                                  4 GAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNC-TVSQGWKLIMWALSDMVVLSVRP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocal Similarity
                                                                                                            MEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNS---RLHGSAYLTVQV 119
                                                                                                                                                        GALQVKMKP-----KIIRPPTDVRALLGSKVVLPCSTMGNPKPAISWFKDETALKNDQP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EE---RVTCLPPKGLPEPSVWWEHAGVRLPTHGRVY--
                                                                                                                                                                                                                                                     62;
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                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pp-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000
A47299
                                                                                                                                                                                                                                                   Conservative
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                                                                   ---ESGN----LRIRNVQLEDAGKYRCLARNSLGFEYSRSAALEVQV 213
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25.3%;
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                                                                                                                                                                                                                                                                     Score 115.5;
Pred. No. 1.1
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                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                     105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain
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                                                                                                                                                                               Best
                       63
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titin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                                                                                                                                                   C;Superfamily: titin; fibronectin type III repeat homology;
C;Keywords: muscle
                                                                                                                                                                                                                                                                                                                                          A;Reference number: S20897; MUID:92258380; A;Accession: S20900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;McMurray, A.
submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C06A1.6 - Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct.1999 C;Accession: T18975
                                                                                                                                                                                                                             A; Note: the nucleotide sequence was submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                A; Cross-references: EMBL: X64700; NID: g54807; PIDN: CAA45941.1; PID: g54808
                                                                                                                                                                                                                                                                          A; Residues: 1-531 <LAB>
                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                  A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Towards a molecular understanding of titin
                                                                                                                                                                                                                                                                                                                                                                                                            R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick, EMBO J. 11, 1711-1716, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: S20900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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A; Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-152 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z19054
A; Accession: T18975
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                                                                                                                                    Query Match
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    93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 SILALTPQSNGTLTCVATWKSLKARKSATVNLTVIR-----CPQDTGGGINIPGVLSS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
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                                                                                                                 Local
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AGVGEHADVPGPVMVEEKLEAPD---IDLDLELRKVINIRAGGSLRLF-----VPIKGRP 144
                                            AGAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSLPSLGFSLPTWGKVGLGLAG
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                                                                                           62;
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                                                                                                              Similarity
                                                                                         Conservative
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24.2%;
                                                                                                              5.5%;
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                                                                                         36;
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                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 114.5; D
Pred. No. 0.18;
                                                                                                                                 Score 114.5;
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                                                                                       ed. No. 0.6
Mismatches
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                                                                                                              0.67;
                                                                                                                                    DB 2;
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                                                                                                                                                                                                   immunoglobulin homology;
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                                                                                       Gaps
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                                                                                                                                                                                                                           February 1992
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MEPI----ITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQ 118

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GENERAL INFORMATION:
APPLICANT: Bruskin, Arthur
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202.508.9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DOS SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1447 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELLEPHONE: 202_508_9100
TELEFAX: 202_508_9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Vogelstein, Bert
APPLICANT: Zabrecky, James R.
TITLE OF INVENTION: Antibodies Specific for DCC Gene Product
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                     215 RNPASSRTGNEAEVRILSDPGLHRQLYFLQRPSNVVAIEGKDAVLECCVS-GYPPPSFTW 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTWLPDISW-ELGLLVSHSSYY 167
109 LHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTWLPDISW-ELGLLVSHSSYY 167
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                                           274 LRGEEVI----
                                                                              51 ALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSR 108
                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US94/05277
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Kinzler, Kenneth W.
                                                                                                                                                                                                   Conservative
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25.1%;
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                                         -QLRSKKYSLLGG--SNLLISNVTDDDSGMYTCVVTYKNEN 318
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                                                                                                                                                                                                                   Score 136; DB 5; Length 1447; Pred. No. 0.0018;
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US-08-374-834-16
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                                                                                                                                                                                                                                                                                                  Best
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                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (914) 345-7721 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: RETELECOMMUNICATION INFORMATION: TELEPHONE: (914) 345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 21-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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209
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                                                                                                                               159
                                                                                                                                                                                                      113 GALQYKMKP-----KITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGD------ 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 777 Old
CITY: Tarrytown
STATE: New York
                                                                                                                                                                63 MEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAY-LTVQVMG 121
                                                                                                                                                                                                                                                                              Local Similarity
les 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cobert, Robert J
REGISTRATION NUMBER: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                        4 GAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWK-LIMWALSDMVVLSVRP 62
                                                                          ELFIPSVNLVVAENEP---------CEVTCLPSHWTWLPDISW-ELGLLVSHSSYYFVPEP 172
                                                       EVFARILRAPESHNVTFGSFVTLHCTATGIP-----VPTITWIENGNAVSSGSIQESVKD 263
                                                                                                                               -SPLRENSRIAVLE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Regeneron Pharmaceuticals, Inc. 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                 869 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                           6.3%; score 132.5; DB ilarity 20.8%; Pred. No. 0.0018; Conservative 55; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Valenzuela, et al.
/ENTION: NOVEL TYROSINE KINASE RECEPTOR
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                                                                                                                               -SGSLRIHNVQKEDAGQYRCVAKNSL--GTAYSKVVKLEV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REG 190A
                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                178;
                                                                                                                                                                                                                                                                                                                   Length 869;
                                                                                                                                                                                                                                                                                Indels 105;
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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match
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Gapop 10.0 , Gapext 0.5
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2088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6D_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                              808.430 Million cell updates/sec
Sequence 6, Appli
Sequence 24, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 15, Appl
Sequence 21, Appl
Sequence 20, Appl
Sequence 20, Appli
Sequence 1, Appli
Sequence 5, Appli
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Sequence 16, Appl
Sequence 16, Appl
Sequence 29, Appl
Sequence 33, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
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4	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
102.5	102.5	102.5	102.5	102.5	102.5	102.5	103.5	104	104	104	104	104	104	105	106	107	107.5
4.	.9	4.9	4.9	4.9	4.9	4.9	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.1	5.1	5.1
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US-U8-441-1U4A-1	US-08-286-305A-1	-445-	US-08-447-314-2	US-08-170-558-2	US-08-445-640-2	US-08-554-612C-1	US-08-928-383B-26	US-09-553-132-2	US-08-935-433-2	US-09-254-465A-6	US-09-336-536-67	US-09-068-051A-22	US-08-597-495B-22	US-08-482-085B-20	US-07-906-349A-6	US-09-540-245A-17	US-08-415-751-6
Sequence I, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 26, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 67, Appl	Sequence 22, Appl	Sequence 22, Appl	Sequence 20, Appl	Sequence 6, Appli	Sequence 17, Appl	Sequence 6, Appli

ALIGNMENTS

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US-09-041-886-25
                                                                                                                             Query Match
Best Local S
Matches 62
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1447 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Dr
                                                                                                                                                                                                                                TOPOLOGY: 1i MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, De
TITLE OF INVENTION: Polypeptides and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                              215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Diego
STATE: California
COUNTRY: United States
51 ALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRC--SLQNSR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                  9 RDPPGSGSGNEV-------IEGPQNARVLKGSQARFNCTVSQGW--KLIMW 50
                                            RNPASSRTGNEAEVRILSDPGLHRQLYFLQRPSNVVAIEGKDAVLECCVS-GYPPPSFTW 273
                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                   amino acid
)GY: linear
                                                                                                                             Conservative
                                                                                                                                                                                                                              protein
                                                                                                                                                6.5%; Score 136; DB 4; 25.1%; Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                                                                                                                  P-LJ 2626
                                                                                                                          Mismatches 101;
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ds of Use
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US-08-145-617-5/c
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                                                                                                                            Matches
                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Jackle, Herbert
APPLICANT: Tautz, Diethard
                                                                                                                                                                                                                                                                                    TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEPAX: 703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PROCESS FOR ANALYZING LENGTH TITLE OF INVENTION: POLYMORPHISMS IN DNA REGIONS
154
                             911 TGCTGCTGCCGTTGTTTCTGCTG 936
                                                                                       851 CCGACGTGTACTCTTACAATACGCTGCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAAC 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               933 GCTG 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          873 GCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTTTTT 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           Local
                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: DE P
FILING DATE: 11-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Svensson, Leonard R REGISTRATION NUMBER: 30,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                       LENGTH:
                                                           CCGAACTCCAGGCCTCCGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGT 155
TGCTGCTGATGTTGCTGCTGTTG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: BIRCH, STEWART, KOLASCI
T: 301 N. Washington Street,
Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.4%;
Similarity 78.1%;
                                                                                                                                         Similarity
                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                        linear
                                                                                                                                                                                                      DNA (genomic)
                                                                                                                                                                                                                                      single
                                                                                                                                       3.3%; Score 41.2; DB 1; 67.4%; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 07/681,494
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                                                                                                                                                                                                                                                                                                                                                                                    147-122PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KOLASCH & BIRCH
Street, P.O. Box 747
                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                          28;
                                                                                                                                                     Length 379;
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Sequence 23, Applicat Patent No. 5750652 GENERAL INFORMATION:

Application US/08185432

APPLICANT:

APPLICANT:

Diederich, Robert J. Busseau, Isabelle

Artavanis-Tsakonas, Spyridon

APPLICANT:

Matsuno, Kenji Xu, Tian

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RESULT 15
US-08-185-432-23
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                                                                                                                                                                                                                                                           US-08-185-432-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-185-432-3/c
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                                                                                                                                                                                            Matches
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                              1815
                                                                                                                             1875
                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, Tian APPLICANT: Matsuno, Kenji
                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                            933 GCTGTAGAAGAAAAAGAGGATTTCGTATT 961
                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) /50 TELEPHONE: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 18 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                          LOCATION:
                                                              GCTGTTGCTGTCGCGGATGCAGTGGTAAT 1787
                                                                                                                            GCTGCTGCTGCCGCTGTTGCTGCTGTTGCATCTGCAGCTGTTGCTGCTTGTTGCTGCT 1816
                                                                                                                                                                                            59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10036-2711
                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08185432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Busseau, Isabelle
Diederich, Robert J.
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                         unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-1994
                                                                                                                                                                                                                                                                                                                                                         double
                                                                                                                                                                                                         3.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DELTEX PROTEINS, NUCLEIC ACIDS, ANTIBODIES, AND RELATED METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/185,432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18,872
                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7326-006
                                                                                                                                                                                                         Score 41; DB : Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.30
                                                                                                                                                                                                                          DB 1;
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                                                                                                            US-09-817-180-1
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US-09-817-180-1
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Applic
Patent No. 634058
                                       Matches
                                                    Query Match
Best Local Similarity
                                                                                                                                                                                SEQ ID NO 1
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Best Local Similarity
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                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/817,180 CURRENT FILING DATE: 2001-03-27 NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/780,049
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND TITLE OF INVENTION: THEREOF FILE REFERENCE: CL001183
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: GAN, Weiniu et al.
                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24176 TCTTTTGCTAAGGCTGCCACAACAAGCATCAGAGAATAGGTGGCTTAAACAACAGAAAT 24117
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                                                                                                                                                               LENGTH:
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882 GCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCCGCTTGTTGTTTCTGCTGTAGAA 941
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                                     Conservative
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                                                    Score 42; DB 4;
Pred. No. 0.044;
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; ORGANISM: p-2093 plasmid US-09-043-303-7
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                                                                  SEQ ID NO 7
                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09043303 Patent No. 6251589
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Patent No. 6251589
                                                                               CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT FILING DATE: 1998-05-18
EARLIER APPLICATION NUMBER: PCT/JP96/01999
EARLIER FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: PCT/JF96/01999
EARLIER FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and TITLE OF INVENTION: Primers Therefor
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APPLICANT: SANPEI, Kazujiro
                                                                                                                                                                                                       TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type TITLE OF INVENTION: Primers Therefor
                                                                                                                                                                                                                                        APPLICANT: TSUJI, Shoji
APPLICANT: SANPEI, Kazujiro
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                                  TYPE: DNA
                                                LENGTH: 203
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Local 5.
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Similarity, 78.18;
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Pred. No. 0.0088;
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                                                                                                                                        TELEFAX: 617-248-7100 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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                                          MOLECULE TYPE:
ORIGINAL SOURCE:
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                IMMEDIATE SOURCE:
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LOCATION:
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                                                                                                                                                                                                                   NAME: Fenton, Gillian M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                             ORGANISM:
                                                                                                                                                                                                                                NAME: Fenton, Gillia REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                TOPOLOGY:
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Donahue, Brian A
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                               Saccharomyces cerevisiae
                                                                             linear
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Pieter M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recognition
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                                                                                                                                                                                                                                                                                                                 US/08/328,809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42.6;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins
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. 0.033;
34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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US-08-328-809-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 3292 base pairs
                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                             FEATURE:
                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: DNA Structure Specific ReTITLE OF INVENTION: Protein and Uses Therefor
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                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       869 ATACGCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCTAACTGCTGCTGCTGCTTGTTGT 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         758 TGCTGCTGTTGCTGCAACTGCTGTTGTTGTTAATT 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      929 TTCTGCTGTAGAAGAAAAAGAGGATTTCGTATTCAAT 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    818 AGATGATGTTGTTGTTGAAGTTGTTGTTGTTGCTACTGGTGTTGCTGTTGTAGC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Lexington
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                                                                                                                            TOPOLOGY:
                                                                                                                                        STRANDEDNESS:
                                                                                                                                                     TYPE: NUCLEIC ACID
                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                    NAME:
              NAME/KEY:
                                              CLONE:
                                                                              ORGANISM:
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63; Conserv
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                                                                                                                                                                                                                                                                                                  Granahan, Patricia
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                                                                                                                                                                                                                      617-861-9540
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VENTION: DNA Structure Specific Recognition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brown, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
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                                                                            Saccharomyces cerevisiae
                                                                                                                         linear
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                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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Pred. No. 0.033;
0; Mismatches 34;
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TELEPHONE:

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US-07-814-964-12/c
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                                                                           NFORMATION FOR SEQ ID NO: 12:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DNA Structure Specific ReTITLE OF INVENTION: Protein and Uses Therefor
                                              SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     933 GCTGTAGAAGAAAAGAGGATTTCGTATTCAAATTTCAAAAGAAATCTGAA 982
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                                                                                                                                                                                                               REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: UPPLICATION NUMBER: UPPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                          NAME:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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          LENGTH:
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                                                                                                                                                                                                                                                                                   Granahan, Patricia
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3292 base pairs
                                                                                                                  617-861-9540
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Toney, Jeffrey H.
Bruhn, Suzanne L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kellett, Patti
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36..1116
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                                                                                                                                                  617-861-6240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
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US-07-814-964-12
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                                                                          TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 18-JUN-1990
                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: |
ORIGINAL SOURCE:
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                                                                           TELEPHONE: 61/-861-9540
                                                                                                                                        REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02173
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Local Similarity 64.9%;
                                TYPE:
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                STRANDEDNESS:
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ropology:
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o. 5670621
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              nucleic acid
DEDNESS: double
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Toney, Jeffrey H.
Bruhn, Suzanne L.
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linear
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US-08-531-927B-1/c
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                                                                                                                                                                                                            Sequence 1, Application US/08531927B Patent No. 5840491 GENERAL INFORMATION:
                                                                                                                                        Patent No. 5840491
TITLE OF INVENTION:
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NAME/KEY:
LOCATION:
                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Broo
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LENGTH: 325 base pairs
TYPE: nucleic acid
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REGISTRATION NUMBER: 32,227
REFERENCE,DOCKET NUMBER: ATH95-01A
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: JP H6-251600
FILING DATE: 21-SEP-1994
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COMPUTER READABLE FORM:
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                                                                                                                               NUMBER OF SEQUENCES:
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                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                   TGCTGYTGCTGCTTTTGCTGCTGTCTGAAACATTCAAAAGTGAAGTATATTTAAAAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity 57.8
100; Conservative
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                 02173-4799
                                                                Lexington
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617-861-9540
                                 USA
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                              DNA Sequence Encoding the Machado-Joseph
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                                                                                              Brook,
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                                                                                              Smith & Reynolds, P.C
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US-08-531-927B-1
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Best Local S
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            CLASSIFICATION:
ATTORNBY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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LENGTH: 1776 base pairs
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: JP H
FILING DATE: 21-SEP-1994
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TELECOMMUNICATION INFORMATION:
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ZIP: 92122
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                                                                                                                                                                                                                                                                                               STREET: 4370 La
CITY: San Diego
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mes 68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      FILING DATE:
                                                                                                                       APPLICATION NUMBER:
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                  TITLE OF INVENTION: DNA Sequence Encoding the Macl Patent NO. 5840491
TITLE OF INVENTION: Disease Gene and Uses Thereof NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                           Sequence 3, Application US/08531927B Patent NO. 5840491
GENERAL INFORMATION:
APPLICANT: Kakizuka, Akira
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	7-8	9-8	3-3	-267-803B-7	-469-802B-7	5-9	-664-977A-8	5-0	7-8	9-8	7-8	9-8	-267-803B-5	9-8	7-8	9-8	3-3	7-8
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ALIGNMENTS

RESULT 1 US-09-253-691-3/c US-09-253-691-3/c US-09-253-691-3/c US-09-253-691-3/c Patent No. 6124100 Patent No. 612400. GENERAL INFORMATION: APPLICANT: Dong Kyu JIN APPLICANT: Dong Kyu JIN TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases TITLE OF INVENTION: Using Trinucleotide Repeats Sequence FILE REFERENCE: 1942/36 CURRENT APPLICATION NUMBER: US/09/253,691 CURRENT FILING DATE: 1999-02-22 EARLIER APPLICATION NUMBER: KR 98-6,278 EARLIER FILING DATE: 1996-02-26 NUMBER OF SEQ ID NOS: 3 SOFTWARE: WordPerfect 6.1/Windows 873 GCTGCTGCTGCCGCCGCCGTTGTTGTTGTGGCTGCTACTGCTGCTGCTGCTGTTGTTTCT 932 993 CAAACAAAGAAACTGAGACAGAAAGTGGAAA 1023 933 GCTGTAGAAGAAAAAGAGGATTTCGTATTCAAATTTCAAAAGAAATCTGAAAAAGAAGAAGA 992 GCTGTTGCTGCTGTGTGTGTGAAACATTCAAAAGTGAAGTATATTTAAAAAACAA AACTTAAAAGAATAAATACACCATGAGAAAA 50 Similarity Conservative 4.2%; Score 51.8; DE Pred. No. 2.5e: 0; Mismatches 0; .5e-05; DB Length Indels 0, Gaps 0;

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VERSION
KEYWORDS
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295 CACCTCTCAGAGGTACGACCAGGGGGGGAACTTCACCTCGGAGATGATCATCCACACATGT
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                                                           211 TAACCAAATGGTGGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACCGCTT 270
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.A.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: mammary; Vector; pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Glibert Smith, NIH"

193 c 170 g 157 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:3584645"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                               14.8%;
73.4%;
                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                               Score 184; DB 10; Pred. No. 3.4e-32;
                                                                                                                                                                                                                                                                                                              85;
                                                                                                                                                                                                                                                                                                                                                  Length 663;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                        294
                                                                                                                                                                                                                                                                                                              0
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Qy 415 TGCTTACCTTACCGTCCAAG 434

В

391

TGCCTTCCTCTCAGTGCAAG 410

Search completed: April 29, 2003, 09:24:22 Job time: 2018.06 secs

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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  429
                                                                              369
                                                                                                                     355
                                                                                                                                                           309
                                                                                                                                                                                                                                                                                                                        189
                                                                                                                                                                                                                                 249 TAACCAAATGGTGGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACCACCTT
                                                                                                                                                                                                                                                                                                                                                             175
                                                                                                                                                                                                                                                                                                                                                                                          129 AGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAAGGA 188
                                                                                                                                                                                                                                                                                                                                                                                                                               115 AGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGTCCTGAAGGG 174
                                                                                                                                                                                                  295
                                                                                                                                                                                                                                                        235 CAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTT 294
                                                                                                                                                  CACCTATGCCAGTTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCATGATGT 368
                                                                                                                                                                       CACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGGAGATGATCATCCACAATGT 354
TGCCTTCCTCAGTGCAAG
                                   TGCTTACCTTACCGTCCAAG 434
                                                                                           GGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATC 414
                                                                                                                                                                                                                                                                                                                                                     CTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCCTCT 234
                                                                      GCAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGATC 428
                                                                                                                                                                                                                                                                                                              CTCAGAGGCTCACTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Host: SOLR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence[5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="putative"
1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="MGD:MGI:1919308"
/translation="MEGSWRDVLAVLVILAQLTASGSSYQIIEGPQNVTVLKDSEAHF
/translation="MEGSWRDVLAVLVILAQLTASGSSYQIIEGPQNVTVLKDSEAHF
NCTVTHGWKLLMWTLNQMVVLSLTTQGFIITINNRFTYASYNSTDSFISELIIHDVQPS
DSGSVQCSLQNSHGFGSAFLSVQDSIGEEGFALPTWAIILLAVAFSLLLILIIIVLIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPPKSAEVSLPEKRSSSLPYQELNKHQPGPATHPRVSFDIASPQKVRNVTLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FCCCCASRREKEESTYQNEIRKSANMRTNKADPETKLKSGKENYGYSSDEAKAAQTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAB25436.1"
/db_xref="GI:12842010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="FANTOM_DB:2010003D20"
/db_xref="mGD:MGI:1904786"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homolog to IGSF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="small intestine"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="data source:SPTR, source key:Q9NSI5, evidence:ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctone="2010003D20"
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73.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stage="adult"
448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 185.6; DB 1
Pred. No. 1.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11; Length 1552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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ORGANISM
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AI425363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
295 CACCTCTCAGAGGTACGACCAGGGGGGGAACTTCACCTCGGAGATGATCATCCACAATGT
                                                                                                                                                                                                                                                116
                                                                                                                                                                                                                                                                                115 AGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGTCCTGAAGGG 174
                                                                 236 TAACCAAATGGTGGTGGTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACCGCTT
                                                                                                                                                                                          CTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCT 234
                                                                                                                                                                                                                                       AGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGGA 175
                                                                                                                                                      CTCAGAGGCTCACTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTCT 235
                                                                                                          CAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        correct orientation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mx91d09.y1 Soares mouse NML Mus musculus cDNA clone 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI425363
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                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructed and normalized by Bento Soares and \mathbf{M}.\mathbf{Fatima} Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Eco RI sites of the modified pT7T3 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:693713"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               133 c
                                                                                                                                                                                                                                                                                                                                                       14.9%;
73.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         126 g
                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.3e-32;
                                                                                                                                                                                                                                                                                                                                                                           Score 184.6; DB 9;
                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 15-MAR-2000
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                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Library
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RESULT 13
AK008060
                                                                                         REFERENCE
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                                                TITLE
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MEDLINE
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                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCAGAGGCTCACTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCTTCCTCAGTGCAAG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTTACCTTACCGTCCAAG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGCCCAGTGATTCGGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCTATGCCAGTTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCATGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAACCAAATGGTGGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACCGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGGA 216
                                                                                                                                                                                                                                                                                                              Mus musculus adult male small intestine cD1
enriched library, clone:2010003D20:homolog
(FRAGMENT), full insert sequence.
                                                                                                                                                                      Mus musculus (strain:C57BL/6J) adult male small intestine cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:2010003D20.
                                      Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
                                                                                                                                                          Mus musculus
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                            Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                          AK008060.1
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http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop:
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                             CAP trapper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   providing samples: Gilbert Smith, NIH" a 277 c 242 g 179 t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
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                                                                                                        Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                          GI:12842009
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73.8%;
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                                                                                                                                                                                                                                                      Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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cDNA library was prepared and sequenced in Mouse Genome 
Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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Hayashizaki,Y.
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                                                                                                                AUTHORS
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les 236; Conser
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                                                                                                                                                                                                                                                                                                     AW990468 611 bp mRI uf37d05.y1 Soares_mammary_gland_NMLMG IMAGE:1513545 5' similar to TR:060962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop:
                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Email: cgapbs-r@mail.nih.gov
This clone is available roya
                                                                           Tumor Gene Index
                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                          Mus musculus
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clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
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/tissue_type="Liver"
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                                                        1 (bases 1 to 931)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                    mRNA sequence.
BG173684
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                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                      Mus musculus
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                                   BG173684.1 GI:12680387
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cDNA Library Preparation: Life
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares_mammary_gland_NMLMG'
/sex="female (lactating)"
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Technologies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 TCCTGGGAGCTCGGTCTCGTCAGCCATTCAAGCTATTATTTTGTTCCGGAGCCCAGC 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCGCGGAGCTCCCTCGTCAGCCATTCAAGCTATTATTTTGTTCCGGAGCCCAGC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTCGGCGTCCCCAAGGTAAGTGAAGATGT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTCGGTGTCCCCAAGACACTGGAGGTGGT 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCGTGGCTACCTGGAAGAGCCTGAAGGCCCACAAGTCTGCAACTGTAAATCTCACTGTG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTG 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGACTTTGACT 658
                                                  Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishiyo, Nishi-shirakawa, Fuku
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                  Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                 5', mRNA sequence.
AV601192
                                                                                                                                                                                                                                                                                                                                                                                                                                        AV601192 Bos taurus kidney fetus Bos taurus 5', mRNA sequence.
                                                                                                                                                                                                Establishment of a high throughput EST sequencing syspoly(A) tail-removed cDNA libraries and determination
                                                                                                                                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                                                                                                                                                                                                 COW.
                                                                                                                                                                                                                                                                                                                                                                                AV601192.1
EST.
Single
                                   Fax: 81-248-25-5725
                                                                                                                                                                                 bovine ESTs
                                                                                                                                                                                                                                       and Sugimoto,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY
                                                                                                                                                                                                                                                                     (bases 1 to 524)
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                                                                                                                                                            eic Acids Res.
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R.Site 2 : SacI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tracking errors.
pass
              kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
159 c 143 g 207 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism≈"Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="PTB-112N07.F"
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sequencing
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                                                                   961-8061, Japan
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REFERENCE
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AA265274
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 TTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAAT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 GGCTCCCAGGCTCGACTGCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 GCAGCCTGTGGATCCAGCAGTGAAATCATAGAGGGTCCCAAGAATGTCACAGCCCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 GTAGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGTCCTGAAG 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGA 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232;
                                                                                            WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                   1 (bases 1 to 471)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mx91d09.rl Soares mouse 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone was obtained from a polyA-deleted cDNA library. Location/Qualifiers
                                                                                                                                                                             Unpublished (1996)
                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
                                         Email: mouseest@watson.wustl.edu
                                                                                                                                                            Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA265274
                                                                                                                                                                                                                        Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                     house mouse
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clone is available royalty-free through LLNL;
E Consortium (info@image.llnl.gov) for further;
                                                           314 286 1800
314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9913"
/clone="ElKI002H04"
/clone="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"
/lab_host="hH10B"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"

a 135 c 168 g 96 t 5 others
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76.1%;
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Pred. No. 1.3e-33;
0; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NML Mus musculus cDNA clone
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                                                                                                                                                                                                                                           Soares, B.,
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                                                                                                   Louis,
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  further information.
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FEATURES
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  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 GTAGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCCAGAATGCAACAGTCCTGAAG 172
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                                                                                                                                                                                                                                                                                                                                                                                            GCCGCCTTCCTTTCTGTTC 517
                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGCTTACCTTACCGTCC 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGCAACTGAGCGATGCCGGGCAAGTCAAATGCAGCCTTCAGAACAGCAATCGGGATGGA 498
                                                                                                                                     BAC Library clor
Pan troglodytes
                                                                                                                                                                                                         GSS
                                                                                                                                                                                                                       Pan troglodytes DNA, clone: AG069679
AG069679.1 GI:16621481
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 27 row: H column: 19
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.989904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 km 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Unpublished
                Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                 Pan
                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                         AG069679
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                                                                                                                                                          troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Library clone:PTB-060F12.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

a 133 c 165 g 102 t
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/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                 Eutheria;
                                                                                                                        Metazoa;
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76.2%;
                                                                                                 Chordata;
Primates;
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                                                                                                                                                                                                                                                                                         622
                                                                                                                                                                                                                                                                    2 bp DNA
PTB-060F12.F,
                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
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                                                                                                                                                                                                                                                                                       GSS 03-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  677 bp DNA
Pan troglodytes DNA, clone: PTB-112N07.F,
AG107877.1 GI:16728395
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-112N07.F.
Pan troglodytes
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Tel:81-45-603-9111, Fax.81-45-503-9170)
Tel:80-45-503-9170, Tel:80-45-503-9170,
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Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                   Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                     Fujiyama, A., Hattori, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                 BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                   (bases 1 to 677)
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R.Site 1 : SacI
R.Site 2 : SacI.
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/clone_lib="PTB Chimpanzee
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Pred. No. 8.9e-34;
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                                                                                                                                                                                                                                                                                                                                     Taylor, T.D.,
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                                                                                                                                                                                                                                                                                       pig.
Sus scrofa
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BE032610.1 GI:8327619
                                                                                                                                                                                                                                                                                                                                                                                         BE032610
132035 MARC
                                                                                             Unpublished (2000)
Contact: Smith TPL
                  WSDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, U
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                Design and use of two pooled tissue EST discovery in swine
                                                                                                                                                                         Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., and Keele, J.W.
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 527)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L.,
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smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." a 167 c 161 g 149 t
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Pred. No. 1.4e-49;
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Best Local
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                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCAGTGACATGGTGGTGCTAAGGGTCAGGGCCCATGGAGCCCATCATCACCAATGACCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGCTTGTGGATCCGGCAATGAAATCTTAGAGGGTCCCAGGAACGTCACGGCGGTGAAG
                                                                                                                                                                                                                                                                                                                                                    GTCCTTGCGGA 527
                                                                                                                                                                                                                                                                                                                                                                                  GTCGCTGAGAA 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAAAGGCACGGTGGTTCTGAGCGTCACGCCCACCGAGCCCATCATCACCAACGACCGA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCT
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                                                                                                                                                                                                                                BE476432
159670 BARC
BE476432
                                                                                                                                                                                                 EST.
Unpublished (2000)
Contact: Sonstegard TS
                                 gland cDNA library
                                             Wells, K.D.
Mapping of Expressed Sequence
                                                                                             Bovidae; Bovinae; Bos. 1 (bases 1 to 517)
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                 Bos taurus
                                                                                                                                                                                 COW
                                                                                                                                                                                                                BE476432.1 GI:9595965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
Plate: 63 row: E column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: AGGAAACAGCTATGACCAT
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                                                                                Sonstegard, T.S.,
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Library made from pooled tissue from day 11, 13, 1
and 30 embryos."
147 c 176 g 99 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                5BOV Bos taurus
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79.0%;
                                                                                 Capuco, A.V.,
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Pred. No. 1.2e-46;
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                                                Tags from a normalized
                                                                              Van Tassell, C.P., Ashwell, M.S.
                                                                                                                                                                                                                                                                 mRNA
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                                                bovine mammary
                                                                                                                                                                                                                                                                   28-AUG-2000
                                                                                                                                  Bovoidea;
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                 1211 GAGAAGGTCAGTAATACAACTGTAGTATA 1239
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                                                                                                                                                                                                                                                                                                                                          971 AAGAAATCTGAAAAAGAGAAGACAAACAAAGAAACTGAGACAGAAAGTGGAAATGAAAAC 1030
                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                           GATCAACGTCCACCCAGGCCAGCCAGGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCCT
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                                                                                                                                                                     TGTGAATCCAGTGATCCTGAACAAAGAACAGTAGCTGTGGCCCTCCTCACCAGCGGGCT
                                                                         GATCAACGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCCT
                                                                                                                                                   TGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCTCCTCACCAGCGGGCT
                                                                                                                                                                                                                             TCCGGCTACAATTCAGATGAACAAAAGACCACAGACACCGCTTCTCTCCCCCAAATCC
                                                                                                                                                                                                                                                                TCCGGCTACAATTCAGATGAACAAAAGACCACAGAAACCGCTTCTCTCCCCCAAATCC
                                                                                                                                                                                                                                                                                                   GACTTGCGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://image.llnl.gov
Plate: LLAM10635 row: b column:
High quality sequence stop: 725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) I Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 725)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
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602633817F1 NCI_CGAP_Skn3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Skn3"
/lab_host="DHIUB (TI phage-resistant)"
/note="Organ: skin, Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 163 c 159 g 176 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:4778789"
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99.3%;
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Pred. No. 3.7e-51;
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BB663870
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., e Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing pipeline with 384 multicapillary sequencer. Geno 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., K., M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., S., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sa, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 631)
Arakawa, T., Carninci, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with numan Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN integrated sequence analysis (RISA) system -- 384 format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    631 bp mRNA linear
RIKEN full-length enriched, 0 day neonat
cDNA clone E030016M12 5', mRNA sequence.
prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory RIKEN. Division of Experimental Animal Research in Rik
                                                                                                                                                           /dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                           /clone="E030016M12"
                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                              /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                /tissue_type="lung"
                                                                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, 0
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                                                                                                                                                                                                                                                                                                                                                TATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGTTCCGGAGCC 594
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                                                                                                                                    TGTGGTTCAGCTTCCAC
                                                                                                                                                                TGTGATTCGGTGTCCCC 731
                                                                                                                                                                                            GACTTGTGTGGCAGAGCTGAAGGACTTGCAGGCCAGCAAGTCCTTAACTGTCAA-CTGAC
                                                                                                                                                                                                                                                       GGGCAACTTTATGAGGGTCTTGAGTGTCCTGGACCTCACAACA-TGGGCAACGGGACCTT
                                                                                                                                                                                                                                                                                                                  TATTTCCTGGGAGCTTGAGGTTCCCGTAAGCCATTCGAGTTACAATTCCTTTCTGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                             CGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACCCGGCTCCCGGA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCTTACCTTACCGTCCAAGTTATGGGAGAGCTGTTCATTCCCCAGTGTTAATCTTGTAGT 474
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      BE784177 794 bp mRNA linear EST 12-JAN-20 602108039F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4236489 BF784177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DHIOB"
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/organism="Mus musculus"
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70.88;
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Query Match
Best Local Similarity
595 CAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGACTTT
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                                                                                                                                                                                 CACTGAGGGTGAACCCTGTAATGTGACTTGCTATGCCGTGGGCTGGACCTCACTCCCGGA
                                                                                                                                                                                                                                       CGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACCCGGCTCCCGGA 534
                                                                                                                     TATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGTTCCGGAGCC
                                                                                                                                                                                                                                                                                                          TGCCTTCCTCTCAGTGCAAGTCATGGGGACCCTGAACATTCCTAGCAACAACCTTATAGT
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9844 row: n column: 10
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.A.G.E. Consortium
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lib="MCI_CGAP_Kid14"
/clone_lib="MCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
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/strain="FVB/N"
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10830 row: b column: 12
High quality sequence stop: 768.
Location/Qualifiers
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 784)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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BG173684 602336823

AK008060 Mus muscu

AI425363 mx91d09.y

BE376590 661226419

BB625217 BB625217

AZ379923 1M0134G22

BG206666 RST26117

AI788300 uk56d01.y

AI790785 uk28a12.y

BB846577 BB846577

AZ411779 1M0185804

BF040046 BP250004B

BB846133 BB846133

AG142221 Pan trog1

B1452873 603170211

B1452873 603171509

N47851 yw95h05.r1
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AI788973 uk56d01.x
BB531388 BB531388
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BB561363 BB564363
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; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Plasmid pGRO403R
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US-08-479-913E-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08479913E Patent No. 6416998
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Query Match 3.5%; Score 40.8; DB 4; Length 6177; Best Local Similarity 75.0%; Pred. No. 0.097; Matches 51; Conservative 0; Mismatches 17; Indels 0,
                                                                                                                                                                                                                              SOFTWARE: MicroSoft Word 97
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                 APPLICANT: O'MAILEY, Bert W.
APPLICANT: Tsai, Ming-Ter
APPLICANT: Tsai, Ming-Ter
APPLICANT: Ledebur, Harry C.
APPLICANT: Kittle, Joseph D.
FILE REFERICE: 121/133
CURRENT APPLICATION NUMBER: US/08/479,913E
CURRENT APPLICATION NUMBER: US/08/479,913E
CURRENT FILING DATE: 1995-06-07
PRIOR APPLICATION DATE: US/07/939,246
PRIOR FILING DATE: 1992-09-02
NUMBER OF SEQ ID NOS: 6
PRIOR FILING DATE: 1992-09-02
NUMBER OF SEQ ID NOS: 6
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APPLICATION NUMBER: US/0:
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
                                                                                                                                                                                                           LENGTH: 6177
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LOCATION:
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STRANDEDNESS: double
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Local Similarity 66.3%;
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864..1349
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3439..3736
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Search completed: April 29, 2003, 10:49:49 Job time: 81.8976 secs

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                                                                                                         Patent No. 5750652
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Patent No. 5750652
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-999
                                                                                                    GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
                                                                                                                                                                                                                  1815 GCTGTTGCTGTCGCGGATGCAGTGGTAAT 1787
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LENGTH: 3771 base pairs
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                   APPLICANT:
                                 APPLICANT:
                                                  APPLICANT:
                                                                  APPLICANT: Artavanis-Tsakonas, Spyridon APPLICANT: Busseau, Isabelle
                                                                                                                                                                                                                                                                                   FEATURE
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                                                                                                                                                                                                                                                    861 GCTGTAGAAGAAAAAGAGGATTTCGTATT 889
                                                                                                                                                                                                                                                                                                                   801 GCTGCTGCTGCCGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGGTTGTTTCT 860
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LOCATION:
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TELEX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                      ocal Similarity
 OF INVENTION:
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                                             Busseau, Isabelle
Diederich, Robert J.
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Busseau, Isabelle
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                                    Xu, Tian
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345..2558
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66.3%;
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DELTEX PROTEINS, NUCLEIC ACIDS,
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Pred. No. 0.064;
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RESULT 14
US-08-185-432-1/c
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TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUIENCE CHARACTERISTICS:
FENGTH: 3771 base pairs
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Best Local Similarity
Matches 59; Conserv
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                                                                                                                                                                                                                                                                                                         APPLICANT:
              COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1957 GCTGTTGCTGTCGCGGATGCAGTGGTAAT 1985
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                  CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) /90-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 10036-2711
 SOFTWARE:
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                                                                                                                                                                       ADDRESSEE:
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PatentIn Release #1.0,
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                                                                                                                                                                                                       Renji DELTEX PROTEINS, NUCLEIC ACIDS, AND ANTIBODIES, AND RELATED METHODS AND 23
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Pred. No. 0.064;
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 Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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PCT-US92-11107-12

Query Match Best Local :

3.6%; 64.9%;

Length 3292;

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US-09-043-303-7
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Patent No. 6251589
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                               SEQ ID NO 7
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Best Local Similarity
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 Query Match
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CURRENT FILING DATE: 1998-05-18
EARLIER APPLICATION NUMBER: PCT/JP96/01999
EARLIER FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
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                                                                                                                                               EARLIER APPLICATION NUMBER: PCT/JP96/01999
EARLIER FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                  FILE REFERENCE: 0760-0241P
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT FILING DATE: 1998-05-18
                                                                                                                                                                                                                                                APPLICANT: TSUJI, Shoji
APPLICANT: SANPEI, Kazujiro
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2
TITLE OF INVENTION: Primers Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and TITLE OF INVENTION: Primers Therefor FILE REFERENCE: 0760-0241P
                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 78
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TSUJI, Shoji
APPLICANT: SANPEI, Kazujiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                          ENGTH: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          801 GCTGCTGCCGCCGCCGCCGTTGTTGTGGCTGCCAACTGCTGCTGCTGCTTGTTTCT 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     861 GCTG 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          758 TGCTGCTGCTGCCAACTGCTGTTGTTGTAATT 722
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les 63; Conserv
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 3.6%;
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Pred. No. 0.02;
""" matches 34;
 Score 41.6;
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Pred. No. 0.0047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 78;
 DВ
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Length 203;
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US-08-145-617-5/c
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                                                                                                                                          Matches
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                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 78.1%; Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,494
FILLING DATE: 10-JUN-1991
APPLICATION NUMBER: DE P3834636.2
FILLING DATE: 11-OCT-198
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
                                                                                                                                                                                                                                                                                                                                  TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,617
                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 379 base pairs
                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PROCESS FOR ANALYZING LENGTH TITLE OF INVENTION: POLYMORPHISMS IN DNA REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jackle, Herbert
APPLICANT: Tautz, Diethard
154 TGCTGCTGCTGATGTTGCTGCTGTTG 129
                                839 TGCTGCTGCCGTTGTTTCTGCTG 864
                                                                      214 CCGAACTCCAGGCCTCCGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGT 155
                                                                                        779 CCGACGTGTACTCTTACAATACGCTGCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAAC 838
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                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: /UJ - 703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 301 N. Washington Street, P.O. Box CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                          58;
                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                379 base pairs
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                                                                                                                                          Conservative
                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIRCH, STEWART,
                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                         3.5%;
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147-122PCT
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                                                                                                                                                       Score 41.2; DB Pred. No. 0.015;
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                                                                                                                                          Mismatches
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US-08-258-442-12
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Best Local Similarity 64.9
Matches 63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                    TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kellett, Patti
TITLE OF INVENTION: Uses For DNA Structure-Specific
TITLE OF INVENTION: Recognition Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: MITTELECOMMUNICATION INFORMATION: 617-248-7000
                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 3292 base pairs
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
GORTMANDO: PC-DOS/MS-DOS
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ORIGINAL SOURCE:
                 IMMEDIATE SOURCE:
                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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CLONE: lambda yPt
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STREET: STREET: BOSTON
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                                     ORGANISM:
                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                       NAME: Fenton, Gillian REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 02109
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                                                                                                 nucleic acid
EDNESS: double
lambda yPt
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Essigmann, John M.
Donahue, Brian A.
Toney, Jeffrey H.
Bruhn, Suzanne L.
Pil, Pieter M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brown, Steven
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                                 Saccharomyces cerevisiae
                                                                                     linear
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                                                                   DNA (genomic)
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                                                                                                                                                                                                                                                       36,508
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                                                                                                                                                                                                                                      MIT-023 (5473/24)
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RESULT 8
PCT-US92-11107-12/c
Sequence 12, Application PC/TUS9211107
GENERAL INFORMATION:
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                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
EFILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,22
                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 3292 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: DNA Structure Specific ReTITLE OF INVENTION: Protein and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
ORIGINAL SOURCE:
               MOLECULE TYPE:
                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2 Milit:
% CITY: Lexington
% STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   818 AGATGATGTTGTTGTTGAAGTTGTTGTTGTTGTTGCAACTGGTGTTGCTTGTTAGC 759
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                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PILING DATE: 19921218
                                                                            LENGTH:
                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP:
                                 TOPOLOGY:
                                               STRANDEDNESS:
                                                                                                                                               TELEPHONE:
                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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                                                                NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lippard, Stephen J. VENTION: DNA Structure Specific Recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brown, Steven
Kellett, Patti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Essigmann, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                               617-861-6240
                DNA (genomic)
                                                 double
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                                                                                                                                                                                                                                                               us 07/539,906
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                                                                                                                                                                               MIT-4787AAA

 Mismatches

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FEATURE:

NAME/KEY:

CDS 1..1626 IMMEDIATE SOURCE:

lambda yPt

ORGANISM: Saccharomyces cerevisiae

TELEPHONE:

(619)

(619) 535-9001 519) 535-8949

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RESULT 5
US-07-814-964-12/c
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US-09-041-886-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                          INFORMATION FOR SEQ ID NO:
                                                          REFERENCE/DOCKET NUMBER: MIT-4787AAA TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   SEQUENCE CHARACTERISTICS:
LENGTH: 3292 base pair
                                                                                                       APPLICATION NUMBER: US 07
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,7
                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                             APPLICATION NUMBER: US
FILING DATE: 19911226
                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                      ZIP: 02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68;
                                                                                                                                                                                                                                                                                                                                                                           Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2, Application US/07814964
5359047
                                                                                                                                                                                                                                                                                                                                                               MA
3292 base pairs
                                                                                                                                                                                                                                                                                                                                                                                           3: Hamilton, Brook, Smith & Reynolds, P.C
2 Militia Drive
                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Essigmann, John M.
Lippard, Stephen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toney, Jeffrey
Bruhn, Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kellett, Patti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
36..1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Donahue, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pieter M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.7%;
61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein and Uses Therefor 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Structure Specific Recognition
                                                                                                                                                                    US 07/539,906
                                                                                                                                                                                                                             US/07/814,964
                                                                                                       32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42.8; DB Pred. No. 0.012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
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Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILLING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patticia
REGISTRATION NUMBER: 32,27
REFERENCE/DOCKET NUMBER: MIT-4787AA.
TELECOMMUNICATION INFORMATION:
TELECHONE: 617-861-6240
                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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LOCATION:
                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
   TOPOLOGY:
                 STRANDEDNESS:
                                TYPE:
                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UZIP: 02173
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                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Lexington
                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 Militia Drive
                                           3292 base pairs
                                                                                              617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lippard, Stephen J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Essigmann, John M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kellett, Patti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brown, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pil,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toney, Jeffrey
Bruhn, Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamilton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pieter M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Structure Specific Recognition Protein and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brian
                                                                                                                                                                                                                                                                                    US/08/258,442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brook, Smith & Reynolds,
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                                                                                                                                            MIT-4787AAA
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Pred. No. 0.02;
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                                                                                                                                                                                                                              Sequence 1, Application US/08531927B Patent No. 5840491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                               TITLE OF INVENTION:
cent No. 5840491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: ATH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPRAY. 617-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER
                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                             ent No. 5
                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP H6
FILING DATE: 21-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                904 ATCTGAAAAAGAGAAGAACAAAGAAACTGAGACAGAAAGTGGAAATGAAA 956
                                                                                                                                                                                                                                                                                                                                                                                                   150 TGCTGYTGCTGTTTTGCTGCTGTCTGAAACATTCAAAAGTGAAGTATATTTAAAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                  845 TGCCGTTGTTGTTTCTGCTGTAGAA-GAAAAAGAGGATTTCGTATTCAAATTTCAAAAGAA 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            785 TGTACTCTTACAATACGCTGCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGC 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
               COUNTRY: USA
ZIP: 02173-4799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                90 AAACTTAAAAGAATAAATACACCATGAGAAAAACTATTCATAAGGAAAATACA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Mil:
CITY: Lexington
                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 21-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02173-4799
                                                             Lexington
READABLE FORM:
                                                                                                                                            INVENTION: Disease Gene and Uses Thereof
                                               Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
                                                                              Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 base pairs
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                                                                                                                                                                                              Kakizuka, Akira
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Pred. No. 0.00012;
                                                                                            Smith & Reynolds, P.C
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RESULT 4
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Patent No. 6235872
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bredesen, I
APPLICANT: Rabizadeh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 617-861-624
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC-DOS/MS-DOS
OPERATING SYSTEM: DC-DOS/MS-DOS
           ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: ATTELECOMMUNICATION INFORMATION:
TELEPHONE: 617,861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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APPLICATION NUMBER:
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                861 GCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAA 910
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LOCATION:
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                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1776 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                       FILING DATE:
                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                    United States
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61.8%;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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      Length
                                 203
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US-09-041-886-12
US-09-043-303-12
US-09-043-303-12
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US-08-185-432-3
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Sequence 3, Application US/08531927B
Patent No. 5840491
GENERAL INFORMATION:
APPLICANT: Kakizuka, Akira
TITLE OF INVENTION: DNA Sequence En
TITLE OF INVENTION: Disease Gene an
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

Encoding the Machado-Joseph

and Uses

Thereof

ADDRESSEE:

Hamilton, Brook, Smith & Reynolds, P.C

RESULT 2 US-08-531-927B-3/c · Semence 3. Application US/08531927B	US-09-253-691-3/c US-09-253-691-3/c Sequence 3, Application US/09253691 Patent No. 6124100 GENERAL IMPORMATION: APPLICANT: Dong Kyu JIN TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases TITLE OF INVENTION: Using Trinucleotide Repeats Sequence FILE REFERENCE: 1942/36 CURRENT FILING DATE: 1999-02-22 FEARLIER APPLICATION NUMBER: US/09/253,691 CURRENT FILING DATE: 1996-02-26 NUMBER OF SEQ ID NOS: 3 SOFTWARE: WordPerfect 6.1/Windows SED ID NO SOFTWARE: WordPerfect 5.1/Windows SOFTWARE: WordPerfect 5.1/Windows SOFTWARE: WordPerfect 5.1/Windows SED ID NO SOFTWARE: WordPerfect 5.1/Windows SOFTWARE: WordPerfect 6.1/Windows SOFTWARE: Wor	ALIGNMENTS	39 40 3.4 477 4 US-09-133-994-1 Sequence 1, 40 40 3.4 506 1 US-08-469-802B-7 Sequence 7, 41 40 3.4 506 2 US-08-267-803B-7 Sequence 7, 42 40 3.4 506 2 US-08-267-803B-7 Sequence 5, 43 40 3.4 3366 1 US-08-469-802B-1 Sequence 1, 44 40 3.4 3366 2 US-08-267-803B-1 Sequence 1, 46 40 3.4 3376 1 US-08-320-559-29 Sequence 29, 45 40 3.4 3376 1 US-08-320-559-29	C 29 40 3.4 168 2 US-08-267-803B-5 Sequence 5, Appli C 31 40 3.4 171 1 US-08-267-803B-5 Sequence 5, Appli C 31 40 3.4 171 1 US-08-267-803B-5 Sequence 5, Appli C 32 40 3.4 171 2 US-08-267-803B-5 Sequence 5, Appli C 32 40 3.4 195 1 US-08-267-803B-2 Sequence 2, Appli C 34 40 3.4 195 2 US-08-267-803B-2 Sequence 2, Appli C 35 40 3.4 234 1 US-08-267-803B-3 Sequence 3, Appli C 36 40 3.4 234 1 US-08-267-803B-3 Sequence 3, Appli C 37 40 3.4 234 2 US-08-267-803B-3 Sequence 3, Appli C 38 40 3.4 270 4 US-09-146-054-8 Sequence 8, Appli C 38 40 38	28 40 3.4 165 4 US-09-043-303-17 Sequence 17, 29 40 3.4 168 1 US-08-469-802B-4 Sequence 4,
2 531-927B-3/c 530-3. Application US/08531927	US/09253691 N Signostic Method and Kit for Neuropsychiatric Diseasing Trinucleotide Repeats Sequence Signostic Method and Kit for Neuropsychiatric Diseasing Trinucleotide Repeats Sequence Signostic Method and Kit for Neuropsychiatric Diseasing Trinucleotide Repeats Sequence Signostic Method and Kit for Neuropsychiatric Diseasing Trinucleotide Repeats Sequence Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Kit for Neuropsychiatric Diseasing Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Kit for Neuropsychiatric Diseasing Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Kit for Neuropsychiatric Diseasing Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Kit for Neuropsychiatric Diseasing Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Kit for Neuropsychiatric Diseasing Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Kit for Neuropsychiatric Diseasing Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Kit for Neuropsychiatric Diseasing Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Repeats Sequence 1.4.4%; Score 51.8; DB 3; Length 397; Signostic Method and Repeats Sequence 1.4.4%; Score 51.8;		9 40 3.4 477 4 US-09-135-994-1 Sequence 1, 0 40 3.4 506 1 US-08-469-802B-7 Sequence 7, 1 40 3.4 506 2 US-08-67-803B-7 Sequence 7, 2 40 3.4 623 4 US-09-043-305 Sequence 7, 3 40 3.4 3366 1 US-08-469-802B-1 Sequence 1, 4 40 3.4 3366 2 US-08-267-803B-1 Sequence 1, 4 40 3.4 3376 1 US-08-320-559-29 Sequence 29, 5 40 3.4 3376 1 US-08-320-559-29	1 40 3.4 158 2 US-08-267-803B-5 Sequence 4, 171 1 US-08-469-802B-5 Sequence 5, 2 40 3.4 171 2 US-08-267-803B-5 Sequence 5, 3 40 3.4 195 1 US-08-8902B-2 Sequence 2, 4 40 3.4 195 2 US-08-267-803B-2 Sequence 2, 4 40 3.4 295 2 US-08-267-803B-3 Sequence 3, 5 40 3.4 234 1 US-08-267-803B-3 Sequence 3, 6 40 3.4 234 2 US-08-267-803B-3 Sequence 3, 6 40 3.4 270 4 US-09-146-054-8 Sequence 8, 7 40 3.4 270 4 US-09-664-977A-8 Sequence 8, 8 40 3.4 270 4 US-09-664-977A-8 Sequence 8,	10 3 TE -00-207 -003h - 1



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RESULT 15
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Best Local
                       Claim 1;
                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          containing a neuropsychiatric gene containing trinucleotide repeats. Tri-nucleotide repeats and their expansion areknown to be involved in a number of diseases including fragile X syndrome, spinocerebellar ataxia type III, hereditary hypertrophic, cardiomyopathy, dentatorubral and pallidoluysian atrophy (DRPLA), spinocerebellar ataxia, Marfan syndrome, X-linked spinoubar atrophy. The present sequence represents a nucleotide sequence of the invention showing the
                                                                                                                                                                                23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                         WO200171042-A2
                                                                                                                                                                                                                                                                                                                          pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                         Drosophila;
                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genomic polynucleotide SEQ ID NO 1963.
                                                           New isolated nucleic acid genes from Drosophila and
                                                                                                                            Venter JC, Adams M,
                                                                                                                                                      (PEKE ) PE CORP NY.
                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                               27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to the use of a plasmid vector array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 12; 23pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid vector arraying neuropsychiatric gene more than copy number containing trinucleotide repeats its use thereof -
                                                  interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the CAG tri-nucleotide repeats.
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                    SEQ ID NO 1963; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                       developmental biology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 A; 108 C; 105 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.4%;
58.9%;
                                                                                                                                                                                                                                                                                                                           ds.
                                                                                                                            Ľ
                                                                                                                            , DWG
                                                           detection reagent for for elucidating cell s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51.8; DB 21
Pred. No. 0.00036;
0; Mismatches 62
                                                                                                                            Myers EW
                                                                                                                                                                                                                                                                                                                                       cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                            r detecting
signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 403;
                                                                                                                                                                                                                                                                                                                                       insecticide;
                                                            1000
and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                           0 or more
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The invention relates to an isolated nucleic acid detection reagent

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Search completed: April 29, 2003, 11:05:24 Job time: 342.628 secs
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                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     16836 ACGATGGTGCTGCCGATGATGTGGATGCTCTGGATGATGCTGCTGCTGCTGCAGATGCAA 16895
                                                                                   16956 AAAGTTACAATTTCAAAACAAAT
                                                                                                                                                                     16896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling the local interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 46954 BP; 13370 A; 9970 C; 9854 G; 13760 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification, but was obtained in electronic format directly from
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                             764 ACCATGCTTCTGACGCCGACGTGTACTCT-TACAATACGCTGCTGCTGCTGCTGCCGCCGTCG 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABB57737-ABB72072)
                                                                                                                                                                                                            823 TTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTGTTTCTGCTGTAGAAGAAAAAGAGGATT 882
                                                                                                                          TCGTATTCAATTTCAAAAGAAAT
                                                                                                                                                                     TTGCTGCCGCTGCTGCTGCTGCTGCTGCTGCAGTTGCGGATGCGGATGAGTGCA 16955
                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                        4.2%;
                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                        Score 49.4;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                        .021;
                                                                                                                                                                                                                                                                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                             Length 46954
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                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
AAX89891/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                containing a neuropsychiatric gene containing trinucleotide repeats. Tri-nucleotide repeats and their expansion are known to be involved in a number of diseases including fragile X syndrome, spinocerebellar ataxia type III, hereditary hypertrophic, cardiomyopathy, dentatorubral and pallidoluysian atrophy (DRPLA), spinocerebellar ataxia, Marfan syndrome; X-linked spinobubar atrophy. The present sequence represents a tri-nucleotide repeat related sequence #5 disclosed in the scope
                    Diagnosis of spinocerebellar ataxia type III (SCA III) syndrome
          using techniques which ensure highly accurate diagnosis
                                                   WPI; 1999-527634/44
                                                                                                                          (JIND/) JIN D K.
                                                                                                                                                    26-FEB-1998;
                                                                                                                                                                                18-FEB-1999;
                                                                                                                                                                                                            02-SEP-1999.
                                                                                                                                                                                                                                        W09943852-A1
                                                                                                                                                                                                                                                                                             repeat_unit
                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           SCAIII syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                         PCR-microplate hybridisation; PCR-MPH; trinucleotide repeat; TNR;
                                                                                                                                                                                                                                                                                                                                                                                                                       Spinocerebellar ataxia type III; SCAIII; reverse dot hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Spinocerebellar ataxia type III (SCAIII) gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX89891 standard; DNA; 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 389 BP; 107 A; 92 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         been represented by an n to keep nucleotide numbering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note; Nucleotides which were illegible in the specification have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the invention.
                                                                                                         (SMSU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to the use of a plasmid vector array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  921 CAAACAAAGAAACTGAGACAGAAAGTGGAAATGAA 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      861 GCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAAAAAGAGAGAAGA 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   801 GCTGCTGCTGCCGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCTGCTTGTTTCT 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 AANTTAAAAGAANACCTACACCATGAGNTANAAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGTTGCTGCTGTGTGTGAAACATTCAAAAGTGAAGTATATTTAAAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
89; Conserv
                                                                                                           SAMSUNG FINE CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                    98KR-0006278.
                                                                                                                                                                                99WO-KR00078.
                                                                                                                                                                                                                                                                                             /*tag= 8
                                                                                                                                                                                                                                                                /note= "trinucleotide repeat"
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
137..355
                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.48;
                                                                                                                                                                                                                                                                                                          a
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 G; 93 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ыв 21;
n.00035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           correct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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ABK10240/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the diagnosis of spinocerebellar ataxia type III (SCAIII) syndrome using reverse dot hybridisation or PCR-microplate hybridisation (PCR-MPH). The method comprises attaching a potion of the SCAIII gene containing 73 copies of the trinucleotide (CAG) repeat unit (the present sequence) to a substrate, and hybridisting with amplified testee genomic DNA containing copies of the trinucleotide units, PCR amplified with labeled primers (AAX89889-90). The new method is useful for diagnosis of SCAIII syndrome, and for determining the severity of the disease. The present sequence represents the SCAIII gene fragment containing 73 trinucleotide (TNR) repeats.
                                                                                                                                                                                                                                                                                                                                                                            hereditary hypertrophic cardiomyopathy; Marfan synds
dentatorubral and pallidoluysian atrophy;
spinocerebellar ataxia; x-linked spinobubar atrophy
Jin DG
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trinucleotide repeat sequence #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK10240 standard; DNA; 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 12-13; 28pp; English.
                            (SMSU ) SAMSUNG MEDICAL CENT
(JIND/) JIN D G.
                                                                         25-JUN-1998;
                                                                                                     25-JUN-1998;
                                                                                                                                     15-JAN-2000
                                                                                                                                                                  KR2000003004-A
                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                           repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                           spinocerebellar ataxia type III;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Trinucleotide repeat; fragile X syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                921 CAAACAAAGAAACTGAGACAGAAAGTGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  861 GCTGTAGAAGAAAAAGAGGATTTCGTATTCAAATTTCAAAAGAAATCTGAAAAAGAGAAAGA 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 AACTTAAAAGAATAAATACACCATGAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGTTGCTGCTTTTGCTGCTGTCTGAAACATTCAAAAGTGAAGTATATTTAAAAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 124 A; 104 C; 104 G; 65 T; 0 other;
                                                                         98KR-0024064
                                                                                                       98KR-0024064.
                                                                                                                                                                                                                                                                                                      Location/Qualifiers 152..347
                                                                                                                                                                                                                                                           /rpt_type=
152..154
                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.4%;
                                                                                                                                                                                                                             "CAG type repeat"
                                                                                                                                                                                                                                             ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                         TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51.8; DB 20;
Pred. No. 0.00035;
0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                           DRPLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        951
                                                                                                                                                                                                                                                                                                                                                                                                                             neuropsychiatric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 397;
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RESULT 1:
ABL29756
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Best Local S
Matches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and pallidoluysian atrophy (DRPLA), spinocerebellar ataxia, Marfan syndrome; X-linked spinobubar atrophy. The present sequence represents a nucleotide sequence of the invention showing the the CAG tri-nucleotide repeats.
                                                                    useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genomic polynucleotide SEQ ID NO 40741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL29756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 277 BP; 80 A; 66 C; 62 G;
                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                   Claim 1; SEQ ID NO 40741; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                               New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                     Venter JC,
                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL29756 standard; DNA; 7029
                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95
                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                         2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACTTAAAAGAATAAATACACCATGAGAAAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAACAAAGAAACTGAGACAGAAAGTGGAAA 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGTTGCTGCTTTTGCTGCTGTCTGAAACATTCAAAAGTGAAGTATATTTAAAAAAACAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAAAAAGAGAAGA 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
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                                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.6%;
                                                                                                                                                                                                                                                                                                                     Li PWD,
                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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Pred. No. 0.00
0; Mismatches
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                                                                                                                                                                                                                                                                                                                     Myers EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.00011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277;
                                                                                                                                                            The invention
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                                            from
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Sequence 7029 BP; 1426 A; 1440 C; 1945 G; 2218 T; 0 other;

Disclosure; Fig 10; 23pp; Korean

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RESULT 12
ABK10248/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5560
                                                                                                                                                                                                                       /note=
misc_difference 203
                                                                                                                                                                                                                                                 /note=
misc_difference 56
                                                                                                                                                                                                                                                                                                                                                                          Trinucleotide repeat; fragile X syndrome; ds; spinocerebellar ataxia type III; DRPLA; neuropsychiatric hereditary hypertrophic cardiomyopathy; Marfan syndrome; dentatorubral and pallidoluysian atrophy; spinocerebellar ataxia; X-linked spinobubar atrophy.
                                                                                                                                                                                                      misc_difference
                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                              Tri-nucleotide repeat related sequence #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK10248;
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               Plasmid vector arraying neuropsychiatric containing trinucleotide repeats its use
                                        WPI; 2000-662424/64
                                                        Jin DG;
                                                                                                   25-JUN-1998;
                                                                                                                                    15-JAN-2000
                                                                                                                                                     KR2000003004-A
                                                                                                                   25-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   801 GCTGCTGCTGCCGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCTGCTTGTTTCT 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        861 GCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAA 904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAMSUNG MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                          /note=
/31
                                                                                                   98KR-0024064
                                                                                                                    98KR-0024064
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                                                                                                                                                                                                        /note=
276
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    Mismatches

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Pred. No. 0.00086;
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                gene more
thereof -
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                        than copy number
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                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and prollferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                 treatment of allergy, asthma and hypersensitivity reactions, nephropathles (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathles (Grave's disease), various pneumopathles (extrinsic alveolitis), vasculopathles, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the coding sequence of mouse B7-L_m2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for enhancing the immune response to tumours. (I) plays a growth and maintenance of cancer cells based on the observation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 6; 135pp; English.
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28-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecules are useful for alleviating the symptoms associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seminal vesicle hyperplasia in transgenic mice overexpressing B7-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Welcher AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC
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228
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                                                                                                                                                                                                       42 CCGGTTCTGGGTACTGAAGTCATAGAAGGCCCCCAAAATGCAAGAGTCCTGAAGG 101
                                                                                                                                                                                                                                                                                         Local Similarity
  TTAACCAAATGGTGGTGCTGAGTCTCACCAACGAGCCCATCATCACCAACAACCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-130881/17.
                                          TCAGTGACATGGTGGTGCTAAGCGTCAGGCCCCATGGAGCCCCATCATCACCAATGACCGCT 221
                                                                                      ACTCAGAGGCTCACTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTC
                                                                                                                                 GCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTC 161
                                                                                                                                                                             CAGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGG
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                                                                                                                                                                                                                                                                                                                                                         895 BP; 250
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2000US-0729264.
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72.9%;
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                                                                                                                                                                                                                                                                                         Score 181.8;
Pred. No. 3.
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RESULT 10
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CCCCCXCXTTXX
                                                                                                                                                                                                                                               PF
         This invention relates to the use of a plasmid vector array containing a neuropsychiatric gene containing trinucleotide repeats. Trinucleotide repeats and their expansion areknown to be involved in a number of diseases including fragile X syndrome, spinocerebella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hereditary hypertrophic cardiomyopathy; neuropsychiatric; dentatorubral and pallidoluysian atrophy; spinocerebellar ataxia; X-linked spinobubar atrophy.
                                                                                              Plasmid vector arraying neuropsychiatric gene more than containing trinucleotide repeats its use thereof -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trinucleotide repeat; fragile X syndrome; ds; DRPLA; spinocerebellar ataxia type III; Marfan syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trinucleotide repeat sequence #2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK10239 standard;
                                                                    Disclosure; Page 12;
                                                                                                                                  WPI; 2000-662424/64
                                                                                                                                                           Jin DG;
                                                                                                                                                                                 (SMSU ) SAMSUNG MEDICAL CENT (JIND/) JIN D G.
                                                                                                                                                                                                                       25-JUN-1998;
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                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        repeat_unit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGAT
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                                                                                                                                                                                                                       98KR-0024064.
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                                                                                                                                                                                                                                                                                                                                                                         /rpt_type=
198..200
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "CAG type repeat" 198..222
                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_type=
152..154
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                                                                                                                                                                                                                                                                                                                                               /note= "CAG type repeat"
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                                                                       23pp; Korean
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cardiomyopathy, dentatorubral
            spinocerebellar
                                                                                                          copy number
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hereditary hypertrophic,

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RESULT 8
ABK13034
ID ABK1
useful for enhancing the immune response to tumours. (1) plays a role in growth and maintenance of cancer cells based on the observation of seminal vestcle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vestcle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat
                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, disorders of conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are
                                   autoLumunne diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective;
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28-NOV-2000;
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                    Grave's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 7; 135pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding mouse B7-like protein, B7-L_m3
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                Hashimoto's thyroiditis and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "B7-like protein, B7-L_m3"
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              They
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
                                                                                                                                                                                                                                                      Mouse; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirtumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer;
                                                                                                                                                                                                  reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coellac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoporoliferative disorders such as multiple myeloma. The present sequence represents the coding sequence of mouse B7-L_m3.
                                                                                                                                                                                                                                                                                                                                                                         DNA encoding mouse B7-like protein, B7-L_m2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and
                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK13033;
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                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                       /*tag=
                                                                                                            53..865
                                                                     /product= "B7-like protein, B7-L_m2"
                                                                                                                              Location/Qualifiers
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                                                                                CTCTCCCTCCCAAATCCTGTGAATCCAGTGATCCTGAACAAGAAGAAACAGTAGCTGTGGCC
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Best Local
                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1119
                                                                                                                                                                                                                          Sequence 401 BP; 105 A; 98 C; 111 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                         analyzing
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
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30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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 374
                                                                 147
                     207
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                                                                                                                                     194
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                                                                                                                                               27 AAAATAGAGACCCACCCGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATG
                                                                                                                                                                                          Local Similarity
                                                             TCATCATGTGGGCTCTCAGTGACATGGTGGTGGTAAGCGTCAGGCCCATGGAGCCCATCA
                                                                                                                                    AAATTGGCTACCTTCCAGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATG
 TCACCAATGACCGCTTCACCTCTCAGAG
                                                                                                  CAAGAGTCCTGAAGGGCTCCCAGGCTCCCACGGCTCCAACCGTCTCCCCAGGGCTGGAAGC
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                                          CAAGAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGC
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                                                                                                                                                                                                                                                                                                                                         gene expression in human placenta
                                                                                                                                                                                                                                                                                                                  SEQ ID No 5268; 654pp; English.
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                                                                                                                                                                                Conservative
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                         16.8%;
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Pred. No. 1.6e-44;
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Mouse; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirhet antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cano reproductive disorder; graft versus host disease; autoimmune diseatoxic shock syndrome; allergy; nephropathy; skin disorder;
                                                                                                                                                                                                                                                                                                             1021
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                                                                                                                              DNA encoding mouse B7-like protein, B7-L_m1.
                                                                                                                                                               23-APR-2002
                                                                                                                                                                                                                              ABK13032 standard; cDNA; 1195
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CC The polypeptide, polynucleotide encoding it and antibody against (I) are CC useful for treating B7-like polypeptide-related disease, disorders or CC conditions including reproductive disorders (e.g. infertility, CC miscarriage, preterm labour and delivery and endometriosis) and CC proliferative disorders. Antibodies, soluble proteins comprising CC extracellular domains and other regulators of B7-L polypeptides are CC useful for enhancing the immune response to tumours. (I) plays a role in CC growth and maintenance of cancer cells based on the observation of CC geninal vesicle hyperplasia in transgenic mice overexpressing B7-L CC polypeptide. Hence modulators of (I) are useful for the treatment of CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian, CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian, CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle cancer sung, brain, breast, ovarian, CC cancer including seminal vesicle seminal vesicle seminal vesicle cancer sung, brain vesicl
                                                                                                               are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain Barre syndrome and mysthenia gravis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endocrinopathy; lymphoproliferative disorder; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 5; 135pp; English.
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28-NOV-2000; 2000US-0729264
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                                                         lymphoproliferative disorders such as multiple myeloma. sequence represents the coding sequence of mouse B7-L_mi
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/product= "B7-like protein, B7-L_ml"
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                                                                                            The present
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Matches 701; Query Match Best Local :

Similarity

32.4%;

BP; 313 A; 304 C;

291 G; 287 T; 0 other;

Conservative

0;

Pred. No. Score 378.4; Mismatches

8e-95

DB 24;

Length 1195;

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Gaps

4;

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ID AAS9
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                                                                                                                                                                       AGTAATACAACTGTAGTATA 1138
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                                          (first entry)
             novel human diagnostic protein #28160
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CC Phe invention relates to isolated polynucleotide (I) and CC polymerase (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags: CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating CC inaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at fitp. Vipub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutatio responsible for genetic disorders or other traits and to assess biodiversity
Sequence 1392 BP; 338 A; 361 C; 341 G; 352 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 28160; 103pp; English
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P-PSDB; ABG28169.
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
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2000US-0649167.
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Query Match 66.6%; Score 777.6; DB 23; Length 1392; Best Local Similarity 87.2%; Pred. No. 6.8e-206; Matches 912; Conservative 0; Mismatches 24; Indels 110;

δõ В Qγ Ъ ρ рЬ Qy DЬ 121 212 Н AATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATC ATGTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACC AATCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACC CTGCATGGATCTGCTTACCGTCCAAGTTATGGGAGAGCTGTTCATTCCCAGTGTT ATCCACAATGTGGAGCCCAGTGATTCGGGGGAACATCAGATGCAGCCTCCAGAACAGTCGC CTGCATGGATCTGCTTACCTTACCGTCCAAGTTATGGGAGAGCTGTTCATTCCCAGTGTT ATCCACAATGTGGAGCCCAGTGATTCGGGGGAACATCAGATGCAGCCTCCAGAACAGTCGC AATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATC Conservative 0; Indels 110; Gaps 451 180 391 60 240 331 271 211

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                                                                                                                                                                                                                                 reproductive disorder; graft versus host disease; autoimmune toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                           Human; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatlo; immunosuppressive; antiarthritlo; antinchematic; antilnflammatory; dermatological; antiporiatic; neuroprotective; antidlabetlo; haemostatlo; antithyroid; antiulcer; antiallergic; antialsethmatic; nephrotropic; antibacterial; virucide; tumour; cancer;
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            28-JUN-2000;
28-NOV-2000;
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                                                                                                             WO200200710-A2
                                                                                                                                                                                                             Homo
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            2000US-214512P
2000US-0729264
                                                      2001WO-US20719
                                                                                                                                                                                                                                                                                                                                                               human B7-like
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                                                                                                                                                                  Location/Qualifiers
1..1134
                                                                                                                                       /*tag=  a
/product= "B7-like protein, B7-L_h4"
                                                                                                                                                                                                                                                                                                                                                             protein,
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diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L molecules are useful for alleviating the symptoms associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) a useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role growth and maintenance of cancer cells based on the observation of
                                                                        nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                 sequence represents the coding sequence of human B7-L_h4.
                                                                                                                                                                                          treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Welcher AA,
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Sequence 1139 BP; 290 A; 300 ü 283 G; 266 T; 0 other;

Query Match Best Local

Similarity

94.48; 97.98;

Score 1102.8; Pred. No. 1.9

DB 24; Length 1139;

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밁 Qy 뭐 δÃ Ъ Qy 밁 Qy Matches 248 181 121 128 61 8 æ ATGGTGGCAGGAGCCATGGAAAATAGAGACCCACCCGGTTCTGGGTCTGGTAATGAAGTC 67 1136; GGGAACTTCACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGGGGAACATC AGGCCCATGGAGCCCATCACCCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGC AGGCCCATGGAGCCCATCATCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGC GTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTC GTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTC ATAGAAGGCCCCCAAAATGCAAGAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACC ATAGAAGGCCCCCAAAATGCAAGAGTCCTGAAGGGCTCCCCAGGCTCGCTTCAACTGCACC 127 ATGGTGGCAGGAGCCATGGAAAATAGAGACCCACCCGGTTCTGGGTCTGGTAATGAAGTC 60 Conservative 0; Mismatches .9e-296; .es 2; Indels 22; Gaps 187 180

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The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) as useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometricsis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                          New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; B7-like protein; B7-L; antiinfertility; gynaecological; antifumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyrold; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder; gene; ss.
                                                                                                                                                                                    Claim 1; Fig 3; 135pp; English.
                                                                                                                                                                                                                                                                                                             WPI; 2002-130881/17.
                                                                                                                                                                                                                                                                                                                                            Welcher AA, Sarmiento UM,
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28-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding human B7-like protein, B7-L_h3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK13030 standard; cDNA; 1240
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2000US-0729264.
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diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfissions, and for
                                                                   treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypepti pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L
                                                sequence represents the coding sequence of human B7-L_h3.
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Sequence 1240 BP; 318 A; 319 C; 305 G; 298 T; 0 other;

Local

Similarity

95.8%; 99.1%;

Score 1119; Pred. No. 6

6.1e-301; DB 24;

Length 1240;

B Q 밁 20 밁 Qγ B Qy 밁 Qy D δÃ 망 Ωy В Ş 뫄 δã Matches 1125; 526 454 466 394 406 334 346 274 286 214 226 154 166 106 94 34 AGACCCACCCGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCCAAAATGCAAGAGT 93 TGGGACTTTGACTTGCGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGT GCTCCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGT TCCGGAGCCCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAA TGGGACTTTGACTTGCGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGT GCTCCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGT TCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACCCG TCCGGAGCCCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAA TCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACCTG GCATGGATCTGCTTACCTTACCGTCCAAGTTATGGGAGAGCTGTTCATTCCCCAGTGTTAA GCATGGATCTGCTTACCGTTCCAAGTTATGGGAGAGCTGTTCATTCCCAGTGTTAA CCACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCT GTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAA CCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCAT CCACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCT TGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCAT CCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCAT AGAAGCTGTAGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCCAGAATGCAACAGT 165 TGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCAT GTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCCATCATCACCAA Conservative 0; Mismatches 10; Indels 0, 633 645 585 465 405 285----

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antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                  proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role in growth and maintenance of cancer cells based on the observation of seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, overlan, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytoxoic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The polypeptide, polypucleotide encoding it and antibody against (1) useful for treating B7-like polypeptide-related disease, disorders of conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New B7-like polypeptides, polynucleotides and their modulators, for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis .
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28-NOV-2000;
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                                                                                                                    are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival.B7-L molecules are also useful for diagnosis and transman.
                                                                                                                                                                         autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC
                                           useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfissions, and for
nephropathies (e.g. glomerulonephritis), skin disorders
                      treatment of allergy, asthma and hypersensitivity reactions
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/product= "B7-like protein,
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GACAGAAAGTGGAAATGAAAACTCCGGCTACAATTCAGATGAACAAAAGACCACAGACAC
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                                                                  CCGTCGTTGTTGTGGCTGCAACTGCTGCTGCTTGTTGTTTTTTTGCTGTAGAAGAAAAG
                                                                                                                                                                          AGCAGGCACCATGCTTCTGACGCCGACGTGTACTCTTACAATACGCTGCTGCTGCTGCCG 823
                                                                                                                                                                                                        AGCAGGCACCATGCTTCTGACGCCGACGTGTACTCTTACAATACGCTGCTGCTGCTGCCCG
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                                                                                                                                                                                                                                                                                                                 TCTCACTGTGATTCGGTGTCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGTATT
                                                                                                                                                                                                                                                                                                                                       TCTCACTGTGATTCGGTGTCCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGTATT 696
                                                                                                                                                                                                                                                                                                                                                                                   GACTTTGACTTGCGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAA
                                    CCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTGTTTCTGCTGTAGAAGAAAAAG
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Pred. No. 6.8e-302;
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28-JUN-2000; 2000US-214512P 28-NOV-2000; 2000US-0729264

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CC Seminal vesicle hyperplasia in transgenic mice overexpressing B7-L CC polypeptide. Hence modulators of (I) are useful for the treatment of CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian, CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian, CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian, CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian, CC cancer including seminal vesicle cancer. Pumphocyte response CC pathway can be manipulated to regulate cytotoxic T-lymphocyte response CC in alloyafit transplantation, graft versus host diseases, T-cell condended B-cell mediated diseases and autoimmune diseases. B7-L CC molecules are useful for alloyafiting the symptoms associated with CC diseases involving chronic immune cell dysfunction or to treat CC autoimmune diseases such as systemic lupus erythematosus, rheumatoid archivitis, multiple sclerosis, diabetes, immune thrombocytopenic CC purpura and psoriasis, chronic inflammatory disease such as colitis), CC grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They CC are also useful as immunosuppressive agents for bone marrow and organ CC transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell CC proliferation, including arteriosclerosis and vascular restenosis. CC shock syndrome or allosensitisation due to blood transfusions, and for CC reatment of allergy, asthma and hypersensitivity reactions, and for CC comparatives (agency asthma and hypersensitivity reactions, and disperse (pembliques and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 1168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a rol growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (crave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the coding sequence of human B7-L_h2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Welcher AA,
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                                                                                                             CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGCT
                                                                                                                                                                                         CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGCT
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GAAGGTCAGTAATACAACTGTAGTATAG
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Minimum DB
Maximum DB
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Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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           N_Geneseq_101002:*
1: /SIDS2/gcgdata/g
2: /SIDS2/gcgdata/g
3: /SIDS2/gcgdata/g
4: /SIDS2/gcgdata/g
5: /SIDS2/gcgdata/g
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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1168
1 agtgatcatggtg
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| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
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| SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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9306.701 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ve	0 00	7	6	5	4	ω	2	1	No.	Result
181.8	181.8	196.8	378.4	777.6	1102.8	1119	1122.4	1168	Score	
15.6	15.6	16.8	32.4	66.6	94.4	95.8	96.1	100.0	Match I	Query
268	754	401	1195	1392	1139	1240	1175	1168	Length DB	
24	24	22	24	23	24	24	24	24	. BB	
ABKI3033	ABK13034	AAI36582	ABK13032	AAS92356	ABK13031	ABK13030	ABK13028	ABK13029	ID	
DNA encoding mouse	DNA encoding mouse	Probe #5268 used t	DNA encoding mouse	DNA encoding novel	DNA encoding human	DNA encoding human	DNA encoding human	DNA encoding human	Description	

epi	AAV08560	20	3263	٠	44.8	45
cDNA sequence #491	ABK36100	24	2614		44.8	44
ep i	AAV08558	20	1310		44.8	43
Polymorphic region	AAZ45758	21	254		44.8	42
	ABL04172	23	6541	٠	45	41
Drosophila melanog	ABL08976	23	5975	3.9	45	40
	ABL03190	23	3624	٠	45	39
melano	ABL08977	23	3210		45	38
	ABL03191	23	2260		45	37
	ABL26940	23	2115	٠	45	36
	ABL26941	23	462		45	<u>3</u> 5
	ABL29757	23	5397		ĹΠ	34
	ABL25652	23	5447		UΠ	33
	ABL28444	23	5215		45.4	32
Ø	ABL25653	23	3135		5	31
מ	ABL28445	23	3042		5	30
la	ABL24570	23	3884		5	29
la	ABL24571	23	1509		45.6	28
la	ABL16096	23	8821		5	27
la	ABL16097	23	2682			26
	ABL24482	23	4044		ი	25
Drosophila melanog	ABL24483	23	1983		σ.	24
7	AAF75339	22	2333			23
	ABL03352	23	22341		7.	22
phila melan	ABL03353	23	3894		47.4	21
brain CNO	AAX84442	20	2733		47.6	20
an prostat	ABV54466	23	381	4.1		19
ndrogen rece	AAN91773	10	4180		•	18
ata	AAQ12002	12	3217		•	17
Rat androgen recep	AAN91578	10	3217		•	16
Drosophila melanog	ABL16830	23	46954		٠	15
ö	ABK10240	21	403	4.4		14
Spinocerebellar at	AAX89891	20	397	4.4	•	13
Tri-nucleotide rep	ABK10248	21	389		•	12
$\mathbf{-}$	7	23	7029	4.5	52.8	11
Trinucleotide repe	ABK10239	21	277	4.6		10

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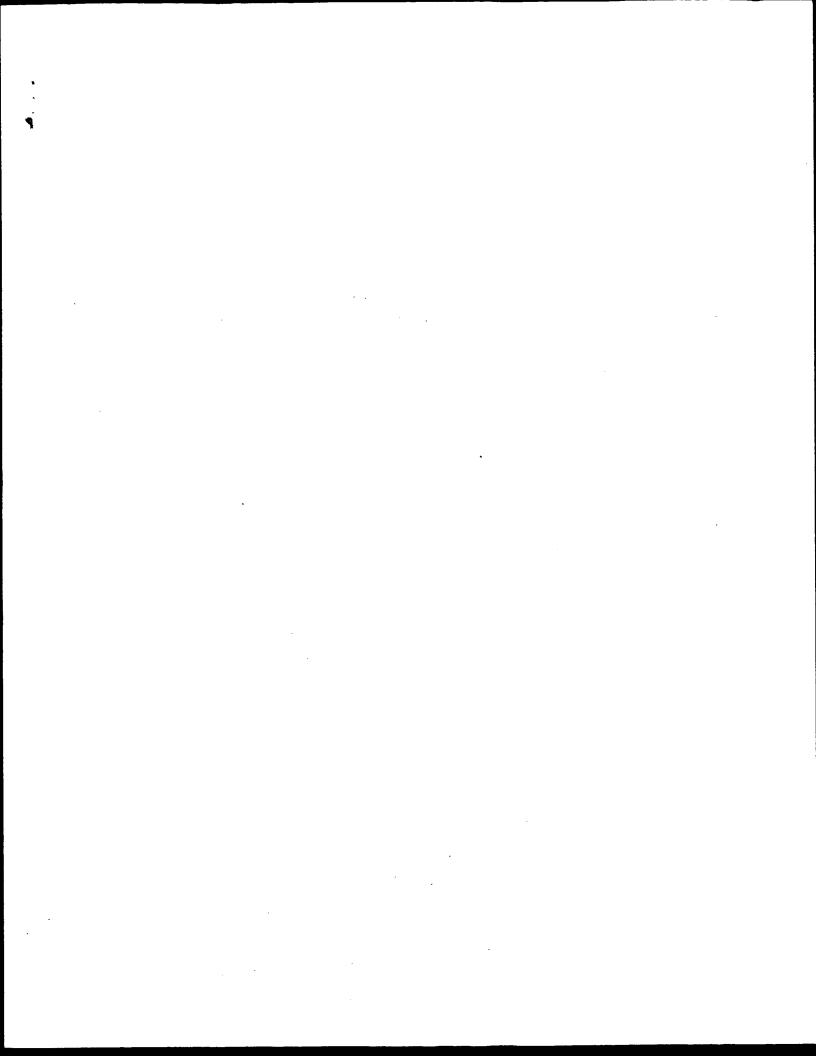
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ALIGNMENTS

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ARESULT 1
ARESULT 1
AREA 3029
ID ABK13029
ID ABK1
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AC ABK1
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DE DNA
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WHUMA
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WW ANTI
KW ANTI
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HOMO
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HOMO
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FT CDS
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WC20
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YN
PF 28-J
                                                                                                                                                                                                                                                 antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                     Human; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirhe; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic;
                28-JUN-2001; 2001WO-US20719
                                                     03-JAN-2002.
                                                                                        WO200200710-A2
                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding human B7-like protein, B7-L_h2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK13029;
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                                                                                                                                                            Location/Qualifiers 8..1168
                                                                                                                       /*tag=  a
/product= "B7-like protein, B7-L_h2"
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APPLICANT: BLOWENFELD, Marta
APPLICANT: BOUGUELERET, Lydie
APPLICANT: CHUMAKOV, Ilya
APPLICANT: COHEN, Daniel
APPLICANT: COHEN, Daniel
APPLICANT: ESSIOUX, Laurent
TITLE OF INVENTION: Genes, proteins and biallelic markers related to central...
FILE REFERENCE: GENEST, 0458US
CURRENT FILING DATE: 1999-10-12
CURRENT APPLICATION NUMBER: US/09/416,384A
PRIOR APPLICATION NUMBER: 60/106,457
PRIOR FILING DATE: 1999-10-30
PRIOR APPLICATION NUMBER: 60/103,955
PRIOR APPLICATION NUMBER: 60/103,955
PRIOR APPLICATION NUMBER: 60/132,277
PRIOR FILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: 60/132,277
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEO ID NOS: 71
Search completed: April 28, 2003, 21:07:44 Job time: 2026.54 secs
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; TYPE: DNA
; ORGANISM: mus musculus
US-09-416-384A-6
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US-09-416-384A-6/c
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 33
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = US-09-864-761-2182
                                                                                                                                                                                                                                         Ouery Match 3.7%; Score 43.2; DB 10; Length 1791; Best Local Similarity 75.0%; Pred. No. 0.018; Matches 54; Conservative 0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patent.pm
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Patent No. US20020081584A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.7
Best Local Similarity 79.7
Matches 51; Conservative
                                                                                                                                                         860 TGCTGTAGAAGA 871
                                                                                   276
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Pred. No. 0.0075;
0; Mismatches 13; Indels 0,
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                                                    Best
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SOFTWARE: Annomax Sequence
SEQ ID NO 18923
LENGTH: 293
                                  Matches
                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/207,456
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OTHER
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                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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801 GCTGCTGCTGCCGCCGTCGTTGTTGTGGCCGAACTGCTGCCGTTGTTGTTTCT 860
                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/774,203 FILING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00668
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                                  Similarity 51; Conser
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                                Conservative
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                                                                                                                  NN: EXPRESSED IN FETAL LIVER, SIGNAL = 16
NN: EXPRESSED IN ADULT LIVER, SIGNAL = 21
NN: EXPRESSED IN HELA, SIGNAL = 29
NN: EXPRESSED IN HARIN, SIGNAL = 29
NN: EXPRESSED IN LUNG, SIGNAL = 33
NN: EXPRESSED IN BONE MARROW, SIGNAL = 21
NN: EXPRESSED IN BONE MARROW, SIGNAL = 21
NN: WIT HIT: Z22828.1, EVALUE 9.00e-59
NN: SWISSPROT HIT: P53360, EVALUE 4.00e-15
NN: EST_HUMAN HIT: AW409956.1, EVALUE 1.00e-58
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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                                                                                                                     OTHER INFORMATION:
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                                                                                                                                                                                    ENGTH:
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APPLICATION NUMBER: PCT/US01/00661
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Chen, Wensheng
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D IN BT474, SIGNAL = 47
D IN PACCENTA, SIGNAL = 53
D IN HBL100, SIGNAL = 69
D IN HEART, SIGNAL = 27
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D IN HELA, SIGNAL = 45
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US-09-728-444-151
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CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,360
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 1206
SOFTWARE: FBSTSEQ for Windows Version 4.0
SEQ ID NO 151
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              PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                  CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                       TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
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APPLICATION NUMBER: JP 00/280988
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OZAKI, AKIO
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Sands, Arthur T.
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-544
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US-09-738-626-1
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RESULT 13
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APPLICANT: OZAKI, AKIO
TITLE OZAKI, NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILLING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILLING DATE: 199-12-16
PRIOR FILLING DATE: 199-12-16
PRIOR FILLING DATE: 2000-04-07
PRIOR FILLING DATE: 2000-04-07
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Best Local Similarity
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APPLICANT:
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SOFTWARE: PatentIn ver. 3.
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APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
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                                                                                                                                                                                                                                                                                                     ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                          LENGTH: 3309400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                          859 CTGCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAA 899
                                                                                                                                                                     799 ACGCTGCTGCTGCCGCCGTCGTTGTTGTGGCCTGCAACTGCTGCTGCCGTTGTTGTTT 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 CTGCTGCAGAAGAAGAAGGACGAGTTCGACGTCGTTCTCGAA 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAYASHI, MIKI
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YOKOI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIZOGUCHI, HIROSHI
                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                            3.78;
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                                                                                                                                                                                                                          Score 43.4;
Pred. No. 2.
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                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                              Length 3309400;
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US-09-864-761-18923/c ; Sequence 18923, Application US/09864761 ; Patent No. US20020048763A1

GENERAL INFORMATION

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                                                                                                                                                                                                                                                                   Sequence 14, Application US/09849243 Patent No. US20020157127A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                          861 GCTG 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   801 GCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTTCT 860
                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: HELLER, EHRMAN, WHITE & MCAULIFFE
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 38005-0148
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)912-2000
TELEFAX: (202)912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPOTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: HELLER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PURIFICATION OF HIGHER ORDER TRANSCRIPTION COMPLEXES FROM TRANSGENIC NON-HUMAN ANIMALS
                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                               APPLICANT: Kirschbaum, Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA
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LENGTH: 3263 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                              NUMBER OF SEQUENCES:
                    STATE: D.C
                                CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/849,243 FILING DATE: 07-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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COUNTRY: USA
                                                                                                                              OF INVENTION: PURIFICATION OF HIGHER ORDER TRANSCRIPTION COMPLEXES FROM TRANSGENIC NON-HUMAN ANIMALS
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                                                                                                                                                                                         Greg
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Pred. No. 0.0087;
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CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1748
LENGTH: 6604
                                                                              ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 D83783 US-09-880-107-1748
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Matches
Query Match
Best Local Similarity 76.4
Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                          LENGTH: 66
                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)912-2020 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
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mes 52; Conserv
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/849,243

FILING DATE: 07-May-2001

ATTORNEY/AGENT INFORMATION:

NEWEY CONSIDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 38005-0148
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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LOCATION:
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                    76.4%;
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Score 44.8; DB Pred. No. 0.014; 0; Mismatches
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                                       DB 10;
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                                       Length 6604;
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Gaps
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APPLICANT:

Owen, Thomas A.

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LENGTH: 3577
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TITLE OF INVENTION: The Canine Androgen Receptor
FILE REFERENCE: PC10893AGPR
CURRENT APPLICATION NUMBER: US/10/008,739A
CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Canine
                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             573 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAAGGAG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   829 TGGCTGCAACTGCTGCTGCCGTTGTTGTTTCTGCTGTAGAAG 870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  769 GCTTCTGACGCCGACGTGTACTCTTACAATACGCTGCTGCTGCTGCCGCCGTCGTTGTTG 828
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                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLITES, Greg
TITLE OF INVENTION: PURLFICATION OF HIGHER ORDER TRANSCRIPTION
COMPLEXES FROM TRANSGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (202)912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: HELLER,
                                                               FEATURE:
                                                                                 MOLECULE TYPE: CDNA
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kirschbaum, Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity
67; Conserv
                                                                                                                                                                                                                                                                                       NAME: Granados, Patricia D. REGISTRATION NUMBER: 33,683 REFERENCE/DOCKET NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                        TOPOLOGY:
                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/849,243 FILING DATE: 07-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: HELLER, EHRMAN, WHITE & MCAULIFFE STREET: 1666 K Street, N.W., Suite 300
                     LOCATION:
                                          NAME/KEY:
                                                                                                                                                               LENGTH: 1310 base pairs
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                                                                                                        linear
                                      exon
                       1..1310
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Pred. No. 0.004;
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                                                                                                                                                                                                                                                                                           38005-0148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 3577;
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US-09-849-243-15/c; Sequence 15, Application US/09849243; Patent No. US20020157127A1; GEMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-846-491
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                                                                                                                                                                     RESULT 7
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
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APPLICANT: Kirschbaum, Bernd
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Gulukota, Kamalakar
Graham, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merberg, David
Treacy, Maurice
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Howes, Steven H.
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Wong, Gordon G.
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Steininger II, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collins-Racie, Lisa
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LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09822846 o. US20030027139A1
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; OTHER INFORMATION: MAP TO AF121782.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
US-09-864-761-16305
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                                                                                                                                                                                                  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 16305
LENGTH: 401
                            Matches 201;
                                          Query Match
Best Local Similarity
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                          FEATURE:
                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                         TYPE: DNA
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FILING DATE: 2001-01-30
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30 APPLICATION NUMBER: US 09/608,408 APPLICATION NUMBER: 2000-06-30
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FILING DATE: 2001-01-30
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Hanzel, David K.
                           Conservative
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96.6%;
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                     Score 196.8;
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US-10-008-739A-1/c
US-10-008-739A-1/c
Sequence 1, Application US/10008739A
Patent No. US20020161194A1
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                                GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
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LENGTH: 398
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 APPLICANT:
                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                        306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 11.7%;
Local Similarity 77.5%;
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Lu, Bihong
               Castleberry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Sequence 4945, Application US/09983965 Patent No. US20020137160A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1998-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: 26-LIB34-017-Q1-E1-G9
366 TCACTTCGGCAAGCTACCAAGAGGGCCGGAACT 398
                                                                                                                                                                                                                                                               102 GCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTC 161
                                                                                                                                                                                                                                                                                                                     186 CAGCCTGTGGATCCAGCAGTGAAATCATAGAGGGTCCCCAAGAATGTCACAGCCCTGAAGG 245
                                                   222 TCACCTCTCAGAGGTACGACCAGGGCGGGAACT 254
                                                                                                                                                                                                               246 GCTCGGAGGCTCGCTTCAACTGCACCATCTCGCAGGGCTGGAAGCTCGTCATGTGGGCTC
                                                                                                                                                                                                                                                                                                                                                    42 CCGCTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATGCAAGAGTCCTGAAGG 101
                                                                                                                                        TCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCT
                                                                                                         TGAGAGGCACAGTGGTGCTGAGCATGACCTAATGAGACCATCATCACCAGTGACCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 136.2; DB : Pred. No. 2.3e-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 398; :
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Run on:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US

2: /cgn2_6/ptodata/1/pubpna/US

3: /cgn2_6/ptodata/1/pubpna/US

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9: /cgn2_6/ptodata/1/pubpna/US

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11: /cgn2_6/ptodata/1/pubpna/US

13: /cgn2_6/ptodata/1/pubpna/US

14: /cgn2_6/ptodata/1/pubpna/US
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Gapop 10.0 , Gapext 1.0
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1 agtgatcatggtggcaggag.....gtaatacaactgtagtatag 1168
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                            .: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
.: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
.: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
.: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
.: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
.: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
.: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
.: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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          /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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ALIGNMENTS

score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution. pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

SUMMARIES

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3.6	3.6	3.6	3.6	3.7	3.7	3.7	3.7	3.7	3.8	3.8	3.8	3.8	3.8	3.8	3.9	11.7	16.8	23.0	Query Match
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US-09-954-456-1996	US-10-029-217A-30	US-10-029-217A-1	US-10-029-217A-25	US-09-416-384A-6	US-09-864-761-2182	US-09-864-761-18923	US-09-738-626-1	US-09-738-626-544	US-09-728-444-151	US-09-880-107-1748	US-09-849-243-14	US-09-849-243-15	US-09-822-846-491	US-09-849-243-13	US-10-008-739A-1	US-09-983-965-4945	US-09-864-761-16305	US-09-918-995-3342	ID
sequence 1996, Ap	Sequence 30, Appl	Sequence 1, Appli	Sequence 25, Appl	Sequence 6, Appli	Sequence 2182, Ap	Sequence 18923, A	Sequence 1, Appli	Sequence 544, App		Sequence 1/48, Ap	Sequence 14, Appl	Sequence 15, Appl	Sequence 491, App		Sequence 1, Appli	Sequence 4945, Ap	Sequence 16305, A	Sequence 3342, Ap	Description

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443 443 443	36 37 38 39 40 41	22222222222222222222222222222222222222	20 21 22 23 24 25 26
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2523 83450 270 488	26/4 216 545 557 572 1143	424 725 2517 2352 2536 6177 6322 5477	238 554 3899 6504 6504 6878 2572
9990	1000	100	100
US-09-4/6-242-15 US-09-811-469-3 US-10-007-557-8 US-09-918-995-19918	US-10-003-299-1 US-09-728-444-25 US-09-919-580-371 US-09-919-580-475 US-09-919-580-570 US-09-919-580-570 US-09-938-842A-1399	US-09-918-995-10212 US-09-919-580-878 US-09-476-242-16 US-09-476-242-26 US-09-822-846-129 US-09-916-145-1 US-09-918-995-11012 US-09-918-995-11012 US-10-078-090-83	US-09-864-761-24079 US-09-864-761-7357 US-09-735-367B-5 US-09-735-367B-1 US-09-735-367B-1 US-09-735-367B-1 US-09-735-367B-1 US-09-925-300-486
Sequence 3, Appli Sequence 8, Appli Sequence 19918, A	135435	Sequence 10412, A Sequence 878, App Sequence 16, Appl Sequence 26, Appl Sequence 129, App Sequence 11, Appl Sequence 11, Appl Sequence 11012, A Sequence 11012, A Sequence 1, Appl	Sequence 24079, A Sequence 7357, Ap Sequence 5, Appli Sequence 171, Appl Sequence 9, Appli Sequence 1, Appli Sequence 486, App

; FEATURE: NAME/KEY: misc_feature ; LOCATION: (1)...(474) ; OTHER INFORMATION: n = A,T,C US-09-918-995-3342 US-09-918-995-3342 RESULT 1 Qy В ; GENERAL INFORMATION: Db QУ 밁 CURRENT APPLICATION NUMBER: US/09/918,995 CURRENT FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: US/09/235,076 PRIOR FILING DATE: 199-01-20 NUMBER OF SEQ ID NOS: 38054 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3342 LENGTH: 474 Sequence 3342, Application US/09918995 Publication No. US20030073623A1 Query Match Best Local Similarity Matches 272; Conserv APPLICANT: Hyseq, Inc. TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756 ORGANISM: Homo sapiens TYPE: DNA 1072 GCGGGCTGATCAACGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGC 1131 1012 CAAATCCTGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCTCCTCACCA 1071 54 ACTITIAAGGAAATCIGAAAAAGAGAAGAACAAAGAAACTGAGACAGAAAGTGGAAA 113 Conservative 23.0%; 0; Mismatches or G Score 269; DB y; L Pred. No. 5.8e-72; DB 9; Length 474; Indels 0; Gaps

0;

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REFERENCE
AUTHORS
TITLE
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Best Local Similarity
                                                                                                                                                                                                                                                                                                              Matches
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162 TCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCT 221
                                                                                                                                                                    102 GCTCCCAGGCTCGACTGCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGGCTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 CTGCCTTCCTCAGTGCNAG 435
                                                             150 ACTCAGAGGCTCACTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 CTGCTTACCTTACCGTCCAAG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 TGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGAT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 TCACCTATGCCAGTTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCATGATG
                                                                                                                                                                                                                           90 CAGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGG 149
                                                                                                                                                                                                                                                                      42
                                                                                                                                                                                                                                                   CCGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATGCAAGAGTCCTGAAGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGAT 414
                                                                                                                                                                                                                                                                                                            233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM8743 row: f column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE376590 663 bp mRNA linear EST 21-JUL-2000 601226419F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:3584645 5', mRNA sequence.
BE376590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 663)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                   143
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
a 193 c 170 g 157 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:3584645"
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/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
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                                                                                                                                                                                                                                                                                                                             15.4%;
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Pred. No. 6.6e-32;
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Search completed: April 29, 2003, 09:24:15 Job time: 1902.29 secs

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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428
                                                                                                                                                                               222 TCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATG
                                                                                                                                                                                                                                             248
                                                                                                                                                                                                                                                                                                                                                                                                          128 CAGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGG 187
                                                                                                                                                              308
                                                                                                                                                                                                                                                                                   162
                                                                                                                                                                                                                                                                                                                         188 ACTCAGAGGCTCACTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTC
                                                                                                                                                                                                                                                                                                                                                                 102 GCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                               42 CCGGTTCTGGGTCTGGAATGAAGGCATAGAAGGCCCCCAAAATGCAAGAGTCCTGAAGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                    CTGCTTACCTTACCGTCCAAG 362
                                                                                                                    TGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGAT 341
                                                                                                                                                                                                                                             TTAACCAAATGGTGGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACCGCT
                                                                                                                                                                                                                                                                                   TCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCT
                                                                              TGCAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGAT
                                                                                                                                                            TCACCTATGCCAGTTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCATGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB25436.1"
/db_xref="GI:12842010"
/db_xref="MGI:H919308"
/db_xref="MEGSWRDVLAVLVILAQLTASGSSYQIIEGPQNVTVLKDSEAHF
/translation="MEGSWRDVLAVLVILAQLTASGSSYQIIEGPQNVTVLKDSEAHF
NCTVTHGWKLLMWTLNQMVVLSLTTQGFIITNNRFTYASYNSTDSFISELIIHDYQPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="putative" 1552
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369 c 374 g
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LPPKSAEVSLPEKRSSSLPYQELNKHQPGPATHPRVSFDIASPQKVRNVTLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSGSVQCSLQNSHGFGSAFLSVQDSIGEEGPALPTWAIILLAVAFSLLLILIIVLIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /HOLE="GALA SOURCE:SPTR, SOURCE key:Q9NSI5, homolog to IGSF5 PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="small intestine"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="FANTOM_DB:2010003D20"
/db_xref="MGD:MGI:1904786"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="2010003D20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 181.8; DB 11,
Pred. No. 3.1e-32;
Pred. No. 3.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 1552;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 14
AI425363
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KEYWORDS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
222 TCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATG
                                                         235
                                                                          162 TCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCT 221
                                                                                                                                                     102 GCTCCCAGGCTCGACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTC 161
                                                                                                                                                                                                            115 CAGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGG
                                                                                                                                                                                                                                                42 CCGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCCAAAATGCAAGAGTCCTGAAGG 101
                                                       TTAACCAAATGGTGGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACCGCT
                                                                                                                                 ACTCAGAGGCTCACTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Pe,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ri,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI425363.1 GI:4271294
EST.
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mx91d09.yl Soares mouse NML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:427273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                   constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:693713"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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72.6%;
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                                                                                                                                                                                                                                                                                       ; 88
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  MEDLINE
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                           JOURNAL
                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 TGCAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 CAGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGG 215
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                                                                                                            Mus musculus (strain:C57BL/6J) adult male mRNA, clone_lib:RIKEN full-length enriched
                                                                                                                                                                                                                                                                                                                                                            AK008060 1552 bp mRNA linear Mus musculus adult male small intestine cDNA, RIKEN enriched library, clone:2010003D20:homolog to IGSF5
                                                                                                                                                                      Mus musculus
                                                                                                                                                                                             clone: 2010003D20.
                                                                                                                                                                                                                                                                 HTC; CAP trapper.
                                                                                                                                                                                                                                                                                          AK008060.1 GI:12842009
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Plate: LLAM10260 row: n column:
                                                                                                                                                                                                                                                                                                                                        (FRAGMENT), full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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277 c 242 g 179 t
                                                                                                                    ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor; biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
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/clone="IMAGE:4459973"
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/strain="FVB/N"
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72.9%;
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Direct Submission

cDNA library was prepared and sequenced in Encyclopedia Project of Genome Exploration

Mouse Genome Research Gro

Group

in Riken

Please visit our web site (http://genome.gsc.riken.go.jp/)

further details

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of

Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and

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REFERENCE
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E 5 (bases 1 to 1552)

S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Tagama, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tenahaka, I., Yoshida, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasanishi, A., Voshida, M., Warantia, Y., Yamamura, T., Yamanaka, I.,
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                                                                                                                                                                                                                                                                             AW990468 611 bp mRNA linear EST 02-JUN-2000 uf37d05.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1513545 5' similar to TR:060962 060962 L549.1. ;, mRNA
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High quality sequence stop: 454.
Location/Qualifiers
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                    Unpublished (1997)
                                                                    Tumor Gene Index
                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                           Mus musculus
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                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
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/tissue_type="Liver"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 GCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCCAGGGCTGGAAGCTCATGTGGGCTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 CTGCTTACCTTACCGTCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 CAGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 TGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGAT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCACCTATGCCAGTTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCATGATG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCCTTCCTCTCAGTGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAACCAAATGGTGGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACCGCT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTCAGAGGCTCACTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTC 243
                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1995)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: '
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMAGE Consortium (info@image.llnl.gov) for further information. MGI:940397
                                                                                                                                                                                                                                                            EST.
                                                                                                                                                                                                                                                                                                                                   BG173684
602336823F1 NCI_CGAP_Mam1 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40RP from Gibco
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                BG173684
BG173684.1 GI:12680387
                                                                                                                                                                                                                                       house mouse.
                                                                                                                                                                                                                                                                                                                            mRNA sequence.
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cDNA Library Preparation: Life Technologies,
                                                                                                                                                (bases 1 to 931)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Wector: pT7T3D-Pac (Pharmacia) with a modified /note="Wector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. " a 155 c 156 g 148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
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72.9%;
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Pred. No. 2.8e-32;
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                                                                                                                                                                                                                                                                                                                                                                    931 bp
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1-7-22 Suehiro-chou, Tsurumi-ku,

Yokohama, Kanagawa 230-0045, Japan

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RESULT 9
AV601192
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Best Local :
                                                                                                                                      MEDLINE
                                                                                                                                                        JOURNAL
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                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCGTGGCTACCTGGAAGAGCCTGAAGGCCCACAAGTCTGCAACTGTAAATCTCACTGTG
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5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                   Shirakawa Institute of Animal Genetics Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                           AV601192 AV601192.1 GI:9723510 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Single
                                                                                                     Contact: Yoshikazu Sugimoto Animal Genetics Division
                                                                                                                                                                                                                          and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                                                                                                                                                                             COW
                 Email: kazusugi@cocoa.ocn.ne.jp
                                     Fax: 81-248-25-5725
                                                                                                                                        21570554
                                                                                                                                                                      bovine ESTs
                                                                                                                                                                                        poly(A) tail-removed cDNA libraries and
                                                                                                                                                                                                      Establishment of a high throughput EST sequencing system
                                                                                                                                                                                                                                        Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H
                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AV601192
                                                                                                                                                     Nucleic Acids Res. 29 (22),
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R.Site 2 : SacT
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 pass
                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus kidney fetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
159 c 143 g 207 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9598"
/clone="PTB-112N07.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pan troglodytes"
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Pred. No. 2.1
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                                                                                                                                                      (2001)
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RESULT 10
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCACAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGC 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCGGAGGCTCGCTTCAACTGCACCATCTCCCAGGGCTGGAAGCTCGTCATGTGGGCTC
                                                                                                       Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                               Marra, M., Hillier, L., Allen, M., Bowles, M., Districh, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                   mx91d09.rl Soares mouse NML Mus 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone was obtained from a polyA-deleted cDNA library. Location/Qualifiers
                                                   4444 Forest Park Parkway, Box 8501, Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                  EST
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                          Unpublished (1996)
                                                                                                                                                                               The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
1 (bases 1 to 471)
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA265274
                                   Email:
                                                                                                                                                                                                  Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                 house mouse.
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                                   mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pZL1; Si
was deleted from a Not1
135 c 168 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"
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/clone="E1KI002H04"
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75.3%;
                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 3.1e-33;
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96 t 5 others
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                                                                                            Louis,
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RESULT 7
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Best Local
                       TITLE
                                                                 AUTHORS
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 TCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 GCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTC 161
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                                                                                                                                                                                                                   622 bp DNA
Pan troglodytes DNA, clone: PTB-060F12.F,
AG069679
AG069679.1 GI:16621481
GSS.
                                                                                                                                                                     BAC
                                                                                                                                                                                                               GSS.
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PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Unpublished
                     BAC end sequences of Library PTB
                                  rujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                  Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 27 row: H column: 19
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                   troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male Library clone:PTB-060F12.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."
                                                                                                          Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
/db_xref="taxon:9913"
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75.5%;
                                                                                                      Primates; Catarrhini; Hominidae;
                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
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Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 TCCGCGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTTGTTCCGGAGCCCAGC 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTCGGTGTCCCCAAGACACTGGAGGTGGT 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTCGGCGTCCCCAAGGTAAGTGAAGATGT 281
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                                                                                                                                                                                                                                                                Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-112N07.F.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                  677 bp DNA linear GSS 03-NOV-200 AG107877 GI:16728395 GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehitro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                                             Direct Submission
                                                                                                                                                                 Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                              GSS
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 622)
Fujiyama, A., Hattor
                                                                Totoki,Y., Watanabe,H.
                                                                                  Fujiyama,A.,
                                                                                                                       Unpublished
                                                                                                                                            BAC end sequences of Library PTB
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                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
1 153 c 128 g 176 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-060F12.F"
                                                                                                       1 to 677)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 622
                                                                Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., atanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 190.8; DB 17; Pred. No. 2.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                     Taylor, T.D., Yada, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                        GSS 03-NOV-2001
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 CAGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCCTTCCTCAGTGCAAGTCATGGGGACCCTGAACATTCCTAGCAACAACCTTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCCCAGGCTCCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTC 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATATTTCCTGGGAGCTTGAGGTTCCCGTAAGCCATTCGAGTTACAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCACTGAGGGTGAACCCTGTAATGTGACTTGCTATGCCGTGGGCTGGACCTCACTCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACCTGGCCTCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336;
                                   USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, UTel: 402 762 4366
                                                                                                                                                                       Stone,R.T., Heaton,M.P.,
and Keele,J.W.
                                                                                                                                                                                                                                                                                                                            BE032610.1
EST.
                                                                                                                                                                                                                                                                                                                                                                              BE032610 527 bp mrNA linear 132035 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                             EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 527)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L.,
                                                                                                                                                                                                                                                                                                                                                                  BE032610
                                                                                               Contact: Smith TPL
                                                                                                                                                   Design and use of two pooled tissue normalized
                                                                                                                                                                                                                                                                                         sus scrora
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                   402 762 4366
402 762 4390
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smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." a 167\ c 161\ g 149\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:8327619
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                                                                                                                                                                                       Grosse, W.M.,
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No. 6.3e-50;
                                                                                                                                                                                       Bennett, G.A.,
                                                         USA
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                                                                                                                                                                                         Laegreid, W.W.
                                                                                                                                                                                                                                                                     Euteleostomi;
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RESULT 6
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               JOURNAL
                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 CCGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATGCAAGAGTCCTGAAGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTTACCTTACCGTCCAAGTTATGGGAGAGCTGTTCATTCCCAGTGTTAATCTTGTAG
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                                                                                                                                                                                                                                                                                                                                        TCCTTGCGGA 527
                                                                                                                                                                                                                                                                                                                                                                     TCGCTGAGAA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCACGTCTGCAAGTTATGAAGAGGGCGGTAACTTCATCTCTGAGATGATCATCCATGACG
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                                                                                                                                                                                                                                          BE476432
159670 BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
           gland cDNA library
Unpublished (2000)
                                                              Sonstegard, T.S., Capuco, A.V., Wells, K.D.
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                           COW.
                                                                                                                                                                                            ESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
Plate: 63 row: E column: 1
Contact: Sonstegard TS
                                             Mapping of Expressed Sequence
                                                                                                           Bovidae; Bovinae; Bos.
                                                                                                                                                            Bos taurus
                                                                                                                                                                                                          BE476432.1 GI:9595965
                                                                                                                                                                                                                            BE476432
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                                                                                           (bases 1 to 517)
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                                                                                                                                                                                                                                           BARC 5BOV Bos taurus cDNA 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV SPUKID; JILL
Library made from pooled tissue
and 30 embryos." 99 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="MARC 1PIG"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Pred. No. 1.9e-46;
0; Mismatches 80;
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rom pooled tissue from day 11, 13, :
                                                                                                                                                                                                                                                           517 bp
                                             Tags
                                                                             Van Tassell, C.P., Ashwell, M.S. and
                                                                                                                                                                                                                                                         mRNA
                                               from a normalized
                                                                                                                                                                                                                                           mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 527;
                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                            EST
                                               bovine mammary
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                                                                                                                              Bovoidea;
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15, 20,
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RESULT

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Plate: LLAM10635 row: b column: 06
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Tissue Procurement: James Cleaver, M.D.
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National Institutes of Health, N
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="ImAGE:4778789"
/clone="ImAGE:4778789"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SpOR76; Site_1: NotI;
/note="Organ: skin; Vector: pCMV-SpOR76; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Sutheria; Primates; Catarrhini; Hominidae
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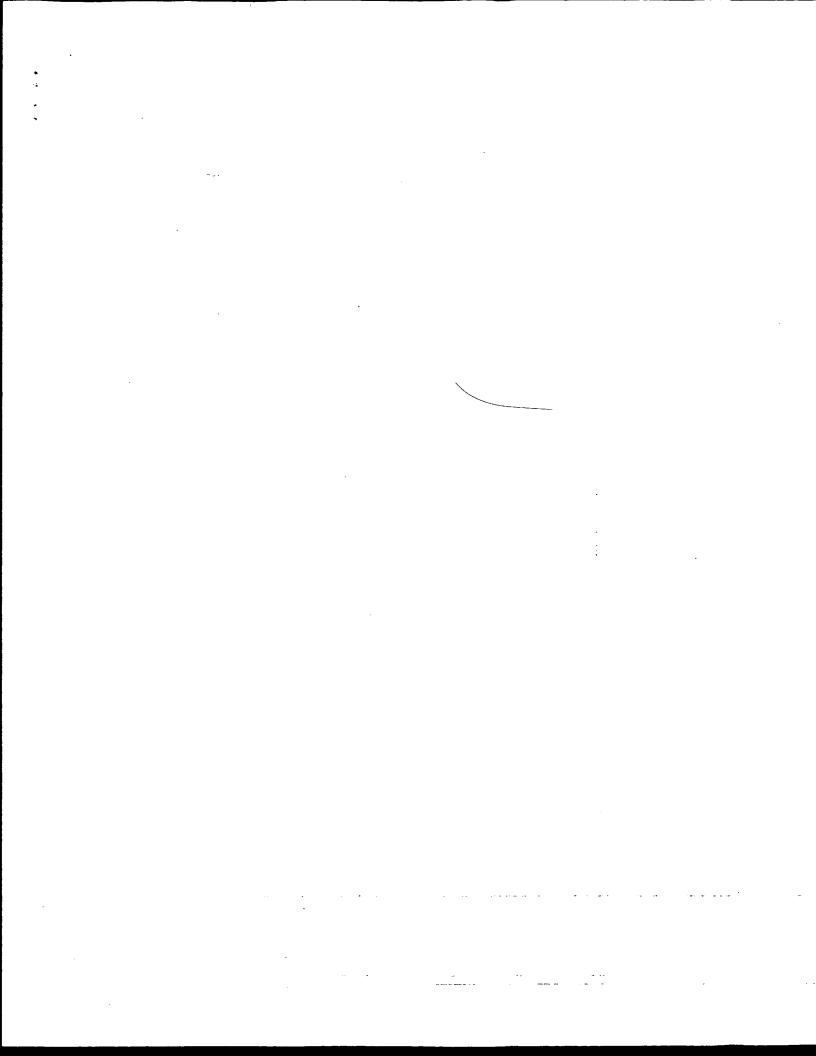
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URL:http://genome.gsc.riken.go.jp/
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
N., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tanaka,T., Matsuura
%.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizav,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
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EST.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computational Analysis of Full-Length Mouse cDNAs Compared with fuman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="E030016M12"
                                                                                                                                                                                                                                              /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                    /dev_stage="0 day neonate"
/lab_host="DH10B"
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to, M., Kawai, J., Konno, H
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 BE784177 794 bp mRNA linear EST 12-JAN-2001 602108039F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4236489 5', mRNA sequence.
BF784177
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/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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Query Match
Best Local Similarity
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CCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGACTT
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plate: LLM9844 row: n column: 10
High quality sequence stop: 694.
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1 (bases 1 to 794)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Contact: Robert Strausberg, Ph.D.
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Clone distribution: MGC clone distribution information can
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/dlone="IMAGE:4236489"
/clone="IMAGE:4236489"
/clone="IND="NCI_CGAP_Kid14"
/lab_host="0H10B (T1 phage=resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT:
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT:
/rechnologies. Note: this is a NCI_CGAP Library. | "
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/strain="FVB/N"
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Pred. No. 1.6e-54;
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  306
276.4
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: L/LAM10830 row: b column: 12
High quality sequence stop: 768.
Location/Qualifiers
                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                            mRNA sequence.
BG863468
                                                                                                                                                                                                                                              BG863468 784 bp mRNA linear EST 29-MAY-2001
602796941F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4917803 5',
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                                                                                                Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla
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                                                                                                                                                         Mammalia; Eutheria;
1 (bases 1 to 784)
                                                                                                                                                                                                 house mouse.
                                               CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Consortium (Clone distribution: MGC clone distribution information car
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7 AG107877
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AI648720
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AK008060 Mvs muscu
AI425363 mx51d09, y
BE376590 6612264619
BB625217 BB625217
AZ379623 1M0134622
BG206666 RST2611.7
AI788300 uk56d01.y
AI79875 uk28a12.y
AZ41179 1M0185B04
BB846577 BB846577
BF040046 BP250004B
AG142221 Pan trog1
BB846133 BB846133
BH452873 603170211
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BH452873 603170211
BH452873 BB846133
BH452873 Uk56609.r1
AQ403719 Hx_5049_A
AI647601 uk41f12.x
AI788973 uk56d01.x
BB531388 BB531388
BB531388 BB531388
AW112084 MC7851 mc
BB556363 BB564363
BG445021 GA_EB002
AI756062 EKESTead9
AV43123 AV43123
AA695064 GM02059 5
AL232043 Tetraodon
AL065607 Drosophil
BE017134 KR6f60.y
BQ599899 MI-P-E6-a
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AG107877 Pan trogl
AVG01192 AVG01192
AA265274 mx91d09.r
AW990468 uf37d05.y
BG173684 602336823
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Db 121168 AGAGGCTCACCTCAACTGCACTGTGACTCATGGCCTGA 121205

Search completed: April 29, 2003, 14:10:30 Job time: 4555.27 secs

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 169879 bases at least Q40
Consensus quality: 172188 bases at least Q30
Consensus quality: 173133 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 176000; agarose-fp
Quality coverage: 8.3 in Q20 bases; agarose-fp
Quality coverage: 8.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the accession number will be preserved.

1 28835: contig of 28835 bp in length
28836 28935: gap of 00 bp
28936 29562: contig of 627 bp in length
29563 29662: gap of 100 bp
29663 30328: contig of 666 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996–1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: Plasmid; n/a; 10
Chemistry: Dye-terminator Big Dye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: L20921
Center clone name: 147_E_11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
                                                                                                               56471 64079: contig of 7609 bp in length 64080 64179; gap of 100 bp 64180 72619: contig of 8440 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                           36080 36179; gap of 100 bp
36180 37483; contig of 1304 bp in length
37484 37583; gap of 100 bp
37584 39166; contig of 1583 bp in length
39167 39266; gap of 100 bp
39267 41065; contig of 1799 bp in length
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30429 32005: contig of 1577 bp in length
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33228; ga
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             81666: gap of
96774: contig
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34512: contig of 1284 bp in length
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contig of 1467 bp in length
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                               Db 121108 TTCTGGATCCCGTTATCAGATCATAGACGGCCCTAAGAATATAACAGTCCTACAGGGCTC 121167
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   113 CCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGA 150
                                                53 TTCTGGGTCTGGTAATGAAGGCAAGAGGCCCCCAGAATGCAACAGTCCTGAAGGGCTC 112
                                                                                                            Local
                                                                                               1 Similarity
73; Conserv
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                                                                                             Conservative
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.74658 175861: contig of 1204 bp in length
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/clone="RP23-147E11"
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174557: ~~
74657
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47772: contig of 28025 l
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contig of 26685 bp in length
ap of 100 bp
                                                                                               0,
                                                                                                              Score 58; DB 2;
Pred. No. 0.0043;
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                                                                                               Mismatches
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                                                                                                                                                                              2103 others
                                                                                                                             Length 175861;
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        Matches 100;
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        Conservative
                                                                              /evidence=not_experimental
/rpt_family="MIR"
48905. .49310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family=:
39884. .40122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
/rpt_family="L2"
39552..39861
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/rpt_family="L2"
38477, .39376
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37518. .38158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="THE1B" 34563. .34620
                                                                                                                                         complement(48002. .48132)
                                                                                                                                                                                                                                                        complement(46792. .47084)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(42066. .42114)
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complement(40243. .40542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(37064. .37364)
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/evidence=not_experimental
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complement(35785. .35824)
                                                                                                                                                         /evidence=not_experimental
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/rpt_family="L1PB1"
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/rpt_family="L1PB1"
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/rpt_family="L2"
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/rpt_family="MIR"
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/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
/rpt_family="Aluy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="MER67C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/rpt_family="MLT2CB"
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/rpt_family="MLT2CB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="homology = 98.40%, score = 29, counts =
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8.5%; Score 100; DB 9;
100.0%; Pred. No. 3.3e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                      _family="L1MA"
                                                                                                                                                                                                                                                                                                                   lement (42758. .46751)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17615
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Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nuguen, C., Nicol, R.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murph, T., Naylor, J., Ngyyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riaback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Riaback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Vienber, T., Stange, S., Tresdare, J., Tresdare, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Vienber, J., Stanger, D., Ye, W.J., Young, G., Vienber, J., Stanger, D., Ye, W.J., Young, G., Vienber, J., Stanger, P., Wall, W., Wall, N., Ye, W.J., Young, G., Vienber, J., Wall, N., Wyman, D., Ye, W.J., Young, G., Vienber, J., Wall, N., Wyman, D., Ye, W.J., Young, G., Vienber, J., Wall, N., Wyman, D., Ye, W.J., Young, G., Vienber, J., Wall, N., Wyman, D., Ye, W.J., Young, G., Vienber, J., Wall, N., Wyman, D., Ye, W.J., Young, G., Vienber, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Vienber, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Vienber, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Vienber, B., Wu, X., Wyman, D., Ye, W.J., Ye, W.J., Young, G., Wall, W.J., Young, G., Wall,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 175861)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus, clone RP23-147E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 175861)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC120346 175861 bp
Mus musculus clone RP23-147E11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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WORKING DRAFT SEQUENCE, 22 ordered
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repeat_region complement(73877491) /evidence=not_experimental /rpt_family="LlME3A" repeat_region 77818020	complement(7057. /evidence=not_exp /rpt_family="MER2	repeat_region 6671. 6969 /evidence=not_experimental /rpt family="AluJb"	<pre>repeat_region complement(02450668) /evidence*not_experimental /rpt_family="LIMS3A"</pre>	<pre>/evidence=not_exp /rpt_family="MIR"</pre>				^	repeat_region 1499. 1588	repeat_region complement(1345. 1500) /evidence=not experimental	repeat_region 747814 /evidence=not_experimental	/evidence=not_experimental /rpt_family="L1"	<pre>/map="21q22.3" repeat_region complement(1383)</pre>	/db_xref="taxon:9606" /chromosome="21"	source 11990b5 /organism="Homo sapiens"	Biotechnology, Beutenbergstrasse II, Jena Location/Qualifiers	sion -MAY-1998) Genome Ar	REFERENCE I (DASSES I CO 19900) RUTHORS Taudien,S., Nordsiek,G., Korenberg,J., Drescher,B., Weber,J., Schattevov,R. and Rosenthal,A.	Euk	MS	ACCESSION AF064857 VERSION AF064857.1 GI:3171149 KEYWORDS HTG	LOCUS AF064857 199665 bp DNA linear PRI 23-JUN-1998 DEFINITION Homo sapiens BAC derived from chromosome 21q22.3, complete sequence, containing PEP19 (PCP4) gene.		Db 120238 GGTTTGGATCTGCCTTCCTCTCAGTGCAAGGT 120207	120298 TCCATGATGTGCAGCCCAGTGACTCGGGATCCC	280 TCCACAATGTGGAGCCCAGTGATTCGGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCC	Db 120358 ACAACCGCTTCACCTATGCCAGTTACAACAGCACTGACAGCTTCATCTCGGGAGTTGATCA 120299
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Center project Information Center project name: L20921 Center clone name: 147_E_11

Center code: WIBR Center: Whitehead

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* 72620 72719; gap of 100 bp in length

* 72620 72719; gap of 100 bp

* 72720 81566: contig of 8847 bp in length

* 81567 81666: gap of 100 bp

* 81667 96774: contig of 15108 bp in length

* 96775 96874; gap of 100 bp

96875 119647: contig of 22773 bp in length

119648 119747; gap of 100 bp

119748 147772: contig of 28025 hm in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the accession number will be preserved.

1 28835: contig of 28835 bp in length
28836 28935: gap of 100 bp
28836 29562: contig of 627 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is believed to be correct as given, however the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: plasmid: n/a; 100% of read Sequencing vector: plasmid: n/a; 100% of read Chemistry: Dye-terminator Big Dye; 100% of read Assembly program: phrap; version 0.960731 consensus quality: 159879 bases at least Q40 Consensus quality: 172188 bases at least Q20 Consensus quality: 173133 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 8.3 in Q20 bases; Quality coverage: 8.4 in Q20 bases;
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Insert size: 173761; sum-of-contigs
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100 bp μp in length
100 bp μp in length
1663 30328: contig of 667 bp in length
329 30428: gap of 100 bp
329 32005: contig of 1577 bp in 166 33128: contig of 1577 bp in 16 33128: contig of 177 bp in 17 33228.
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590 50604: contig of 3015 bp in length
605 50704: gap of 100 bp
705 56370: contig of 5666 bp in length
71 56470: gap of 100 bp
71 64079: contig of 7609 bp in length
80 64179: gap of 100 bp
0 72619: contig of 600 bp
0 77619: contig of 7609 bp
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179: gap of 100 bp
37483: contig of 1304 bp in length
183: gap of 100 bp
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43203: contig of 2038 bp in
100 bp
17489: contig of 4186 bp in
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  220 ATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCA 279
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174658. .175861
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41166. .43203
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96875. .119647
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81667...96774
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72720. .81566
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50705. .56370
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47590. .50604
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43304. .47489
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37584. .39166
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32106. .33128
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29663. .30328
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FEATURES

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Location/Qualifiers

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COMMENT
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                                                                                                                             ACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGC 323
                                                                                                                                                                                                                                                                                                                                                                                               CCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAG 143
                                                                                                                                                                                                                                    GAGCCCATCATCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTC 263
                                                                                                                                                                                                                                                                                    GGCTGGAAGCTTCTCATGTGGACTCTTAACCAAATGGTGGTGCTGAGTCTCACCACCCAA 264
                                                                                                                                                                                                                                                                                                                          GGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCCATG 203
                                                                                                                                                                                                                                                                                                                                                                      CCTCAGAATGTAACAGTCCTAAAGGACTCAGAGGCTCACTTCAACTGCACCGTGACTCAC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGCTGGTCATCCTGGCTCAGCTGACAGCTTCCGGATCCAGTTATCAGATCATAGAAGGT 144
                                                                                                                                                                                             GGACCCATCATCACCAACAACCGCTTCACCTATGCCAGTTACAACAGCACTGACAGCTTC
                  CTGCAGAACAGCCATGGGTTTGGATCTGCCTTCCTCTCAGTGCAAG 430
                                                                                                      ATCTCGGAGTTGATCATCCATGATGTGCAGCCCAGTGACTCGGGATCCGTGCAATGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLIL at: http://lmage.llnl.gov Series: IRAK Plate: 10 Row: m Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gunaratne, P.H., Garcia, A.M., Lu, Yoon, V.S., Kowis, C.R., Lawrence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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/db_xref="LocusID:72058"
/translation="MEGSWRDYLAVLVILAQLTASGSSYQIIEGPQNVTVLKDSEAHF
/translation="MEGSWRDYLAVLVILAQLTASGSSYQIIEGPQNVTVLKDSEAHF
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DSGSYQCSLQNSHGFGSAFLSYQDSIGEEGPALPTWAIILLAVAFSLLLILIIVLIII
FCCCCASRREKEESTYQNEIRKSANMETNKADPETKLKSGKENYGYSSDEAKAAQTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="MGC:7960 IMAGE:3584645"
/tlssue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy." /clone_lib="NCI_CGAP_Maml" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPPKSAEVSLPEKRSSSLPYQELNKHQPGPATHPRVSFDIASPQKVRNVTLV"
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/protein_id="AAH04806.1"
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Gord, S., Goyette, M., Gaqe, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Gale, D., Galagan, J., Gardyna, S., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacChan, P., Major, J., Marquis, N., Matthews, C., MacLean, C., MacChan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Muyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Senaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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submitted (09-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 9, 2002 this sequence version replaced gi:20503171.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                         Sequence 11
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                               house mouse
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NCTVTHGWKLLAWTLNGMVVLSLTTQGPIITNNRFTYASYNGTUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVLSUNGMVVL
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53. .724
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Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                            GI:19575336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246;
                                                                                                                                                                                                                                                                            Mus musculus, RIKEN cDNA 2010003D20 gene, IMAGE:3584645, mRNA, complete cds. BC004806
                                Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                             Mus musculus
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                     Strausberg, R.
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                  Direct Submission
                                                                                                                                                                                                                                                           BC004806.1
                                                                                                                                                                                                                      house mouse
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FCCCCASRREKEESTYQNEIRKSANMRTNKADPETKLKSGKENYGYSSDEAKAAQTAS
LPPKSAEVSLPEKRSSSLPYQELNKHQPGPATHPRVSFDIASPQKVRNVTLV"
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Pred. No. 4.4e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 15, 2000 this sequence version replaced gi:6686457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 19690)
DOE Joint Genome Institute.
Sequencing of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 164618 bases at least Q40 Consensus quality: 180887 bases at least Q20 Consensus quality: 180777 bases at least Q20 Consensus quality: 183777 bases at least Q20 Estimated insert size: 147000; pulse field gel estimation Estimated insert size: 193700; sum-of-contigs estimation Quality coverage: 5.67 in Q20 bases; pulse field gel estimation Quality coverage: 4.3 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces consists of 33 contigs. The true order of the pieces consists of 33 contigs. The true order of the pieces consists of 33 contigs. The true order of the pieces consists of 33 contigs. The true order of the pieces consists of 33 contigs. The true order of the pieces consists of 33 contigs. The true order of the pieces consists of 33 contigs. The true order of the pieces consists of 33 contigs. The true order of the pieces consists of 33 contigs. The true order of the pieces consists of 33 contigs. The true order of the pieces consists of 33 contigs. The true order of the pieces consists of 35 contigs. The true order of the pieces consists of 35 contigs. The true order of the pieces consists of 35 contigs. The true order of the pieces consists of 35 contigs. The true order of the pieces consists of 35 contigs.
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   67736 GTTTGGATCTGCCTTCCTCAGTGCAAGGT 67766
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                                GCATGGATCTGCTTACCTTACCGTCCAAGTT 371
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/clone="RP21-467L12"
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complement(9989. .10077)
                                                      complement(9723. .9882)
/note="L2"
                                                                                                                                                                                               complement(8865. .8964)
/note="L2"
                                                                                                                                                                                                                                                                                                                                                      complement(6887. .7067)
                                                                                                                                                                                                                                                                                                                                                                                                            5542. .5829
/note="AluSx"
                                                                                       /rpt_family="SINE/Alu"
/rpt_type=DISPERSED
                                                                                                                         /note="AluSq"
                                                                                                                                                                                                                                                                                complement(8482. .8762)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_type=DISPERSED
2398. .2495
                    rpt_type=DISPERSED
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/rpt_type=DISPERSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="21-Glutamic Acid Rich protein 21-GARP"
/protein_id="CAB90445.1"
/db_xref="G1:7717370"
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/clone="BAC-291B3, 3' partial"
/clone_lib="BAC library"
                                                                                                                                                          rpt_type=DISPERSED
                                                                                                                                                                                                                                                 rpt_family="SINE/Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SH3BGR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Accession No. X93498"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SH3BGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   )oin(<3473. .3565,12649. .12678,15331. .15460,18739. .19157)
"gene="SH3BGR"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oin(3473. .3565,12649. .12678,15331. .15426)
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RESULT 9
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                                                               Db 268745 CATGGATCTGCTTACCTTACCGTCCAAGGTGTG 268777
                                                                                                                                                                                                                                                                           Db 268685 CACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTG
                                                                                                                                                                                                         Db 268625 GACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATC
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                                                                                                    342 CATGGATCTGCTTACCTTACCGTCCAAGTTATG 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                       42 TTCCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGTC 101
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/note="Alusx"
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/rpt_family="LINE/L2"
/rpt_type=DISPERSED
complement[10078..10429)
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/note="L2"
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/note="(CA)n'
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10980. .11חחח
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|2649. .12678
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97.6%;
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                                                                                                                                                                                                                                            340000 bp DNA 1
Homo sapiens chromosome 21 segment HS21C080.
Hattori,M., Fujiyama,Â., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 340000)
                                                                                                                                                   Homo sapiens
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complement(18643. 24647)
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/evidence=not_experimental
complement(18397. .18584)
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complement(17633. .17969)
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/rpt_family="HERV17"
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* e.mail: shimizu@dmb-med.keio.ac.jp
* URL: http://adenine.dmb.med.keio.ac.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (05-MAY-2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
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* e.mail: sakaki@gsc.riken.go.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Mascheroder Weg 1, D-38124 Bra
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/note="Accession No. AF064860"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGCTGATGCTTAAGCGTCAGGCCCATG
                                   TCAAGCTATTATTTTGTTCCGGAGCCCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCT 563
                                                                                                  CCCTCACACTGGACCCGGCTCCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCAT 503
                                                                                                                                                         AACATTCCTAGCAACAACCTTATAGTCACTGAGGGTGAACCCTGTAATGTGACTTGCTAT 502
                                                                                                                                                                                                                                                                                                                  ATCTCGGAGTTGATCATCCATGATGTGCAGCCCAGTGACTCCGGGATCCGTGCAATGCAGC
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TCGAGTTACAATTCCTTTCTGGAGCCGGGCAACTTTATGAGGGTCTTGAGTGTCCTGGAC 622
                                                                             GCCGTGGGCTGGACCTCACTCCCGGATATTTCCTGGGAGCTTGAGGTTCCCCGTAAGCCAT
                                                                                                                                                                                                 TTCATTCCCAGTGTTAATCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTA 443
                                                                                                                                                                                                                                         CTGCAGAACAGCCATGGGTTTGGATCTGCCTTCCTCTCAGTGCAAGTCATGGGGGACCCTG
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AX380404
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1 (bases 1 to 142742)
Taudien,S., Dagand,E., Hildmann,T., Nordsiek,G., Drescher,B., Schattevoy,R., Weber,J., Schilling,M., Menzel,U., Yaspo,M.L. and
                                                                                                                                                                                                 Submitted (21-JAN-1999) Genome Analysis, Institute for Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
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/rpt_family="MIR"
                    /evidence=not_experimental
                                                          /clone="PAC 206A10"
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                                                                                                                   /db_xref="taxon:9606"
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GAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCCAGGGCTGGAAGCTCATCATGTG
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                                                                    CCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCCAGAATGCAACAGTCCT 103
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Eukaryota; M
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                                                                                                Conservative
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/db_xref="G1:19575333"
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CCCCRCCFCCRKRGNLKKRRQTKKLRQKVENKTPATIQmNRRpQTPLLSLPNPVNPV
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                                                                                                                                                                                                                                                                                                                         /note="unnamed protein product"
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/db_xref="taxon:9606"
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97.5%;
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          Welcher, A.A.,
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                                                    Eukaryota;
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 Patent:
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                                         ; Metazoa;
Eutheria;
lecules and 0200710-A
                      Sarmiento, U.M., Schultz, H.J.
                                         Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
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AAAGTGGAAATGAAAACTCCGGCTACAATTCAGATGAACAAAAGACCACAGACACACCGCTT
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/clone_lib="pLACE6"
/note="cloning vector: phace6"
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Pred. No. 1.9e-260;
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GINIPGVLSSLPSLGFGSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRECGCRCCC
RCCFCCRRKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKTTDTASLPPKSC
ESSDPEQRNSSGGPPHQRADQRPPRPASHPQASFNLASPEKVSNTTVV*
307 c 286 g 287 t
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/db_xref="GI:19575327"
/db_xref="GI:19575327"
/translation="MGLYIFLHGSGSGNEVIEGPQNATVLKGSQARFNCTVSOGWKLI
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SRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLDDISWELGILVSHS
SRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEVTCLPSHWTRLDDISWELGILVSHS
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/db_xref="taxon:9606"
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                                                              submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81'438-52-3986) NEDO human cDNA sequencing project supported by Mnistry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-& 3'-end one pass, sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligo capping; fis (full insert sequence).
Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE6 clone:PLACE6017788.
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Homo sapiens cDNA FLJ35197 fis,
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Isogai, T. and Yamamoto, J.
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                                                 Evaluation; clone selection for full insert sequencing: HRI and
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Isogai,T.
                           annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                               human cDNA sequencing project
Location/Qualifiers
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clone PLACE6017788,
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highly similar
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/organism="Homo sapiens" /db_xref="taxon:9606"

Title:
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Sequence: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
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Gapop 10.0 , Gapext 1.0 April 28, 2003, 23:25:03; Search time 3244.94 Seconds (without alignments) 10538.186 Million cell updates/sec GenEmbl:*
1: gb_ba:* 2054640 seqs, 14551402878 residues 1 ctgtctgcccatctgaataa.....gtaatacaactgtagtatag 1175 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. em_htgo_hum:*
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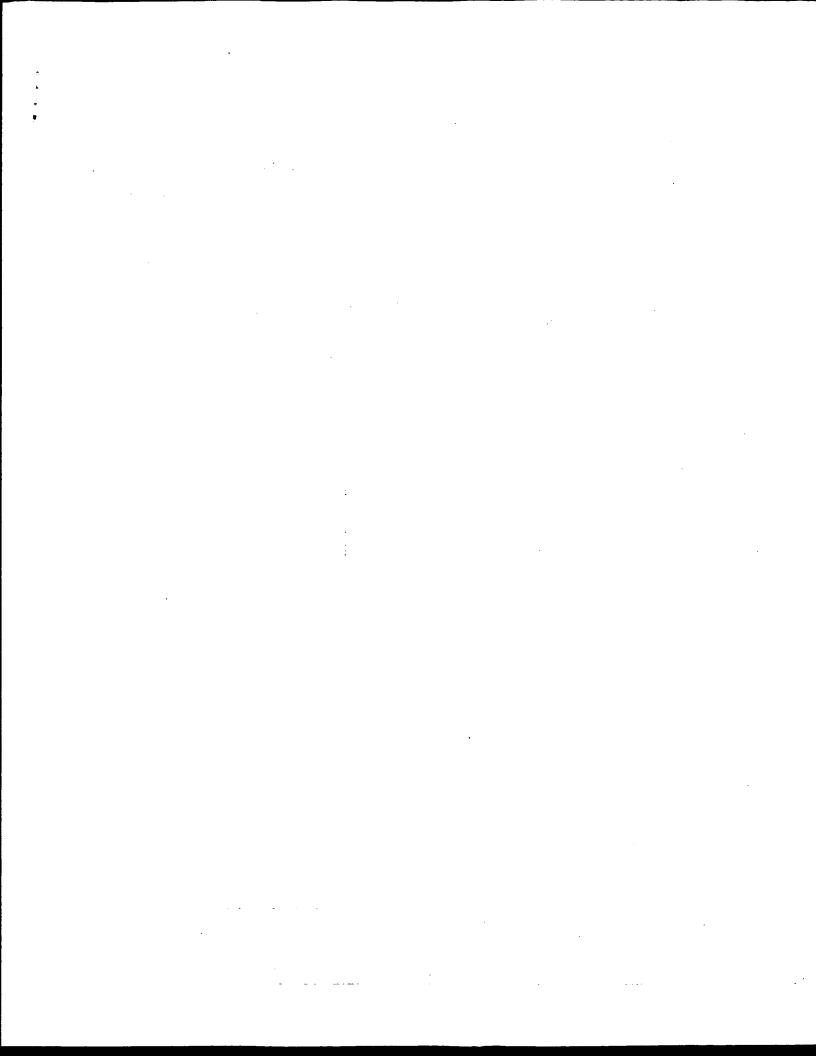
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AUTHORS TITLE JOURNAL	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 AX380396
Welcher, A.A., Sarmiento, U.M., Schultz, H.J. and Chute, H.T. B7-like molecules and uses thereof Patent: WO 0200710-A 1 03-JAN-2002;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	human.	•	AX380396.1 GI:19575326	AX380396		AX380396 1175 bp DNA linear	
hute,H.T.	ta; Euteleostomi; dae; Homo.					•		r :PAT 18-MAR-2002	•

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                         Claim 1; SEQ ID NO 1963;
                                                      interactions
                                                              New isolated nucleic acid
genes from Drosophila and
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL16830 standard; DNA; 46954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represents a nucleotide sequence of the invention showing the the CAG tri-nucleotide repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   containing a neuropsychiatric gene containing trinucleotide repeats. Tri-nucleotide repeats and their expansion areknown to be involved in a number of diseases including fragile X syndrome, spinocerebellar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to the use of a plasmid vector array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid vector arraying neuropsychiatric gene more than copy number containing trinucleotide repeats its use thereof -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-662424/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              808 GCTGCTGCCGCCGCCGTCGTTGTTGTGGCGCAACTGCTGCTGCCGTTGTTTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 AACTTAAAAGAATAAATACACCATGAGAAAA 65
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                                                                                                          2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAACAAAGAAACTGAGACAGAAAGTGGAAA 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGTTGCTGCTGTTTTGCTGCTGAAACATTCAAAAGTGAAGTATATTTAAAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAAAAAGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 4.48;
Similarity 58.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 12;
                                                                                                                                                                                          2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                    Li
                      21pp + Sequence Listing; English
                                                                                                                                    PWD,
                                                                 detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51.8; DB 21
Pred. No. 0.00039;
                                                                                                                                    Myers
                                                                                                                                                                                                                                                                                                                                                        cell signalling; insecticide;
                                                                                                                                    EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 403;
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and c
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Search completed: April 29, 2003, 11:04:24

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The invention relates to an isolated nucleic acid detection reagent

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Best Local
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                                                                                                                                                 16836 ACGATGCTGCCGATGATGTGGATGCTCTGGATGATGCTGCTGCTGCTGCAGATGCAA 16895
16956 AAAGTTACAATTTCAAAACAAAT 16978
                                                                         16896
                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryctes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                    Sequence 46954 BP; 13370 A; 9970 C; 9854 G; 13760 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                   (ABB57737-ABB72072)
                                                                                                               830
                                                                                                                                                                                       771 ACCATGCTTCTGACGCCGACGTGTACTCT-TACAATACGCTGCTGCTGCTGCCGCCGTCG 829
                                     TCGTATTCAATTTCAAAAGAAAT 912
                                                                         TTGCTGCCGCTGCTGCTGCTGCTGCTGCTGCAGTTGCGGATGCGGATGAGTGCA 1695
                                                                                                           91;
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                              4.2%;
63.6%;
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                                                                                                                                                                                                                                            Score 49.4; DB Pred. No. 0.022;
                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                DB 23;
                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                              Length 46954;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to the use of a plasmid vector array containing a neuropsychiatric gene containing trinucleotide repeats. Tri-nucleotide repeats and their expansion are known to be involved in a number of diseases including fragile X syndrome, spinocerebellar ataxia type III, hereditary hypertrophic, cardiomyopathy, dentatorubral and pallidoluysian atrophy (DRPLA), spinocerebellar ataxia, Marfan syndrome; X-linked spinobubar atrophy. The present sequence represents
       Diagnosis of spinocerebellar ataxia type III (SCA III) syndrome using techniques which ensure highly accurate diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                  Spinocerebellar ataxia type III; SCAIII; reverse dot hybridisation; PCR-microplate hybridisation; PCR-MPH; trinucleotide repeat; TNR;
                                                 WPI; 1999-527634/44.
                                                                                                       (JIND/) JIN D K.
(SMSU ) SAMSUNG FINE CHEM CO LTD
                                                                                                                                                  26-FEB-1998;
                                                                                                                                                                              18-FEB-1999;
                                                                                                                                                                                                          02-SEP-1999.
                                                                                                                                                                                                                                     W09943852-A1
                                                                                                                                                                                                                                                                                          repeat_unit
                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        SCAIII syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Spinocerebellar ataxia type III (SCAIII) gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX89891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX89891 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 389 BP; 107 A; 92 C; 91 G; 93 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a tri-nucleotide repeat related sequence #5 disclosed in the scope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     been represented by an n to keep nucleotide numbering correct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note; Nucleotides which were illegible in the specification have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 928 CAAACAAAGAAACTGAGACAGAAAGTGGAAATGAA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  868 GCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAAAAAGAGAAGA 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                808 GCTGCTGCCGCCGCCGCCGTCGTTGTTGTGGCTGCCAACTGCTGCTGCTGCTTGTTTCT 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 AANTTAAAAGAANACCTACACCATGAGNTANAAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                   98KR-0006278
                                                                                                                                                                              99WO-KR00078
                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         ss.
                                                                                                                                                                                                                                                             /note= "trinucleotide repeat"
                                                                                                                                                                                                                                                                             *tag=
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57.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51.8; DB 21; Pred. No. 0.00038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66;
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Best Local
Jin DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the diagnosis of spinocerebellar ataxia type III (SCAIII) syndrome using reverse dot hybridisation or PCR-microplate hybridisation (PCR-MPH). The method comprises attaching a potion of the SCAIII gene containing 73 copies of the trinucleotide (CAG) repeat unit (the present sequence) to a substrate, and hybridising with amplified testee genomic DNA containing copies of the trinucleotide units, PCR amplified with labeled primers (AAX89889-90). The new method is useful for diagnosis of SCAIII syndrome, and for determining the severity of the disease. The present sequence represents the SCAIII gene fragment
                            (SMSU ) SAMSUNG MEDICAL CENT (JIND/) JIN D G.
                                                                          25-JUN-1998;
                                                                                                        25-JUN-1998;
                                                                                                                                                                   KR2000003004-A
                                                                                                                                                                                                                                                                                                                                                                                  spinocerebellar ataxia; X-linked spinobubar atrophy
                                                                                                                                                                                                                                                                                                                                                                                              spinocerebellar ataxia type III; DRPLA; neuropsychiatric; hereditary hypertrophic cardiomyopathy; Marfan syndrome; dentatorubral and pallidoluysian atrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trinucleotide repeat sequence #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK10240 standard; DNA; 403
                                                                                                                                       15-JAN-2000
                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                            repeat_unit
                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            Trinucleotide repeat; fragile X syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 397 BP; 124 A; 104 C; 104 G; 65 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 12-13; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 trinucleotide (TNR) repeats.
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                                                                          98KR-0024064.
                                                                                                        98KR-0024064.
                                                                                                                                                                                                                                                           /rpt_type=
152..154
                                                                                                                                                                                                                                                                                                       Location/Qualifiers 152..347
                                                                                                                                                                                                                            /note= "CAG type repeat"
                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                          /*tag=
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Pred. No. 0.00
0; Mismatches
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RESULT 11
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Best Local
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                                                                  useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                  Claim 1; SEQ ID NO 40741; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genomic polynucleotide SEQ ID NO 40741.
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                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                           New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                          genes from Drosophila
                                                                                                                                                                                                                                                                                                               Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY
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11-JUL-2000;
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                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAG tri-nucleotide repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                     2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 A; 66 C; 62 G; 69 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.5%;
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                                                                                                                                                                                                                                                                                                                PWD,
                                                                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53.4; D
Pred. No. 0.00
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                Myers
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es 61;
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                                                                                                                                                          The invention
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                                            WIPO
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Sequence 7029 BP; 1426 A; 1440 C; 1945 G; 2218 T; 0 other;

Disclosure; Fig 10; 23pp; Korean

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5560
                                                                                                                                                                                                                                                                                                                                                                                Trinucleotide repeat; fragile X syndrome; ds;
spinocerebellar ataxia type II. DRPLA; neuropsychiatric
hereditary hypertrophic cardiomyopathy; Marfan syndrome;
dentatorubral and pallidoluysian atrophy;
               Plasmid vector arraying neuropsychiatric containing trinucleotide repeats its use
                                                                                                                                                                                                                              misc_difference
                                                                                                                                                                                                                                                       misc_difference
                                                                                                                                                                                                                                                                              misc_difference
                                                                                                                                                                                                                                                                                                         misc_difference
                                                                                                                                                                                                                                                                                                                                 misc_difference
                                                                                                                                                                                                                                                                                                                                                                         spinocerebellar
                                                                                                                                                                                                                                                                                                                                                                                                                           Tri-nucleotide repeat related sequence #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK10248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK10248 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-662424/64
                                                                          (SMSU)
                                                                                                                                                                                                      misc_difference
                                                                                                                                                                                                                                                                                                                                                         Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-2002 (first entry)
                                                                                                   25-JUN-1998;
                                                                                                                                    15-JAN-2000
                                                                                                                                                    KR2000003004-A
                                                                                                                                                                     Homo sapiens
                                                          Jin DG;
                                                                                                                    25-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      868 GCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       808 GCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCCGCTTGTTGTTTCT 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGTATTTGCTAAAAAGAAGTAATCATTAATTTCCGGTAAAAA 5603
                                                                           SAMSUNG MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                   98KR-0024064.
                                                                                                                    98KR-0024064
                                                                                                                                                                                                                               /note=
203
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         ataxia; X-linked spinobubar atrophy
                                                                                                                                                                                                       /note=
276
                                                                                                                                                                                                                                                                                 46
                                                                                                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                        /note=
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"Illegible :
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"Illegible in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Β₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52.8; Db 22,
Pred. No. 0.00094;
                                                                                                                                                                                       in
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                 gene more
thereof -
                                                                                                                                                                                      specification"
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                         than copy number
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The polypeptide, polynucleotide encoding it and antibody against (I) are useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, and conditions including seminal conditions of B7-L polypeptides are consecuted for enhancing the immune response to tumours. (I) plays a role in a consecution of consecution consecution.

CC polypeptide. Hence modulators of (I) are useful for the treatment of concer including seminal vesicle cancer, lung, brain, breast, ovarian, concer and cancers of hemantopoietic system. B7-L polypeptide concer including seminal vesicle cancer lung, brain, breast, ovarian, concerticular cancer and cancers of hemantopoietic system. B7-L polypeptide concerticular cancer and cancers of hemantopoietic system. B7-L polypeptide concerticular cancer and cancers and autoimmune diseases. B7-L concerticular cancer and cancers and autoimmune diseases. B7-L concerticular cancer and cancers and autoimmune diseases. B7-L concerticular cancer and cancer and autoimmune diseases and autoimmune diseases and autoimmune diseases and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune diseases such as systemic lupus environments of a continuous and psoriasis, chronic inflammatory disease such as purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions, comphigus and pemphigoid, endocrinopathies (Grave's disease, anaemia, thromborytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple mysloma. The present
                                                                                                                                                                                                                                                                                                                 Matches 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 895 BP; 250 A; 223 C; 212 G; 210 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-2000;
28-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 6; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUN-2001; 2001WO-US20719
     203
                                                        144
                                                                                                           143
                                                                                                                                                           84
                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                         24 GAGATGGGGCTTGTGATTTTCCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGC 83
                                                GGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATG
                                                                                                                                CCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTCCAACTGCACCGTCTCCCAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-130881/17.
GGCTGGAAGCTTCTCATGTGGACTCTTAACCAAATGGTGGTGCTGAGTCTCACCACCCAA 262
                                                                                                     CCTCAGAATGTAACAGTCCTAAAGGACTCAGAGGCTCACTTCAACTGCACCGTGACTCAC
                                                                                                                                                                                                        GTGCTGGTCATCCTGGCTCAGCTGACAGCTTCCGGATCCAGTTATCAGATCATAGAAGGT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sarmiento
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2000US-0729264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the coding sequence of mouse B7-L_m2
                                                                                                                                                                                                                                                                                                                                    15.8%;
71.1%;
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                                                                                                                                                                                                                                                                                                                                      Score 186; DB 24;
Pred. No. 3.6e-41;
                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chute HT;
                                                                                                                                                                                                                                                                                                                                                            Length 895;
                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
ABK10239/c
       This invention relates to the use of a plasmid vector array containing a neuropsychiatric gene containing trinucleotide repeats. Tri-nucleotide repeats and their expansion areknown to be involved in a number of diseases including fragile X syndrome, spinocerebella
                                                                                        Plasmid vector arraying neuropsychiatric gene more than copy number containing trinucleotide repeats its use thereof \cdot
                                                                                                                                                      Jin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trinucleotide repeat; fragile X syndrome; ds; DRPLA; spinocerebellar ataxia type III; Marfan syndrome; hereditary hypertrophic cardiomyopathy; neuropsychiatric; dentatorubral and pallidoluysian atrophy;
                                                                     Disclosure;
                                                                                                                               WPI; 2000-662424/64.
                                                                                                                                                                           (SMSU ) SAMSUNG MEDICAL CENT (JIND/) JIN D G.
                                                                                                                                                                                                                25-JUN-1998;
                                                                                                                                                                                                                                      25-JUN-1998;
                                                                                                                                                                                                                                                            15-JAN-2000.
                                                                                                                                                                                                                                                                                    KR2000003004-A
                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                         repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spinocerebellar ataxia; X-linked spinobubar atrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trinucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK10239 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cepeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCAGAACAGCCATGGGTTTGGATCTGCCTTCCTCAGTGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACCCATCATCACCAACAACCGCTTCACCTATGCCAGTTACAACAGCACTGACAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCCCATCATCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGGGGGAACATCAGATGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCTCGGAGTTGATCATCCATGATGTGCAGCCCAGTGACTCGGGGATCCGTGCAATGCAGC
                                                                   Page 12; 23pp; Korean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat sequence #2
                                                                                                                                                                                                               98KR-0024064.
                                                                                                                                                                                                                                      98KR-0024064
                                                                                                                                                                                                                                                                                                                                                        /rpt_type=
198..200
                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= b
/note= "CAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 152..194
                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_type=
152..154
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                          198..222
                                                                                                                                                                                                                                                                                                                               /note= "CAG type repeat"
                                                                                                                                                                                                                                                                                                                                               /*taq=
                                                                                                                                                                                                                                                                                                                                                                                *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                    type repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428
        spinocerebellar
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hereditary

hypertrophic,

cardiomyopathy,

dentatorubral

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RESULT 8
ABK13034
ID ABK1
  conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometricsis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a rogrowth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder; gene; ss.
                     arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They
                                                                                              dependent B-cell mediated diseases and autoimmune diseases. B7-L molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumato
                                                                                                                                                                            polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 7; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirhe antiinflammatory; dermatological; antipsoriatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding mouse B7-like protein, B7-L_m3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK13034 standard; cDNA; 754 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Welcher AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUN-2000; 2000US-214512P
28-NOV-2000; 2000US-0729264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200200710-A2
                                                                                                                                                                                                                                                                                    seminal vesicle hyperplasia in transgenic mice overexpressing B7-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to an isolated B7-like (B7-L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B7-like polypeptides, polynucleotides and their modulators, useful diagnosing, preventing and treating reproductive, immune and
                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide, polynucleotide encoding it and antibody against ()
ul for treating B7-like polypeptide-related disease, disorders
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/product= "B7-like protein, B7-L_m3"
immunosuppressive agents for bone marrow and organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UM,
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                                                                                                                                                                                                                                                                                                                            plays a role
                                                                                                     rheumatoid
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Best Local :
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                                                                                                                                                                                                                    antiasthmatic; nephrotropic; antibacterial; virucide; tumo reproductive disorder; graft versus host disease; autoimmu toxic shock syndrome; allergy; nephropathy; skin disorder;
                                                                                                                                                                                                                                                                               Mouse; B7-like protein; B7-L; antiinfertility; gynaecological; antiithmour; cytostatlc; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic;
                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                       endocrinopathy;
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                                                                                                                                                                                                         lymphoproliferative disorder; gene; ss
                                                                                                           Location/Qualifiers 53..865
                                                                          /product= "B7-like protein, B7-L_m2"
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71.1%;
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                            CCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCCTGAGAAGGTCAGTAATACA 1163
                                                                                        GAACAAAGAAACAGTAGCTGTGGCCCTCCTCACCAGCGGGCTGATCAACGTCCACCCAGG
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 401 BP; 105 A; 98 C; 111 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human placenta \boldsymbol{\cdot}
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GACCGCTTCACCTCTCAGAG
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                                                                                                         TGGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAAT
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2000US-0236359.
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2000US-0608408.
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97.0%;
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Pred. No. 1.4e-42;
0; Mismatches 6
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RESULT 6
ABK13032
           antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder;
                                                                     Mouse; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirhe antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antilicer; antiallergic;
endocrinopathy;
                                                                                                                                                                         DNA encoding
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                                                                                                                                                                         mouse B7-like protein,
                                                                                                                                                                                                               (first entry)
 lymphoproliferative
 disorder;
                                                                                                                                                                         B7-L_m1.
                                                                                                             antirheumatic;
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GAGATGGGGCTTGTGATTTTCCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGC GTGCTGGTCATCCTGGCTCAGCTGACAGCTTCCCGGATCCAGTTATCAGATCATAGAAGGT

Query Match Best Local S Matches 712

Local Similarity nes 712; Conserv

Conservative

32.4%; 61.9%;

Score 381; DB 24; Pred. No. 3.4e-95; Mismatches

Length

Indels

69;

Gaps

4

83

Sequence

1195

BP;

313 A;

304 C;

291 G;

287 T; 0 other;

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The invention relates to an isolated B7-like (B7-L) polypeptide (I). CC The polypeptide, polynucleotide encoding it and antibody against (I) are useful for treating B7-like polypeptide-related disease, disorders or cc conditions including reproductive disorders (e.g. infertility, and inscarriage, preterm labour and delivery and endometriosis) and consistent of the immune response to tumours. (I) plays a role in growth and maintenance of cancer cells based on the observation of cc seminal vesicle hyperplasia in transgenic mice overexpressing B7-L colypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, ct testicular cancer and cancers of haematopoietic system. B7-L polypeptide concert including seminal vesicle cancer, lung, brain, breast, ovarian, ct testicular cancer and cancers of haematopoietic system. B7-L polypeptide concert including seminal vesicle cancer, lung, brain, breast, ovarian, ct testicular cancer and cancers of haematopoietic system. B7-L polypeptide concert including seminal vesicle cancer, lung, brain, breast, ovarian, ct dependent B-cell mediated diseases and autoimmune diseases. B7-L conceutes are useful for alleviating the symptoms associated with cd diseases involving chronic immune cell dysfunction or to treat conceutes are useful for alleviating the symptoms associated with cc autoimmune diseases such as systemic lupus erythematosus, rheumatoid care also useful as immunosuppressive agents for bone marrow and organ cc useful for diagnosis and treatment of diseases involving abnormal cell conceils as mannosuppressive agents for bone marrow and organ custification, including arretriosciers and vaccular restencies.
                                                      proliferation, including arteriosclerosis and vascular restenosis.

Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New B7-like polypeptides, polynucleotides and their modulators, for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis.
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28-NOV-2000; 2000US-0729264
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                                     represents the coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
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                                            of mouse
                                       B7-L_m1.
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RESULT 5
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   Homo sapiens
                                                                                                        13-FEB-2002 (first entry)
                                                                                                                                                                    AAS92356 standard; cDNA; 1392 BP
                                                                          DNA encoding novel human diagnostic protein #28160
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                              supplement;
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                                             chromosome mapping; gene mapping; gene therapy;
                             medical imaging; diagnostic; genetic
                                 disorder;
                                              forensic;
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CGGCTCCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTT

AATCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACC AATCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACC CTGCATGGATCTGCTTACCTTACCGTCCAAGTTATGGGAGAGCTGTTCATTCCCAGTGTT

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159 ATGTGGGCTCTCAGTGACATGGTGGTGGTGCTAAGCGTCAGGCCCCATGGAGCCCCATCATCACC

AATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATC AATGACCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATC ATGTGGGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACC

ATCCACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGC

338

120

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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II), (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polypucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed coat for the polymeration of the chiral patent of the polymeration of the printed coat for the polymeration of the chiral patent of the printed coat for the polymeration of the printed coat for the patent of the patent did not appear in the printed coat for the patent of the patent 
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Matches 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess beddings.
                                                                                                           Sequence 1392 BP; 338 A; 361 C;
                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
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23-AUG-2000;
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  Local Similarity
nes 913; Conserv
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Score 779.2; DB 23; Length 1392; Pred. No. 1.3e-205; O; Mismatches 23; Indels 110; Gaps
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                                                                                                                                                                                                 Human; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumat antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder; gene; ss.
         28-JUN-2000;
28-NOV-2000;
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2000US-0729264
                                             2001WO-US20719
                                                                                                                                         Location/Qualifiers
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                                                                                                                  /product=
                                                                                                                                /*tag=
                                                                                                                "B7-like protein,
                                                                                                                  B7-L_h4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer. Lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytoxic T-lymphocyte response in allograft transplantation, graft versus host disease. T-Cell dependent B-cell mediated diseases and autoimmune diseases. B7-L molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory bosed in the symptoms are such as inflammatory bosed disease and alternative collitics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus pemphigoid), endocrinopathies (Grave's disease), various pneumopat (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain Barre syndrome and myasthenia gravis, lymphoproliferative disorders such as multiple myeloma. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The polypeptide, polynucleotide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, discretes conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a roluprotth and maintenance of cancer cells based on the observation of growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1139 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents the coding sequence of human B7-L_h4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and
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CAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCA
                                                                    CCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCA
                                                                                                                                                                    GGCTCTCAGTGACATGGTGGTGCTAAGCCTCAGGCCCATGGAGCCCATCATCACCAATGA
                                             CCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACCTCACCTCGGAGATGATCATCCA
                                                                                                                                              GGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGA
                                                                                                                                                                                                                                           GAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTG
                                                                                                                                                                                                                                                                                                                                            CCCACCCGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATGCAAGAGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 A; 300 C; 283 G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.8%;
97.5%;
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Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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ies 6;
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ibody against (I)
ease, disorders o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present
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The polypeptide, polynucleotide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic;
antiasthmatic; nephrotropic; antibacterial; virucide; tumour; ca
                                                                                                                                                                  Claim 1;
                                                                                                                                                                                              proliferative
                                                                                                                                                                                                                        New B7-like polypeptides, polynucleotides and their modulators, useful
                                                                                                                                                                                                                                                                                                     Welcher AA,
                                                                                                                                                                                                                                                                                                                                                                28-JUN-2000;
28-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200200710-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding human B7-like protein, B7-L_h2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK13029 standard;
                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                            28-JUN-2001; 2001WO-US20719
                                                                                                                                                                                                             diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCCCTCCCAAATCCTGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCT 1070
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                                                                                                                                                                                                                                                           AAU75541.
                                                                                                                                                                Fig 2; 135pp; English.
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2000US-0729264
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                                                                                                                                                                                               disorders,
                                                                                                                                                                                            preventing and treating reproductive, immusorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=  a
/product= "B7-like protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                     HT;
                                                                                                                                                                                                            immune and
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Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coellac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the coding sequence of human B7-L_h2.
                                                                                                                                                                                                                                                                                                                                                                                                       arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell useful for diagnosis and treatment of diseases involving abnormal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (1) are useful for the treatment of cancer including seminal vesicle cancer lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid autoimmune diseases such as systemic lupus erythematosus, rheumatoid
Sequence 1168 BP; 299 A; 302 C; 288 G; 279 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 proliferation, including arteriosclerosis and vascular restenosis
                                                                                                                                                                                                          various pneumopathies
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Qγ QУ Вþ 밁 QΥ DЬ δÃ рь Вb δÃ Вb δÃ DЬ Qy 망 Ωy Д Qy Qγ Matches 1126; Query Match 404 584 517 524 457 464 397 337 344 277 284 224 157 164 104 97 44 37 CCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGTTCC TGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACCCGGCT CCTCCACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGTCCT GGAGCCCAGGGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGG TGGATCTGCTTACCTTACCGTCCAAGTTATGGGAGAGCTGTTCATTCCCAGTGTTAATCT CAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCA CCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCA GAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTG CCCACCCGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATGCAAGAGTCCT GACTTTGACTTGCGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAA CCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGTTCC TGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACCTGGCT TGGATCTGCTTACCTTACCGTCCAAGTTATGGGAGAGCTGTTCATTCCCAGTGTTAATCT CAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCA CCGCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCA GGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGA GGCTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGA GAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTG GGAGCCCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGG Similarity Conservative 95.5%; 99.5%; 0; Score 1122.4; DB 24 Pred. No. 7.4e-301; DB 24; Length 1168; Indels 0; Gaps 216 96 103 636 643 576 583 516 463 396 403 336 276 163 456 0

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cc useful for enhancing the immune response to tumours. (I) plays a role in c growth and maintenance of cancer cells based on the observation of c seminal vesicle hyperplasia in transgenic mice overexpressing B7-L cc polypeptide. Hence modulators of (I) are useful for the treatment of c cancer including seminal vesicle cancer, lung, brain, breast, ovarian, c testicular cancer and cancers of haematopoietic system. B7-L polypeptide cancer sticular cancer and cancers of haematopoietic system. B7-L polypeptide c pathway can be manipulated to regulate cytotoxic T-lymphocyte response c in allograft transplantation, graft versus host disease, T-cell c dependent B-cell mediated diseases and autoimmune diseases. B7-L c molecules are useful for alleviating the symptoms associated with c diseases involving chronic immune cell dysfunction or to treat c autoimmune diseases such as systemic lupus erythematosus, rheumatoid c arthritis, multiple sclerosis, diabetes, immune thrombocytopenic c inflammatory bowel disease (Crohn's disease and ulcerative colitis), c Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They care also useful as immunosuppressive agents for bone marrow and organ c transplantation or to prolong graft survival. B7-L molecules are also cuseful for diagnosts and treatment of diseases involving abnormal cell coroliferation, including arteriosclerasis and vaccular restancis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynuclectide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, disorders o conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and
                                       proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxi shock syndrome or allosensitisation due to blood transfusions, and treatment of allergy, asthma and hypersensitivity reactions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New B7-like polypeptides, polynucleotides and their modulators, for diagnosing, preventing and treating reproductive, immune any proliferative disorders, e.g. cancer and arteriosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are
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28-NOV-2000;
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reproductive disorder; graft versus host disease; autoimmune disease;
reproductive disorder; graft versus host disease; autoimmune disease;
toxic shock syndrome; allergy; nephropathy; skin disorder;
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)B; AAU75542.
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2000US-0729264
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(e.g.
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/pròduct= "B7-like protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polynucleotide encoding it and antibody against (I) are useful for treating B7-like polypeptide-related disease, disorders or conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New B7-like polypeptides, polynucleotides and their modulators, for diagnosing, preventing and treating reproductive, immune an proliferative disorders, e.g. cancer and arteriosclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for enhancing the immune response to tumours. (I) plays a growth and maintenance of cancer cells based on the observation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proliferative disorders. Antibodies, soluble proteins comprising proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are extracellular domains and other regulators of tumours. (I) plays a role reaching for enhancing the immune response to tumours.
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28-NOV-2000; 2000US-0729264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the coding sequence of human B7-L_hl.
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                                                                                                                                                                                                                                                                                                     GCAACTGCTGCTGCCGTTGTTGTTTCTGCTGTAGAAGAAAAAGAGATTTCGTA(TCAAT
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GGGCTGATCAACGTCCACCCAGGCCAGCCAAGTCATCCACAGGCTTCTTTTAATCTGGCCA
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ABK13030 standard;

CDNA; 1240 BP

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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length:
      N_Geneseq_101002:*

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1175
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9306.701 Million cell updates/sec
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and score Pred. No. is derived No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

										NO.	Result
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!	186	186	190.4	381	779.2	1067.4	1122.4	1123.4	1175	Score	
	15.8	15.8	16.2	32.4	66.3	90.8	95.5	95.6	100.0	Match Length DB	Query
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pun curcoatily mouse	DNA encoding mouse	DNA encoding mouse	Probe #5268 used t	DNA encoding mouse	DNA encoding novel	DNA encoding human	DNA encoding human	_	DNA encoding human	Description	

45	44	43	42	41	40	39	38	37	36	35	34	<u>3</u>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	
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AAV08560	ABK36100	AAV08558	AAZ45758	ABL04172	ABL08976	ABL03190	ABL08977	ABL03191	ABL26940	ABL26941	ABL29757	ABL25652	ABL28444	ABL25653	ABL28445	ABL24570	ABL24571	ABL16096	ABL16097	ABL24482	ABL24483	AAF75339	ABL03352	ABL03353	AAX84442	ABV54466	AAN91773	AAQ12002	AAN91578	ABL16830	ABK10240	AAX89891	024	ABL29756	023	
Transgene for epit	ence	Ħ	0	la		Drosophila melanog															Drosophila melanog	Human TGF-beta rec	Drosophila melanog	Drosophila melanog	brain	an prostat	ndrogen re	l-length rat a		Drosophila melanog	Trinucleotide repe	н.	Tri-nucleotide rep	a melan	Trinucleotide repe	

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ALIGNMENTS

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RESULT 1 ABK13028 ABK13028 standard; cDNA; 1175 BP

Human; B7-like protein; B7-L; antiinfertility; gynaecological; antilumour; cytostatic; immunosuppressive; antiarthritic; antiinhemmatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder; gene; ss.

Homo sapiens

×	ΡF	×	PD	×	PN	XX	ŦΤ	ŦŢ	FT	FH	XX	SO	XX	X	ΚW	ΚW	ΚW	KW	ΚW	ΚW	KΨ	XX	DE	XX	DT	XX	AC	×	Ħ
	28-JUN-2001; 2001WO-US20719.		03-JAN-2002.		WO200200710-A2.		/product= "B7-like protein, B7-L_h1"	/*tag= a	CDS 271175	Key Location/Qualifiers		Homo sapiens.		endocrinopathy; lymphoproliferative disorder; gene; s	toxic shock syndrome; allergy; nephropathy; skin disc	reproductive disorder; graft versus host disease; aut	antiasthmatic; nephrotropic; antibacterial; virucide;	antidiabetic; haemostatic; antithyroid; antiulcer; ar	antiinflammatory; dermatological; antipsoriatic; neur	immunosuppressive; anti	Human; B7-like protein; B7-L; antiinfertility; gynaec		DNA encoding human B7-like protein, B7-L_h1.		23-APR-2002 (first entry)		ABK13028;		ABK13028 standard; cDNA; 1175 BP.

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; NAME/KEY: misc_feature
; OTHER INFORMATION: Plasmid pGRO403R
US-08-479-913E-1
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US-08-479-913E-1/c
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; LOCATION:
US-08-185-432-1
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5063 base pairs
TYPE: nucleic acid
STRANDEDMESS: double
 Query Match 3.5%;
Best Local Similarity 75.0%;
Matches 51; Conservative
                                                                                                                                                           NUMBER OF SEQ ID NOS: 6
SOFTWARE: MicroSoft Word 97
SEQ ID NO 1
LENGTH: 6177
TYPE: DNA
                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.5%;
Best Local Similarity 66.3%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 1, Application US/08479913E Patent No. 6416998
                                                                                                                                                                                                                                      APPLICANT: O'Malley, Bert W.
APPLICANT: Tsai, Ming-Jer
APPLICANT: Tsai, Ming-Jer
APPLICANT: Ledebur, Herry C.
APPLICANT: Ledebur, Joseph D.
TITLE OF INVENTION: MODIFIED STEROID HORMONES FOR GENE THERAPY AND METHODS FOR THEIR
FILE REFERENCE: 212/13
CURRENT APPLICATION NUMBER: US/08/479,913E
CURRENT FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 07/939,246
PRIOR FILING DATE: 1992-09-02
                                                                                                                            FEATURE:
                                                                                                                                         ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2928 GCTGTTGCTGTCGCGGATGCAGTGGTAAT 2900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                868 GCTGTAGAAGAAAAAGAGGATTTCGTATT 896
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/185,432
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864..1349
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3439..3736
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1944..3370
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 Score 40.8; DB 4;
Pred. No. 0.14;
0; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length 5063; Pred. No. 0.11;
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 17;
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                                Length 6177;
 Indels
0;
Gaps
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0;
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Search completed: April 29, 2003, 10:49:16 Job time: 88.1906 secs

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RESULT 12
US-08-185-432-3/c
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Patent No. 5750652
                                                                                                                      Sequence 23, Application US/08185432
Patent No. 5750652
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Artava
APPLICANT: Bussea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 869-8864/9
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
                                                                                                           GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TITLE OF I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 790-9090
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                                                                                                                                                                                                                                                                                                    1875 GCTGCTGCTGCTGCTGCTGCTGCTTGCATCTGCAGCTGTTGCTGCTGCTTGTTGCTGCT 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                    APPLICANT:
                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: cDNA
                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                          808 GCTGCTGCTGCCGCCGCCGTCGTTGTTGTGGCTGCCAACTGCTGCTGCTGCTGCTTGTTTCT 867
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STATE: New York
COUNTRY: U.S.A.
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/185,432 FILING DATE: 21-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 59; Conserv
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     INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 869-8864/9741
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                                                   Artavanis-Tsakonas, Spyridon
Busseau, Isabelle
Diederich, Robert J.
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                                      Xu, Tian
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Kenji
DELTEX PROTEINS, NUCLEIC ACIDS, AND
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RESULT 14
US-08-185-432-1/c
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Best Local Similarity 66.3%;
Matches 59; Conservative
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TELEX: 66141 PENNIE
TRELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
EENGTH: 3771 base pairs
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS,
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS
NUMBER OF SEQUENCES: 23
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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TELEFAX: (212) 869-8864/9741
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                                                                                              COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                       CITY: New York
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STREET: 11
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                                                                                                                                    STATE: New York
SOFTWARE:
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EDNESS: double
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1155 Avenue of the Americas
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1155 Avenue of the Americas
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PatentIn Release #1.0,
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Version #1.30
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Indels

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78.1%;

Pred. No. 0.014;

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; LENGTH: 203
; TYPE: DNA
; ORGANISM: p-2093 plasmid
US-09-043-303-7
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                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
   Query Match
                                                                                                        SOFTWARE: PatentIn SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/09043303
Patent No. 6251589
                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09043303 Patent No. 6251589
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                                                                                                                                                                          APPLICANT: TSUJI, Shoji
APPLICANT: SANPEI, Kazujiro
APPLICANT: SANPEI, Kazujiro
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
TITLE OF INVENTION: Primers Therefor
FILE REFERENCE: 0750-0241P
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT FILING DATE: 1998-05-18
EARLIER APPLICATION NUMBER: PCT/JP96/01999
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Best Local Similarity
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CURRENT FILING DATE: 1998-05-18
EARLIER APPLICATION NUMBER: PCT/JP96/01999
EARLIER FILING DATE: 1996-07-18
                                                                                                                                               EARLIER FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and TITLE OF INVENTION: Primers Therefor FILE REFERENCE: 0760-0241P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TSUJI, Shoji
APPLICANT: SANPEI, Kazujiro
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ORGANISM: Homo sapiens
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 3.5%;
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Score 41.6;
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DВ
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US-08-145-617-5/c
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                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                  MOLECULE TYPE:
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APPLICATION NUMBER: US 07/681,494
FILING DATE: 10-JUN-1991
APPLICATION NUMBER: DE P3834636.2
                                                                                                                                                                                                                                                                                                                          TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jackle, Herbert APPLICANT: Tautz, Diethard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
 846 TGCTGCTGCCGTTGTTGTTTCTGCTG 871
                               214 CCGAACTCCAGGCCTCCGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGT 155
                                                786 CCGACGTGTACTATACAATACGCTGCTGCTGCTGCCGCCGTTGTTGTGGCTGCAAC 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 301 N. Washington S
CITY: Falls Church
STATE: Virgin'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       808 GCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCTGCTTGTTTCT 867
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                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                               TELEPHONE: 703-2--
703-241-2848
                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                            LENGTH: 379 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                             nucleic acid
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                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                              single
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                                                                                                                3.5%;
67.4%;
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                                                                                                                                                                                                                                                                                                                                                                       30,330
                                                                                               0,:
                                                                                                           Score 41.2; DB 1;
Pred. No. 0.025;
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Street, P.O. Box 747
                                                                                              Mismatches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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APPLICANT: Lippar
                                                                                                                           TELEFAX: 617-248-7100 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 3292 base pair
                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Uses For DNA Structum
TITLE OF INVENTION: Recognition Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                              MOLECULE TYPE: 1
ORIGINAL SOURCE:
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NAME: Fenton, Gillian M.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                  IMMEDIATE SOURCE:
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CITY: Boston
STATE: MA
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CLONE:
                               ORGANISM:
                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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                                                                                                          nucleic acid
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Donahue, Brian A.
Toney, Jeffrey H.
Bruhn, Suzanne L.
Pil, Pieter M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kellett, Patti
VENTION: Uses For DNA Structure-Specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brown, Steven
                               Saccharomyces cerevisiae
                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                            DNA (genomic)
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                                                                                             double
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64.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 0.031;
0; Mismatches 34;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                  FEATURE:
                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                   CLONE:
                                                                               ORGANISM:
                                                                                                                               TOPOLOGY:
                                                                                                                                             STRANDEDNESS:
                                                                                                                                                            TYPE: NUCLEIC ACID
                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                             NAME: Granahan, Patricia REGISTRATION NUMBER: 32,
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CITY: Lexington
                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                               lambda yPt
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                                                                                                                                                                           3292 base pairs
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Toney, Jeffrey H.
Bruhn, Suzanne L.
                                                                                                                               linear
                                                                              Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pil, Pieter M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                            DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                              US 07/539,906
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                                                                                                                                                                                                                                                                                          32,227
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RESULT 5
US-07-814-964-12/c
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SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
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           TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
                                                            REFERENCE/DOCKET NUMBER: MIT-4787AAA TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                    APPLICATION NUMBER: US FILING DATE: 19911226 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
                                                                                                           FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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LOCATION:
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CITY: Lexington
STATE: MA
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STRANDEDNESS: single
                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                SOFTWARE:
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Similarity 61.8%;
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3292 base pairs
                                                                                                                                                                                                                                                                                                                                                              USA
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Bruhn, Suzanne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Donahue, Brian A.
                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
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519) 535-8949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pieter M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steven
                                                                                                                                                                          US 07/539,906
                                                                                                                                                                                                                                      US/07/814,964
                                                                                                       32,227
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Pred. No. 0.02;
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US-07-814-964-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12,
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Best Local Similarity
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                                                                  INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
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                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                   FILING DATE: 18-JUN-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                SEQUENCE CHARACTERISTICS:
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STRANDEDNESS:
                 TYPE:
                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                    NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                              LENGTH:
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              nucleic acid
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Toney, Jeffrey H.
Bruhn, Suzanne L.
Pil, Pieter M.
                              3292 base pairs
                                                                                    617-861-9540
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double
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                                                                                                                                                                                                                                                                                               US/08/258,442
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                                                                                                                                                                                                             TITLE OF INVENTION: DNA Sequence Encoding the MacIPatent No. 5840491
TITLE OF INVENTION: Disease Gene and Uses Thereof NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
CORRESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08531927B Patent No. 5840491
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NAME/KEY:
LOCATION:
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NFORMATION FOR SEQ ID NO:
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SOTTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MINISTERM
COMPUTER READABLE FORM:
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APPLICATION NUMBER: JP HO
FILING DATE: 21-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                             STREET: Two Militia | CITY: Lexington STATE: Massachusetts
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LOCATION:
                                     COUNTRY: USA
ZIP: 02173-4799
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STRANDEDNESS: single
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REGISTRATION NUMBER: 32,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequence Encoding the Machado-Joseph
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Pred. No. 0.00023;
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US-09-041-886-12/c
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Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: Granning
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COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                  ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A
REGISTRATION NUMBER: 31,8:
                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  868 GCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAA 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          808 GCTGCTGCTGCCGCCGCCGTTGTTGTGGCTGCAACTGCTGCTGCTGCTTGTTTCT 867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4370 La
CITY: San Diego
STATE: Californ:
                   REFERENCE/DOCKET NUMBER:
                                                                                         CLASSIFICATION:
                                                                                                              FILING DATE
                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                            ZIP: 92122
                                                                                                                                                                                                                                                                           COUNTRY:
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REFERENCE/DOCKET NUMBER: ATH95-01A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 21 CLASSIFICATION:
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TELEFAX: 617-861-9540
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               31,815
ER: P-LJ 2626
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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   seq length: 0 seq length: 2000000000
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1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

3: /cgn2_6/ptodata/1.

4: /cgn2_6/ptodata/1.

5: /cgn2_6/ptodata/1.

6: /cgn2_6/ptodata/1.
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Listing first 45 summaries
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    /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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US-09-253-691-3
US-08-531-927B-3
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US-09-041-886-12
US-09-041-886-12
US-08-258-442-12
US-08-328-809-7
PCT US92-11107-12
US-09-043-303-7
US-09-043-303-7
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US-08-456-9803B-6
US-08-453-265-5
US-09-041-886-14
US-08-453-265-5
US-09-043-303-10
US-09-043-303-11
US-08-459-802B-6
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Sequence
                   Sequence 3, Appli
Sequence 1, Appli
Sequence 12, Appli
Sequence 14, Appli
Sequence 5, Appli
Sequence 23, Appli
Sequence 1, Appli
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Sequence 10, Appli
Sequence 11, Appli
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GENERAL INFORMATION:
APPLICANT: Kakizuka, Akira
TITLE OF INVENTION: DNA Sequ
Patent No. 5840491
PITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

Disease Gene

DNA Sequence Encoding the Machado-Joseph and Uses Thereof

ADDRESSEE:

Hamilton, Brook, Smith & Reynolds,

P.C.

RESULT 2 US-08-531-927B-3/c

Sequence 3, Application US/08531927B Patent No. 5840491

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es 62; AACTGCTGCT TGCTGCTGCT CAAAAGAAAT AAAGTGAAGT AAAGTGAAGT	Method and Kit for ucleotide Repeats Sc /09/253,691 2 98-6,278 6 Score 51.8; DB 3; ows	ALIGNMENTS	US-09-043-303-17 US-08-469-802B-4 US-08-267-803B-4 US-08-267-803B-5 US-08-469-802B-5 US-08-267-803B-2 US-08-267-803B-3 US-08-267-803B-3 US-08-267-803B-3 US-09-146-054-8 US-09-146-054-8 US-09-135-994-1 US-08-267-803B-7 US-08-267-803B-7 US-09-043-303-5 US-08-267-803B-1 US-08-267-803B-1 US-08-267-803B-1 US-08-267-803B-1 US-08-267-803B-1
Gaps T 867 T 141 T 141 A 927 A 81	Neuropsychiatric Diseases quence .		Sequence 17, Appli Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 8, Appli Sequence 8, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli
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RESULT 15
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US-09-416-384A-6/c
Sequence 6, Application US/09416384A
Patent No. US20020081584A1
Patent No. US20020081584A1
Patent No. US20020081584A1
PAPLICANT: BLUMENFELD, Marta
APPLICANT: BOUGUELERET, Lydie
APPLICANT: CHUMAKOV, 11ya
APPLICANT: CHUMAKOV, 11ya
APPLICANT: ESSIGUX, Laurent
TITLE OF INVENTION: Genes, proteins and biallelic markers related to central.
FILE REFERENCE: GENSET 045AUS
CURRENT FILING DATE: 1999-10-12
CURRENT APPLICATION NUMBER: US/09/416,384A
PRIOR APPLICATION NUMBER: 60/106,457
PRIOR APPLICATION NUMBER: 60/103,955
PRIOR APPLICATION NUMBER: 60/103,955
PRIOR APPLICATION NUMBER: 60/103,955
PRIOR FILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: 60/132,277
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 71
SOPTWARE: Patent.pm
SEQ ID NO 6
Search completed: April 28, 2003, 20:36:16 Job time: 2140.37 secs
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; ORGANISM: mus musculus
US-09-416-384A-6
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Best Local s
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Best Local Similarity 79.7%;
Matches 51; Conservative
                                                                                 867 TGCTGTAGAAGA 878
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276 TGCTGTTGGTGA 265
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                                                                                                                                                                                                                                                          y Match 3.7%; Score 43.2; DB 10; Length 1791; Local Similarity 75.0%; Pred. No. 0.017; hes 54; Conservative 0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43.2; DB 10; Length 459; Pred. No. 0.0067; 0; Mismatches 13; Indels 0
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OTHER INFORMATION: EXPRESSED IN BY474, SIGNAL = 47
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 53
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 69
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 27
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 16
OTHER INFORMATION: EXPRESSED IN BLAIN, SIGNAL = 21
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 29
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 29
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OTHER INFORMATION: SWIRESSED IN BORN MARROW, SIGNAL = 21
OTHER INFORMATION: SWIRESSED IN BORN MARROW, SIGNAL = 21
OTHER INFORMATION: SWISSPROT HIT: P53360, EVALUE 4.00e-15
OTHER INFORMATION: EST_HUMAN HIT: AW409956.1, EVALUE 1.00e-58
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04
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                                                      Matches
                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Annomax
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MAP TO AC009954.1 OTHER INFORMATION: EXPRESSED IN BT47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 293
808 GCTGCTGCTGCCGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTGTTCT 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                              Local
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                                                                                 Similarity
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Hanzel, David K.
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                                                        Score 43.2; DB Pred. No. 0.005; 0; Mismatches
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RESULT 14
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
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PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: 2000-08-03
PRIOR APPLICATION NUMBER: 2002-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
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CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: US 60/207,456
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                                 OTHER INFORMATION: MAP TO AC009954.1
OTHER INFORMATION: EXPRESSED IN BT477.
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ORGANISM: Homo sapiens
FEATURE:
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2000-06-30
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INFORMATION: INFORMATION:
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Chen, Wensheng
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    XI EXPRESSED IN BT474, SIGNAL = 43

X EXPRESSED IN PLACENTA, SIGNAL = 53

X EXPRESSED IN HEART, SIGNAL = 69

X EXPRESSED IN HEART, SIGNAL = 27

X EXPRESSED IN FETAL LIVER, SIGNAL = 45

X EXPRESSED IN HELA, SIGNAL = 45
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                                                       FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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APPLICANT:
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CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,360
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 1206
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 151
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Best Local Similarity
                    PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                          TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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PRIOR APPLICATION NUMBER: JP 00/280988
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LOCATION: (1)...(455)
OTHER INFORMATION: n = A,T,C or G
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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Pred. No. 0.0038;
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US-09-864-761-18923/c
                                                                 Db 510748 CTGCTGCAGAAGAAGGACGAGTTCGACGTCGTTCTCGAA 510788
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US-09-738-626-1
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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APPLICANT:
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NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
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PRIOR FILING DATE: 1999-12-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 CTGCTGCAGAAGAAGGACGACGTTCGACGTTCTCGAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866 CTGCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAA 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   806 ACGCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTGTTT 865
                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 ACGTAACCGCAGCTGCTCCAGTTGCAGTTGCTGCTGCAGGCGCGCGAGGCGGCGAAGCTG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                           65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAYASHI, MIKII
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIZOGUCHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENOH, AKIHIRO
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HARUHIKO
                                                                                                                                                                                                                                      3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIROSHI
                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                  Score 43.4; DB 9; Length 3309400; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43.4; DB 9; Length 384; Pred. No. 0.0052;
                                                                                                                                                                                                                 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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; GENERAL INFORMATION

; Sequence 18923, Application US/09864761
; Patent No. US20020048763A1

WPI; 2000-662424/64

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RESULT 15
AAI95221
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to the use of a plasmid vector array containing a neuropsychiatric gene containing trinucleotide repeats. Tri-nucleotide repeats and their expansion areknown to be involved in a number of diseases including fragile X syndrome, spinocerebellar ataxia type III, hereditary hypertrophic, cardiomyopathy, dentatorubral and pallidoluysian atrophy (DRPLA), spinocerebellar ataxia, Marfan syndrome; X-linked spinobubar atrophy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid vector arraying neuropsychiatric gene more than copy number containing trinucleotide repeats its use thereof \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 403 BP; 121 A; 108 C; 105 G; 69 T; 0 other;
                                                                          Nucleic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour marker
                                                                                                                                                                                                                                                07-MAR-2000; 2000JP-0159195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI95221 standard; cDNA; 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the CAG tri-nucleotide repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents a nucleotide sequence of the invention showing the
                                 Claim 1; Page 977-978; 2979pp; Japanese.
                                                                                                                                                                                                                                                                                02-MAR-2001; 2001WO-JP01629.
                                                                                                                                                                                                                                                                                                                                          WO200166719-A1
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                      Human; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human neuroblastoma expressed polynucleotide SEQ ID NO 1296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI95221;
The invention relates to novel genes (AAI93926-AAI97963) expressed
                                                                                                                                          WPI; 2001-565584/63.
                                                                                                                                                                       Nakagawara A;
                                                               for anti-cancer agents
                                                                                                                                                                                                    (HISM ) HISAMITSU
                                                                                                                                                                                                                  (CHIB-) CHIBA PREFECTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            933 GCTGTAGAAGAAAAAGAGGATTTCGTATTCAAATTTCAAAAGAAATCTGAAAAAGAGAGAAGA 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            873 GCTGCTGCTGCCGCCGCCGTCGTTGTTGTGGCCTGCCAACTGCTGCTGCTGCTTGTTTCT 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  993 CAAACAAAGAAACTGAGACAGAAAGTGGAAA 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 AACTTAAAAGAATAAATACACCATGAGAAAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGTTGCTGCTGTGTGTGAAACATTCAAAAGTGAAGTATATTTAAAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                     PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                      malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51.8; DB 21
Pred. No. 0.00042;
0; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                        tumour marker; N-myc; TrkA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 403;
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                                                                                                                                          Matches
                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar
                                                                                                                                                                                                              Sequence 742 BP; 180 A; 183 C; 152 G; 219 T; 8 other;
                                                                                                                                                                                                                                                 to that for N-myc and TrkA genes.
403 GAAATCTATTTCTCACAGTTCTGGAGGCTAGAAGT 438
                                                                      343 GTATATTAGTTTATAAGGCTCCCATAACAAAGCACCACAGACTGGGTGGCTTAAACAAAA 402
                    83 GAAAGGCATTTGCTCACGGTTCCAGAAGCTGTAGGT 118
                                                                                                       23
                                                                                        GTGGATCAGTTTCCTAGGCTGCCATAACAAAGCACCATAACCTGGTGGCTTAGAACAATG 82
                                                                                                                                          l Similarity
67; Conserv
                                                                                                                                          Conservative
                                                                                                                                                          4.0%;
                                                                                                                                            0;
                                                                                                                                          Score 49.6; DB 2
Pred. No. 0.0024;
D; Mismatches 2
                                                                                                                                                                             DB 22;
                                                                                                                                              29;
                                                                                                                                              Indels
                                                                                                                                                                               Length
                                                                                                                                              0;
                                                                                                                                              Gaps
                                                                                                                                               0;
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Search completed: April 29, Job time : 322.05 secs 2003, 11:05:46

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ACC XXX ACC XX
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AAX89891/c
ID AAX898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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      Diagnosis of spinocerebellar ataxia type III (SCA III) syndrome using techniques which ensure highly accurate diagnosis
                                                                                                         WPI; 1999-527634/44.
                                                                                                                                                                      Jin DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to the use of a plasmid vector array containing a neuropsychiatric gene containing trinucleotide repeats. Tri-nucleotide repeats and their expansion are known to be involved in a number of diseases including fragile X syndrome, spinocerebellar ataxia type III, hereditary hypertrophic, cardiomyopathy, dentatorubral and pallidoluysian atrophy (DRPLA), spinocerebellar ataxia, Marfan syndrome; X-linked spinobubar atrophy. The present sequence represents
                                                                                                                                                                                                                                                                                                             26-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                       18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                02-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spinocerebellar ataxia type III (SCAIII) gene fragment.
                                                                                                                                                                                                                      (SMSU ) SAMSUNG FINE CHEM CO LTD
                                                                                                                                                                                                                                                    (JIND/) JIN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09943852-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCAIII syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spinocerebellar ataxia type III; SCAIII; reverse dot hybridisation; PCR-microplate hybridisation; PCR-MPH; trinucleotide repeat; TNR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX89891 standard; DNA; 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 389 BP; 107 A; 92 C; 91 G; 93 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           been represented by an n to keep nucleotide numbering correct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note; Nucleotides which were illegible in the specification have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a tri-nucleotide repeat related sequence #5 disclosed in the scope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            873 GCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTGTTTCT 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        993 CAAACAAAGAAACTGAGACAGAAAGTGGAAATGAA 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AANTTAAAAGAANACCTACACCATGAGNTANAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAAAAAGAGAAGA 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGTTGCTGCTGTGTGTGAAACATTCAAAAGTGAAGTATATTTAAAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.28;
Similarity 57.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                          98KR-0006278
                                                                                                                                                                                                                                                                                                                                                                 99WO-KR00078
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137..139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
137..355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "trinucleotide repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
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Pred. No. 0.00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 389;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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PD XX PF YAX YAX PA XX PA AXX PA AXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
ABK10240/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db
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Best Local :
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           Jin DG;
                                                                               25-JUN-1998;
                                                                                                        25-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                        spinocerebellar ataxia type III; DRPLA; neurops hereditary hypertrophic cardiomyopathy; Marfan dentatorubral and pallidoluysian atrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the diagnosis of spinocerebellar ataxia type III (SCAIII) syndrome using reverse dot hybridisation or PCR-microplate hybridisation (PCR-MPH). The method comprises attaching a potion of the SCAIII gene containing 73 copies of the trinucleotide (CAG) repeat unit (the present sequence) to a substrate, and hybridising with amplified testee genomic DNA containing copies of the trinucleotide units, PCR amplified with labeled primers (AAXB9889-90). The new method is useful for diagnosis of SCAIII syndrome, and for determining the severity of the disease. The present sequence represents the SCAIII gene fragment
                                 (SMSU ) SAMSUNG MEDICAL CENT (JIND/) JIN D G.
                                                                                                                                     15-JAN-2000
                                                                                                                                                                KR2000003004-A
                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                  repeat_unit
                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                           spinocerebellar ataxia; X-linked spinobubar atrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Trinucleotide repeat sequence #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK10240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK10240 standard; DNA; 403
                                                                                                                                                                                                                                                                                                                                                                                                      spinocerebellar
                                                                                                                                                                                                                                                                                                                                                                                                                   Trinucleotide repeat; fragile X syndrome; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 397 BP; 124 A; 104 C; 104 G; 65 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the disease. The present sequence בייינים containing 73 trinucleotide (TNR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 12-13; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            993 CAAACAAAGAAACTGAGACAGAAAGTGGAAA 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     873 GCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCTGGTTGTTTCT 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTTAAAAGAATAAATACACCATGAGAAAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGTTGCTGCTTTTGCTGCTGTCTGAAAACATTCAAAAGTGAAGTATATTTAAAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGTAGAAGAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAAAAAGAGAAGA 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                               98KR-0024064
                                                                                                        98KR-0024064
                                                                                                                                                                                                                                                                                         Location/Qualifiers 152..347
                                                                                                                                                                                                                                                  /rpt_type=
152..154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.9%;
                                                                                                                                                                                                            b
"CAG type repeat"
                                                                                                                                                                                                                                                                TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; DB 20;
0.00042;
                                                                                                                                                                                                                                                                                                                                                                                                    neuropsychiatric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
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RESULT 11
ABL29756
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and pallidoluysian atrophy (DRPLA), spinocerebellar ataxia, Marfan syndrome; X-linked spinobubar atrophy. The present sequence represents a nucleotide sequence of the invention showing the the CAG tri-nucleotide repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 277 BP; 80 A; 66 C; 62 G; 69 T; 0 6ther;
                                                                          useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG1840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ ID NO 40741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL29756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL29756 standard; DNA; 7029 BP
                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                                                 New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                Claim 1; SEQ ID NO 40741; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                   Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                  (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         933 GCTGTAGAAAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAAAAAAGAGAGA 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 AACTTAAAAGAATAAATACACCATGAGAAAA 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
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2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds.
                                                                                                                                                                                                                                                                                                                                                                     Li PWD,
                                                                                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                     Myers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
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                                                                                                                                                                                   The invention
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Sequence 7029 BP; 1426 A; 1440 C; 1945 G;

2218

T; 0 other;

Disclosure; Fig 10; 23pp; Korean

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ABK10248/c
ID ABK102
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RESULT 12
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Best Local Similarity
                                                                                                                                                                                                                                                                                                 misc_difference 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5560 GCTGTATTTGCTAAAAAGAAGTAATCATTAATTTCCGGTAAAAA 5603
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misc_difference 46
                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  spinocerebellar ataxia type III; DRPLA; neuropsychiatric; hereditary hypertrophic cardiomyopathy; Marfan syndrome; dentatorubral and pallidoluysian atrophy; spinocerebellar ataxia; X-linked spinobubar atrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trinucleotide repeat; fragile X syndrome; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tri-nucleotide repeat related sequence #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK10248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK10248 standard; DNA; 389
                   Plasmid vector arraying neuropsychiatric gene more than copy number containing trinucleotide repeats its use thereof \boldsymbol{\cdot}
                                                                                                                                                                                                                                               misc_difference
                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                    misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                  misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAY-2002 (first entry)
                                                                     Jin DG;
                                                                                                                                            25-JUN-1998;
                                                                                                                                                                                   KR2000003004-A
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      873 GCTGCTGCTGCCGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTTCT 932
                                                  WPI; 2000-662424/64
                                                                                        (SMSU ) SAMSUNG MEDICAL CENT (JIND/) JIN D G.
                                                                                                                      25-JUN-1998;
                                                                                                                                                               15-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                933 GCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAA 976
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                                                                                                                        98KR-0024064
                                                                                                                                             98KR-0024064
                                                                                                                                                                                                                                                /note=
: 276
                                                                                                                                                                                                                                                                             /note=
203
                                                                                                                                                                                                                                                                                                                                                                      /note= "Illegible in the 31
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.3%;
                                                                                                                                                                                                                                                                                                                                                  "Illegible in the specification"
                                                                                                                                                                                                                             "Illegible in
                                                                                                                                                                                                                                                                                        "Illegible in the specification'
                                                                                                                                                                                                                                                                                                                    "Illegible in the
                                                                                                                                                                                                                                                         "Illegible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52.8; DB 23; Pred. No. 0.001; 0; Mismatches 32;
                                                                                                                                                                                                                                                          ĺ'n
                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                            the specification"
                                                                                                                                                                                                                                                                                                                     specification"
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                                                                                                                                                                                                                                                          specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constitution to the transport of the matter of the seminal verification of the tentum of the observation of the seminal vesicle hyperplasia in transpenic mice overexpressing B7-L cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of (1) are useful for the treatment of the testicular cancer and cancers of haematopoietic system. B7-L polypeptide testicular cancer and cancers of haematopoietic system. B7-L polypeptide concerts of the manual concerts of haematopoietic system. B7-L polypeptide concerts in allograft transplantation, graft versus host disease. B7-L polypeptide concerts in alloyated diseases and autoimmune diseases. B7-L concerts of molecules are useful for alloyating the symptoms associated with concerts of the symptoms associated wi
                                                                                                                                                                                                                                                                                                                                                    Matches 236;
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 895 BP; 250 A; 223 C; 212 G; 210 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferation, including arteriosclerosis and vascular restenosis.
Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The polypeptide, polynucleotide encoding it and antibody again useful for treating B7-like polypeptide-related disease, disor conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and antibody again.
229 TAACCAAATGGTGGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACCGCTT
                                                                                                                            169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents the coding sequence of mouse B7-L_m2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 6; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                  235 CAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTT
                                                                                                                                                                                                                                          109
                                                                                                                                                                                                                                                                          115 AGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCCAGAATGCCAACAGTCCTGAAGGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC
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28-NOV-2000; 2000US-0729264
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                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated B7-like (B7-L) polypeptide (I) polypeptide, polynucleotide encoding it and antibody against (I)
                                                                                                          CTCAGAGGCTCACTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTCT
                                                                                                                                                             CTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCT 234
                                                                                                                                                                                                                     AGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGGA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-130881/17.
                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                              Conservative
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73.8%;
                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                        Score 185.6; DB 2
Pred. No. 5.8e-41;
0; Mismatches 84
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                                                                                                                                                                                                                                                                                                                                                                                           DB 24; Length 895;
                                                                                                                                                                                                                                                                                                                                           84;
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                                                                                                                                                                                                                                                                                                                                  Gaps
                                                        294
                                                                                                             228
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Db
RESULT 10
ABK10239/c
ID ABK102
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                                                       Disclosure; Page 12; 23pp; Korean
                                                                          Plasmid vector arraying neuropsychiatric gene more than copy number containing trinucleotide repeats its use thereof \boldsymbol{\cdot}
                                                                                                             WPI; 2000-662424/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trinucleotide repeat; fragile X syndrome; ds; DRPLA; spinocerebellar ataxia type III; Marfan syndrome; hereditary hypertrophic cardiomyopathy; neuropsychiatric; dentatorubral and pallidoluysian atrophy; spinocerebellar ataxia; X-linked spinobubar atrophy.
                                                                                                                                   Jin DG
                                                                                                                                                      (SMSU ) SAMSUNG MEDICAL CENT (JIND/) JIN D G.
                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                     25-JUN-1998;
                                                                                                                                                                                                         25-JUN-1998;
                                                                                                                                                                                                                              15-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trinucleotide repeat sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK10239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK10239 standard; DNA; 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 TGCTTACCTTACCGTCCAAG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 CACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATGT
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                                                                                                                                                                                     98KR-0024064
                                                                                                                                                                                                         98KR-0024064
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/note= "CAG type repeat"
198..222
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198..200
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152..154
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containing a neuropsychiatric gene containing trinucleotide repeats. Tri-nucleotide repeats and their expansion areknown to be involved in a number of diseases including fragile X syndrome, spinocerebellar ataxia type III, hereditary hypertrophic, cardiomyopathy, dentatorubra

hereditary hypertrophic, cardiomyopathy, dentatorubral

This invention relates to the use of a plasmid vector array

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ABK13034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK13034;
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                                                                                               seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid autoimmune diseases such as systemic lupus erythematosus, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding mouse B7-like protein, B7-L_m3.
                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polypnetide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, disorders oconditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200200710-A2.
                   arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They
                                                                                                                                                                                                                                                                                                                       proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (I) plays a role in growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New B7-like polypeptides, polynucleotides and their modulators, of diagnosing, preventing and treating reproductive, immune and prollferative disorders, e.g. cancer and arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUN-2000; 2000US-214512P.
28-NOV-2000; 2000US-0729264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 7; 135pp; English.
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also useful as immunosuppressive agents for bone marrow and organ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "B7-like protein, B7-L_m3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 754 BP; 220 A; 191 C; 175 G; 168 T; 0 other;
                                                                                                                                                                                                                                   antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; altergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                   Mouse; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirherantiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antipler; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding mouse B7-like protein, B7-L_m2.
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                                           WO200200710-A2
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                                                                                                                                53..865
                                                                                     /product- "B7-like protein, B7-L_m2"
                                                                                                                                                  Location/Qualifiers
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73.8%;
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                                 CTGCAAACATGAGGACAA------ACAAAGCAGATCCGGAGACAAAGTTAAA
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                                                                                                                                                                        AAGTGGAAATGAAAACTCCGGCTACAATTCAGATGAACAAAAGACCACAGAAAACCGCTTC 1074
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                                                                        TCTCCCTCCTAAATCTGCTGAAGTCAGCCTTCCAGAAAAACGCAGCAGTA-----GCCT
                                                                                                                                                 AAGTGGAAAGGAAAACTACGGGTACAGTTCGGATGAGGCAAAGGCTGCACAGACTGCATC
                                                                                                                                                                                                                                                           TTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTTCTGCTGTAGAAGAAAAAAGAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGGTTCAGCCTCCACCTGACAGTATTGGAGAGGA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------AGGCCCAGCACTGCCGACCTGGGCCATCATCCTGCTGGCAGTGGCCTT
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human placenta - \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 401 BP; 105 A; 98 C; 111 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #5268 used to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI36582;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; microarray; human; placenta; antenatal diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2001
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CACCTCTCAGAG 401
                                               CACCTCTCAGAG 306
                                                                                                                                 CAGTGACATGGTGGTGGTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTT
                                                                                                                                                                                                                                      CTCCCAGGCTCGCATCCAACTGCACCGTCTCCCCAGGGCTGGAAGCTCATCATGTGGGCTCT
                                                                                                  CAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTT
                                                                                                                                                                                                          CTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCT
                                                                                                                                                                                                                                                                                                                  AGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATGCAAGAGTCCTGAAGGG 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID No 5268; 654pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
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99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 188.8; DB Pred. No. 5e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
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Mouse; B7-like protein; B7-L; antiinfertility; gynaecological; antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder;
                                                                                                                                                                                                                                                                                                           1021
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                                                                                                                                                                                               ABK13032;
                                                                                                                               DNA encoding mouse B7-like protein, B7-L_m1.
                                                                                                                                                                 23-APR-2002
                                                                                                                                                                                                                               ABK13032 standard;
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                                                                                                                                                                                                                                                                                                           CTCCTCACCAGAGAAGACATAGACCT 1046
                                                                                                                                                                                                                                                                                                                                                                                        CTCTCCCTCCCAAATCCTGTGAATCCAGTGATCCTGAACAAGAAACAGTAGCTGTGGCC
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                                                                                                                                                                                                                               CDNA; 1195
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molecules are useful for alleviating the symptoms associated with diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes, immune thrombocytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and diabetes mellitus. They are also useful as immunosuppressive agents for performance organs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endocrinopathy; lymphoproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seminal vesicle hyperplasia in transgenic mice overexpressing B7-L polypeptide. Hence modulators of (I) are useful for the treatment of cancer including seminal vesicle cancer, lung, brain, breast, ovarian, testicular cancer and cancers of haematopoietic system. B7-L polypeptide pathway can be manipulated to regulate cytotoxic T-lymphocyte response in allograft transplantation, graft versus host disease, T-cell dependent B-cell mediated diseases and autoimmune diseases. B7-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 5; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-2000;
28-NOV-2000;
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                                                              treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present
                                                                                                                                                                                           proliferation, including arteriosclerosis and vascular restenosis. Antagonists of B7-L polypeptides are useful for alleviation of tox shock syndrome or allosensitisation due to blood transfusions, and
                                                                                                                                                                                                                                                       transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for enhancing the immune response to tumours. (I) plays a role growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polypeptide, polynucleotide encoding it and antibody useful for treating B7-like polypeptide-related disease.
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                                            represents the coding sequence
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2000US-0729264
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polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations are expensible for genetic disorders or other traits to assess biodiversity and the produce of the traits and activity and the produce of the traits and activity and the produce of the traits and the produce of the prod
                                                   and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIF at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc useful for enhancing the immune response to tumours. (1) plays a role in cc growth and maintenance of cancer cells based on the observation of cc seminal vesicle hyperplasia in transgenic mice overexpressing B7-L cc polypeptide. Hence modulators of (1) are useful for the treatment of crancer including seminal vesicle cancer, lung, brain, breast, ovarian, ct testicular cancer and cancers of haematopoietic system. B7-L polypeptide cancer including seminal vesicle cancer, lung, brain, breast, ovarian, ct testicular cancer and cancers of haematopoietic system. B7-L polypeptide cancer including transplantation, graft versus host disease, T-cell concerned to transplantation, graft versus host disease. B7-L cc dependent B-cell mediated diseases and autoimmune diseases. B7-L cc diseases involving chronic immune cell dysfunction or to treat autoimmune diseases such as systemic lupus erythematosus, rheumatoid carthritis, multiple sclerosis, diabetes, immune thrombocytopenic confiammatory bowel disease (Crohn's disease and ulcerative colitis), crace is cuseful as immune courts and brease mellitus. They
                                                                                                                                                                                                                                                                                 Matches 1102;
                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                 Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coellar disease, anaemia, thrombocytopenias, Guilliain Barre syndrome and myssthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present sequence represents the coding sequence of human B7-L_h4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival. B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    miscarriage, preterm labour and delivery and endometriosis) and proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 8..1168
                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "B7-like protein,
                                                                                                                                                                                                                           MD,
                                                                                                                     e.g. cancer and arteriosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases such as systemic lupus erythematosus, rheumatoid carthritis, multiple sclerosis, diabetes, immune thrombotytopenic purpura and psoriasis, chronic inflammatory disease such as inflammatory bowel disease (Crohn's disease and ulcerative colitis), Carave's disease, Hashimoto's thyroiditis and diabetes mellitus. They are also useful as immunosuppressive agents for bone marrow and organ transplantation or to prolong graft survival B7-L molecules are also useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis.

Antagonists of B7-L polypeptides are useful for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain Barre syndrome and myasthenia gravis, and lymphoproliferative disorders such as multiple myeloma. The present of sequence represents the coding sequence of human B7-L_h2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 1125;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferative disorders. Antibodies, soluble proteins comprising extracellular domains and other regulators of B7-L polypeptides are useful for enhancing the immune response to tumours. (1) plays a rol growth and maintenance of cancer cells based on the observation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1168 BP; 299 A; 302 C; 288 G; 279 T; 0 other;
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TCCGGAGCCCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAA
                                                                                                             GCTCCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGT
                                                                                                                                                                                                                                                                                           GCATGGATCTGCCTTACCCTTACCGTCCAAGTTATGGGAGAGCTGTTCATTCCCAGTGTTAA
                                                                                                                                                                                                                     TCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACCCG
                                                                                     GCTCCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGT
                                                                                                                                                                           TCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACCTG
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Pred. No. 2.6e-299;
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cc proliferative disorders. Antibodies, soluble proteins comprising cc extracellular domains and other regulators of B7-L polypeptides are cc useful for enhancing the immune response to tumours. (I) plays a role in crowth and maintenance of cancer cells based on the observation of cc growth and maintenance of cancer cells based on the observation of cc cancer including seminal vesicle cancer, lung, brain, breast, ovarian, cc testicular cancer and cancers of (I) are useful for the treatment of cc cancer including seminal vesicle cancer, lung, brain, breast, ovarian, cc pathway can be manipulated to regulate cytotoxic T-lymphocyte response cc in allograft transplantation, graft versus host diseases. B7-L cell cdependent B-cell mediated diseases and autoimmune diseases. B7-L cc dependent B-cell mediated diseases and autoimmune diseases. B7-L cc autoimmune diseases such as systemic lupus crythematosus, rheumatoid cc arthritis, multiple sclerosis, diabetes, immune thrombocytopenic cc inflammatory bowel disease, cronic inflammatory disease such as purpura and psoriasis, chronic inflammatory disease such as computation or to treat also useful as immunosuppressive agents for bone marrow and organ cc useful for diagnosis and treatment of diseases involving abnormal cell proliferation, including arteriosclerosis and vascular restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antidiabetic; heemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; endocrinopathy; lymphoproliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK13028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated B7-like (B7-L) polypeptide (I). The polypeptide, polypnectide encoding it and antibody against (I) useful for treating B7-like polypeptide-related disease, disorders oconditions including reproductive disorders (e.g. infertility, miscarriage, preterm labour and delivery and endometriosis) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; B7-like protein; B7-L; antiinfertility; gynaecological;
antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic;
antiinflammatory; dermatological; antipsoriatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding human
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28-NOV-2000; 2000US-0729264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferative
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/product= "B7-like
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                                                                                     ACCATGCTTCTGACGCCGACGTGTACTCTTACAATACGCTGCTGCTGCTGCTGCCGCCGTCGT
                                                                                                                                                        TTACCGAGTTTAGGTTTTTCATTGCCTACTTGGGGCAAAGTTGGACTTGGACTAGCAGGC
                                                                                                                                                                                                                           GTGATTCGGTGTCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGTATTATCAAGT 775
                                                                                                                                                                                                                                                                            ATTTCCTGGGAGCTCGGTCTGGTCAGCCATTCAAGCTATTATTTTGTTCCGGAGCCC
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 TGTTGTGGCTGCAACTGCTGCTGCTGCTGTTGTTTCTGCTGTAGAAGAAAAAGAGGATTT
                                  TGTTGTGGCTGCAACTGCTGCTGCCGTTGTTTCTGCTGTAGAAGAAAAAAGAGGATTT
                                                                   ACCATGCTTCTGACGCCGACGTGTACTCTTACAATACGCTGCTGCTGCTGCCGCCGTCGT
                                                                                                                                      TTACCGAGTTTAGGTTTTTCATTGCCTACTTGGGGCAAAGTTGGACTTGGACTAGCAGGC
                                                                                                                                                                                                          GTGATTCGGTGTCCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGTATTATCAAGT
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Pred. No. 1.6e-300;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shock syndrome or allowers treatment of allergy, asthma and hypersensitivity reactions, treatment of allergy, asthma and hypersensitivity reactions, nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, and myasthenia gravis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferation, including arterioscierosis and vascului including anterioscierosis and vascului for alleviation of toxic shock syndrome or allosensitisation due to blood transfusions, and for allosensitisation due to blood transfusions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (extrinsic alveolitis), vasculopathies, coeliac disease, anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia gravis, ar lymphoproliferative disorders such as multiple myeloma. The present sequence represents the coding sequence of human B7-L_h3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New B7-like polypeptides, polynucleotides and their modulators, useful for diagnosing, preventing and treating reproductive, immune and proliferative disorders, e.g. cancer and arteriosclerosis
                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1240 BP; 318 A; 319 C; 305 G; 298 T; 0 other;
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181 GGCTGGCTTCAACTGCACCGTCTCCCCAGGGCTGGAAGCTCATGATGATGATGA 240
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28-NOV-2000; 2000US-0729264.
                                                                                                          121 TGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGTCCTGAAGGGCTCCCA 180
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ABK13032 AAI36582		85.8 1139 24 ABK13031 62.7 1392 23 AAS92356	90.6 1175 24 ABK13028 90.2 1168 24 ABK13029	100.0 1240 24 ABK13030	Result Query No. Score Match Length DB ID Descr
DNA encoding mouse	DNA encoding mouse Probe #5268 used t	DNA encoding DNA encoding	DNA encoding	DNA encoding human	Description

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ABL29757 ABL26941	AAF93812	ABL25652	ABL28444	ABL25653	ABL28445	AAS30941	ABL24570	ABL24571	ABL16096	ABL16097	ABV56338	ABV47976	ABV54466	AAK82884	AAS36073	ABL24482	ABL24483	AAK78411	AAF75339	AAX98974	AAX98588	ABL03352	ABL03353	AAX84442	AAN91773	AAQ12002	AAN91578.	ABL16830	AAI95221	ABK10240	AAX89891	ABK10248	ABL29756	023	
Drosophila melanog										mela	ct			Human immune/haema	Human cardiovascul	Drosophila melanog	Drosophila melanog	Human immune/haema	Human TGF-beta rec	Human validated ca	Human cancer cell	Drosophila melanog	Drosophila melanog	Mouse brain CNG-1	Rat androgen recep	Full-length rat an	Rat androgen recep	Drosophila melanog	Human neuroblastom	Trinucleotide repe	Spinocerebellar at	Tri-nucleotide rep	Drosophila melanog	Trinucleotide repe	

ALIGNMENTS

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RRSSULT 1
ABK13030
ID ABK13030
AC ABK1
XX ABK1
XX ABK1
XX ABK1
XX BINA
DT 23-A
DT 23-A
DT ABK1
XX DNA
AX DNA
AX DNA
AX ANTI
KW ANTI
                                                                                                                                                    DNA encoding human B7-like protein, B7-L_h3.
                                                                                                                                                                                 23-APR-2002 (first entry)
                                                                                                                                                                                                            ABK13030;
                                                                                                                                                                                                                                      ABK13030 standard; cDNA; 1240 BP
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Human; B7-like protein; B7-L; antiinfertility; gynaecological: antitumour; cytostatic; immunosuppressive; antiarthritic; antitheumatic; antiinflammatory; dermatological; antipsoriatic; neuroprotective; antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic; antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer; reproductive disorder; graft versus host disease; autoimmune disease; toxic shock syndrome; allergy; nephropathy; skin disorder; gendocrinopathy; lymphoproliferative disorder; gene; ss. Homo sapiens

Ų	X	PD	XX	PN	XX	FΤ	FΤ	FT	FΗ	XX
28-JUN-2001: 2001WO-US20719.		03-JAN-2002.		WO200200710-A2.				CDS	Key	
01WO-US20719.						/product= "B7-like protein, B7-L_h3	/*tag= a	801240	Location/Qualifiers	

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Search completed: April 29, 2003, 14:51:53 Job time: 4716.78 secs

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Query Match
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Conservative
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/rpt_family="MLT1E"
20645. . 20910
                                                                                                    complement(22325. .22806)
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/note="MZEF, score = 79.4%"
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21483...21781
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19945. . 20020
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/evidence=not_experimental
complement(18219. 18349)
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/note="GRAIL, score = 72.000%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="MERVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimenta
15369. .16268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
/rpt_family="MLT1C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="GenScan, score = 2.99%, comment = Internal_exon 131
bp frame: 1 phase: 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/rpt_family="MLT1C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="MIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family-"LTR16C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="GC score = 10.60 (249bp); Region: GC content"
                                                                                                                     /evidence=not_experimental
                                                                                                                                                                             /evidence=not_experimental
/rpt_family="AluJb"
                                                                                                                                                                                                                                                                                     /evidence=not_experimental
/rpt_family="MLT1F"
                                                                                                                                                                                                                                                                                                                                                                                                                              /note="homology = 100.00%, score = 38, counts = 2"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Xpound exon prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="GRAIL, score = 81.000%, comment = excellent shadow"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
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                                                                   /rpt_family="MLT1C"
                                                                                     /evidence=pot_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        frame: 1 phase:
             9.6%; Score 119; DB 9; 100.0%; Pred. No. 1.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _family="MLT1C"
                                                                                                                                                                                                                                                                                                                                                                                              _unit=ttcttgcacacttctctgttgagaggtcggtttatcgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .19350
0;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comment =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           score = 60% (0%)"
                               Length 40205;
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ORGANISM
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MEDLINE
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Matches 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18694 AGGTGTGAGTCCAGCCAACAGTGTGGATCAGTTTCCTAGGCTGCCATAACAAAGCACCAT 18753
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Park,H.-S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.-K., Soeda,E.,
Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
Patterson,D., Reichwald,K., Rump,A., Schilhabel,M.B., Schudy,A.,
Patterson,D., Reichwald,K., Rudoh,J., Kawasaki,K., Asakawa,S.,
Zimmermann,W., Rosenthal,A., Kudoh,J., Kawasaki,K., Asakawa,S.,
Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G.,
Hornischer,K., Brandt,P., Scharfe,M., Schoen,O., Desario,A.,
Hennischer,K., Rauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S.,
Hennig,S., Riesselmann,L., Dagand,E., Haaf,T., Wehrmeyer,S.,
Borzym,K., Gardiner,K., Nizetic,D., Francis,F., Lehrach,H.,
Reinhardt,R. and Yaspo,M.Laure.
The DNA sequence of human chromosome 21
Nature 405 (6784), 311-319 (2000)
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Homo sapiens chromosome 21 clone PAC
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Rump,A., Dagand,E., Hildmann,T., Nordsiek,G., Drescher,B., Weber,J., Schattevoy,R., Yaspo,M.-L. and Rosenthal,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biotechnology, Beutenbergstr. 11, Jena 07745, Germany On Feb 27, 2002 this sequence version replaced gi:3171153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (05-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-FEB-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany 4 (bases 1 to 170121)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rump,A., Dagand,E., Hildmann,T., Nordsiek,G., Drescher,B., Weber,J., Schattevoy,R., Yaspo,M.-L., Rosenthal,A., Yaspo,M.-L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-MAY-1998) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
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                                                                                                                                                                              /map="21q22.3"
/clone="PAC 70124"
/s36756 c 37509 g 50672 t
                                                                                                                                                                                                                                                                                                             /chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
9.6%; Score 119; DB 9;
100.0%; Pred. No. 1.8e-17;
rative 0; Mismatches 0;
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NC 70124 map 21q22.3, complete
                                                                           Length 170121;
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Gaps

0;

/note=" /evider	/rpt_family="L2" exon	<pre>repeat_region complement(43304433) /evidence=not_experimental</pre>	repeat_region complement(3874. 4176) /evidence=not_experimental	/note="Xpound exon prediction, score = 84% (0%)" /evidence=not experimental	/rpt_fa	repeat_region complement(3213558)	-	repeat_region complement(2)96. 3220) /evidence-not_experimental	repeat_region complement(12511859) /evidence-nt-greerimental /rnt fanct-rureur	/evidence=not_e	exon complement(10531176) /note="GenScan, score = 5.19%, comment = Internal_exon 124	<pre>/evidence=not_ex /rpt_family="MER</pre>	<pre>/rpt_family="AluSc" repeat_region complement(643964)</pre>	repeat_region complement(293 .586) /evidence=not experimental	/map="21q22.3" /clone="cosmid 011M15"	/db_xref="taxon:9606" /chromosome="21"	source 140205 /organism="Homo sapiens"	Biotechnology, Beutenbergstrasse 11, Jena 07745, G Location/Qualifiers	Genome Analysis.	REFERENCE 2 (bases 1 to 40205) AUTHORS Taudien.S., Nordsiek.G., Dagand,E., Hildmann,T., Drescher,B., Weber.I. Rosenthal A and Vasno M.	Taudien,S. Unpublishe	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 40205)	NISM Homo sapiens Eukaryota; Metazoa; Chordata;	S HTG.	e 11411, complete	AF045450 40205 bp DNA	RESULT 14 AF045450	עט ביטביב GAICIGCCTICCTCTCAGTGCAAGGT 120207	411 GATCTGCTTACCTTACCGTCCAAGTT	CAGCCCAGTGAC	QY 351 ATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATG 410	Db 120352 GCTTCACCTATGCCAGTTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCATG 120293
misc_feature	repeat_region	exon	10 t C C C C C C C C C C C C C C C C C C		repeat_region	exon	repeat_region	repeat_region		exon	exon	í	repeat region	exon	0 2 2	0	repeat_region	י פ <i>הפמר</i> "ד פא דרוו	+	<pre>repeat_region</pre>	repeat_region		exon	exon	repeat_region		exon	repeat_region	nother Treatment	+	exon	repeat_region
/evIdence=not_experimental /rpt_family="HERVL" 1513015378	15065, 15188	<pre>complement(1348113519) complement(1348113519) /note="GRAIL, score = 65.000%, comment = good" /evidence=ort synoriment=1 /evidence=ort</pre>	/evidence=not_experimental /rot_family="THRIB"	<pre>/evidence=not_experimental /rpt_family="AluSx" 13102</pre>	/evidence=not_experimental 1262312843	<pre>/rpt_family="MLTLE" complement(1182811949) /note="GRAIL, score = 50.000%, comment = good"</pre>	complement(1177412320) /evidence=not_experimental	<pre>complemenc(1168/11/35) /evidence=not_experimental /not familv="MTR"</pre>	<pre>/note="GRAIL, score = 99.000%, comment = excellent shadow" /evidence=not_experimental</pre>	/evidence=not_experimental 1157011704	11570 11704 // // // // // // // // // // // // //	/evidence=not_experimental /rpt_familv="12"	/ House Aponing Experimental 11478 11507	11129)	/notte="GRAIL, score = 86.000%, comment = excellent"		1066210875	<pre>comprement(10100:100:100:100) /evidence=not_experimental /rpt_family="MJT2E"</pre>	/evidence=noc_experimental /rpt_family="LIMC3" complement/10138 10427\	H-1	complement(91909258) /evidence=not experimental	<pre>/note="GRAIL, score = 55.000%, comment = good" /evidence=not experimental</pre>	<pre>/note="GRAIL, score = 55.000%, comment = good shadow" /evidence=not_experimental complement(91139213)</pre>	/rpt_family="MER1A" 88378876	<pre>complement(88099187) /evidence=not_experimental</pre>	<pre>/note="MZEF, score = 67.4%" /evidence=not_experimental</pre>	"L2"	80488178 /evidence=not_experimental	/rpt_family="FLAM_A"	TO 0	598)	<pre>complement(51137899) /evidence=not_experimental</pre>

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NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces in health of the health of the sizes in health of the health of the sizes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 28835; contig of 28835 bp in length
28836 28935; gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 8.3 in Q20 bases; agarose-fp Quality coverage: 8.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: L20921
Center clone name: 147_E_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 169879 bases at least Q40 Consensus quality: 172188 bases at least Q30 Consensus quality: 173133 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-terminator Big Dye; 100% o Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Plasmid; n/a; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 176000; agarose-fp
Insert size: 173761; sum-of-contigs
                                                                                                               119648 119747: gap of 100 bp
119748 147772: contig of 28025 l
                                                                147773 147872: gap of 100 bp 147873 174557; contig of 26685 k
                                                                                                                                                                                    72720 81566: contig of 8847 bp in length 81567 81666: gap of 100 bp in length 81667 96774: contig of 15108 bp in length 96775 96874: gap of 100 bp
                        .74558 174657: gap of .74658 175861: cont:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29563 29662:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 bp
100 bp
100 bp
100 bp
100 bp
100 bp
100 30005: contig of 1577 bp
100 32105: gap of
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            50604: contig of 3015 bp in length
50704: gap of 100 bp
50470: contig of 5666 bp in length
56470: gap of 100 bp
64079: contig of 7609 bp in length
64179: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36079: contig of 1467 bp in length
36179: gap of 100 bp
37483: contig of 1304 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                             41065: contig of 1799 bp in length
41165: gap of 100 bp
43103: contig of 1799 bp in length
43203: contig of 2038 bp in length
43303: gap of 100 bp
47489: contig of 4186 bp in length
7589: gap of 100 hp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43303:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33228: gap of 100 b
34512: contig of 1284
34612: gap of 100 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47589:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39266:
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100 bp
19266: contig of 1583 k
19266: gap of
41065: continued
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                                                                                                                                                                                                                                                                           100 bp 10.19: contig of 8440 bp in gap of 100 km
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62: contig of 627
gap of 100 1
                        contig of 1204 bp in length
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FEATURES

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                                 Db 120412 CTCTTAACCAAATGGTGGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACC
                                                                                                  Db 120472 GGACTCAGAGGCTCACTTCAACTGCACCGTGGGCTCACGGCTGGAAGCTTCTCATGTGGA 120413
                                                                                                                                                                    Db 120532 TCTAGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAA 120473
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                                                                                                                    172 GGGCTCCCAGGCTCGCTTCAACTGCACCGT-CTCCCAGGGCTGGAAGCTCATCATGTGGG 230
                                                                                                                                                                                     112 TGTAGGTTCTGGGTCTGGAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGTCCTGAA 171
                                                                   231
291 GCTTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACA 350
                                                                                                                                                                                                                                                     Local
                                                                   CTCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACC
                                                                                                                                                                                                                                       239;
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                        48903
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clone_end:SP6
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39540 c 39029 g 46286 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81667
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72720. .81566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
50705. .56370
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174658. .175861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="RP23-147E11"
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47873. .174557
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                                                                                                                                                                                                                                     14.2%; Score 176.4; DB 2
73.3%; Pred. No. 4.2e-31;
Live 0; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .32005
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                171 CTCAGAGGCTCACTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                             111 AGCTTCCGGATCCAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGGA 170
                                                                                                                                                                                    291
                                                                                                                                                                                                                        295 CACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATGT 354
                                                                                                                                                                                                                                                                   231 TAACCAAATGGTGGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACCGCTT
                                                                                                                                                                                                                                                                                                  235 CAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 AGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCCAGAATGCAACAGTCCTGAAGGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                          TGCTTACCTTACCGTCCAAG 434
TGCCTTCCTCAGTGCAAG 430
                                                                                     GCAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGATC
                                                                                                                                                                             CACCTATGCCAGTTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCATGATGT
                                                                                                                                                                                                                                                                                                                                                                                                           CTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 10 Row: m Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgebcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.R.
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Glibert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Translation="MEGSWRDVLAVLVILAQLTASGSSYQIIEGPQNVTVLKDSEAHF
/Translation="MEGSWRDVLAVLVILAQLTASGSSYQIIEGPQNVTVLKDSEAHF
NCTVTHGWKLLMWTLNQMVVLSLTTQGPIITNNRFTYASYNSTDSFISELIIHDVQPS
DSGSYQCSLQNSHGFGSAFLSVQDSIGEEGPALPTWAIILAVAFSLLLLIIIVLIII
FCCCCASRREKEESTYQNEIRKSANNRTNKADPETKLKSGKENYGYSSDEAKAAQTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV-SPORT6"
55. .867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPPKSAEVSLPEKRSSSLPYQELNKHQPGPATHPRVSFDIASPQKVRNVTLV"
364 c 367 g 378 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="RIKEN cDNA 2010003D20 gene"
/protein_id="AAH04806.1"
/db_xref="GI:13435933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Mammary tumor. Metallothionien-TGF alpha
model. 10 month old virgin mouse. Taken by biopsy."
/cione_lib="NCI_CGAP_Mam1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="LocusID:72058"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="MGC:7960 IMAGE:3584645"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.0%;
73.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 185.6; DB 10;
Pred. No. 2.2e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
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                                      COMMENT
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AUTHORS
TITLE
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Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Garaham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacConald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stanger, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zalhoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Farreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, M., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Kosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Direct Submission
S
                                                    Submitted (09-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 9, 2002 this sequence version replaced gi:20503171. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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                                                                                                                                                                                     TGCCTTCCTCAGTGCAAG
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NCTVTHGWKLLMWTLNQMVVLSLTTQGP11TNNRFTYASYNSTDSF1SEL11HDVQPS
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aammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                    Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                              Mus musculus, RIKEN cDNA 2010003D20 gene, IMAGE: 3584645, mRNA, complete cds.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                      Direct Submission
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/protein_id="CAD28221.1"
/db_xref="GI:19575337"
/translation="MEGSWRDVLAVLVILAQLTASGSSYQIIEGPQNVTVLKDSEAHF
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DSGSVQCSLQNSHGFGSAFLSVQDSIGEEGPALPTWAIILLAVAFSLLLILIIVLIII
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Consensus quality: 180887 bases at least Q30
Consensus quality: 183777 bases at least Q30
Consensus quality: 183777 bases at least Q20
Estimated insert size: 147000; pulse field gel estimation
Bstimated insert size: 193700; sum-of-contigs estimation
Quality coverage: 5.67 in Q20 bases; pulse field gel estimation
4.3 in Q20 bases; sum-of-contigs estimation
4.00TE: This is a 'working draft' sequence. It currently
5.67 in Q20 bases; sum-of-contigs estimation
5.67 in Q20 bases; sum-of-contigs estimation
6.8 NOTE: This is a 'working draft' sequence of the pieces
6.9 is not known and their order in this sequence record is
6.9 arbitrary. Gaps between the contigs are represented as
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Pred. No. 1e-33;
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
of 9468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
of 9870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown length of 14363 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown length
of 9089 bp in length
unknown length
of 15208 bp in length
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of 7697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 10726 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 3093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 8006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 9441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 10486 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 5555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 4288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 3647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
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                                                                                                                                                                                                       complement(8865. .8964)
/note="I.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_type=TANDEM complement(2496. .2878)
 complement(9989. .10077)
                                                      complement(9723. .9882)
/note="L2"
                                                                                                                                                                                                                                                                                         complement(8482. .8762)
                                                                                                                                                                                                                                                                                                                                          complement(6887. .7067)
/note="L1MD3"
                                                                                                                                                                                                                                                                                                                                                                                                                  5542. .5829
/note="Alusx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="BAC-291B3, 3' partial"
/clone_lib="BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/chromosome="21"
                /rpt_family="LINE/L2"
/rpt_type=DISPERSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ′organism≔"Homo sapiens"
                                                                                       rpt_type=DISPERSED
                                                                                                                            'note="AluSq"
                                                                                                                                           rpt_type=DISPERSED
                                                                                                                                                                                                                                   /rpt_family="SINE/Alu"
/rpt_type=DISPERSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SH3BGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="21-Glutamic Acid Rich protein 21-GARP"
/protein_id="CAB90445.1"
/db_xref="GI:7717370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(<3473. .3565,12649. .12678,15331. .15460,18739. .19157)
//gene_"SH3BGR"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="(TCCA)n"
/rpt_family="Simple_repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="LTR/MaLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="THE1C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="LINE/L1"
                                                                                                            rpt_family="SINE/Alu"
                                                                                                                                                                               rpt_family="LINE/L2"
                                                                                                                                                                                                                                                                          'note="AluJo"
                                                                                                                                                                                                                                                                                                            rpt_type=DISPERSED
                                                                                                                                                                                                                                                                                                                                                                                 rpt_type=DISPERSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMEGAEGEAEEEETAEGEEPGEDEDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="SH3BGR"
                                                                                                                                                                                                                                                                                                                             rpt_family="LINE/L1"
                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="GSEKAEEGGETEAQKEGSEDVGNLPEAQEKNEEEGETATEETEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oin(3473. .3565,12649. .12678,15331. .15426)
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                                                                                                                                                                                                                                                                                                                                                         Db 268513 CTCCCAGGCTCGACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCCTCT 268572
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                                                                                                                                               Db 268693 GGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATC
                                                                                                                                                                                                                      Db 268633 CACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 268453 AGGTTCTGGGTCATGGTAATGAAGTCATAGAAGGCCCCCAAAATGCCAAGAGTCCTGAAGGG 268512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ω
                                                                        Db 268753 TGCTTACCTTACCGTCCAAGGTGTG 268777
                                                                                                                                                                                                                                                                                             Db 268573 CAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCCATCATCACCAATGACCGCTT
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                                                                                             415 TGCTTACCTTACCGTCCAAGTTATG 439
                                                                                                                                                                  355 GGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATC
                                                                                                                                                                                                                                         295 CACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATGT 354
                                                                                                                                                                                                                                                                                                                 235 CAGTGACATGGTGGTGGTAAGCGTCAGGCCCATGGAGCCCATCATCATCACCAATGACCGCTT 294
                                                                                                                                                                                                                                                                                                                                                                                                       175 CTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 AGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGTCCTGAAGGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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/rpt_type=DISPERSED
14013. .14131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(13598. .13892)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(11315. .11556)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(11002. .11282)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(10430. .10651)
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/rpt_type=DISPERSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="Simple_repeat"
/rpt_type=TANDEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="Aluy
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98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 318.6; DB 9;
Pred. No. 7.3e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 340000;
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                                                                       REFERENCE
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                                                                                                                                                                                                    ACCESSION
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                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                               ORGANISM
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Best Local :
                                                                                                                                                                                                                                                                                                                                    44573
                                                                                                                                                                                                                                                                                                                                                                                                           44513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44453 CACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                        GARGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATC 414
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             Hattori,M., Fujiyama,Å., Taylor,T.D., Watanabe,H., Yada,T. Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soed Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 340000)
                                                                                                                             Homo sapiens
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/evidence=not_experimental
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Blechschmidt, K.
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* e.mail: sakaki@gsc.riken.go.jp
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/note="Accession No. AF121782" 286628. .>340000
                                              /clone="P206A10, 3' partial"
/clone_lib="RPCI1,3-5 PAC lil
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Hornischer, K., Brandt, P., Scharfe, M., Schoen, O., Desario, A., Reichelt, J., Kauer, G., Bloecker, H., Ramser, J., Beck, A., Klages, S., Hennig, S., Riesselmann, L., Dagand, E., Wehrmeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and
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Submitted (05-MAY-2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Biology * The Chromosome 21 Mapping and Sequencing Consortium consists of * RIKEN Genomic Sciences Center, Human Genome Research Group, * Genetics (addresses see below)

* URL: http://genome.imb-jena.de, * Institute of Molecular Biotechnology, Genc Beutenbergstrasse 11, D-07745 Jena, Germany, * e_mail: gscj-submit@genome.imb-jena.de Genome Analysis,

* URL: http://adenine.dmb.med.keio.ac.jp/ Keio University School of Medicine, Dept. yo 160-8582, .mail: shimiz shimizu@dmb-med.keio.ac.jp Japan, of Molecular Biology, *

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Max-Planck Institute for Molecular Genetics URL: http://genome.gbf.de/

Germany,

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complement(78198220) /evidence=not_experimental /rpt_family="MLT1J"	<pre>/rpt_tamily="LTR16C" complement(75617696) /evidence=not_experimental /rpt_family="MIR"</pre>	/rpt_tamily="MLFIC" 7347	/evidence=not_experimental	/note="GenScan, score = 1.83%, comment = Initia frame: 1 phase: 0"		<pre>/evidence=not_experimental /rpt_family"HERVL" 6682. 6751</pre>	/note="xpound exon prediction, score = /0% (0%)" /evidence=not_experimental 53856104	1	<pre>/evidence=not_experimental 46744781 /note="GRRIT. score = 42 000% comment = marginal"</pre>	00%, comment = good	<pre>/rpt_family="THELB" 3479. 3618 /evidence=not_experimental</pre>	3123 3478 3123 3478 /evidence-not_experimental	30123122 /evidence=not_experimental /rot_familv="Mr.Trl."	26292831 /evidence=not_experimental /rpt_family="AluSx"	00%, comment = good		/evidence=not_experimental /rpt_family="MIR" complement(1780. 2326)	experimental 931741)	<pre>/evidence=not_experimental 1576 . 1710 /nofe="GRAIL. score = 99.000%, comment = excellent"</pre>	/rpt_family="L2" 15761710 /note="MZEF, score = 66.1%"	1481 .1603 /evidence=not_experimental	11141403 /evidence=not_experimental /rot_familv="Mrrll"	<pre>complement(10781162) /note="GRAIL, score = 86.000%, comment = excellent /evidence=not_experimental</pre>	complement(668881) /evidence=not_experimental /rpt_family="MER58A"	complement(140415) /evidence=not_experimental /rot_family==Mrgper
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/rpt_family="THELA" region 1720917632 /evidence=not_experimental	/evidence=not_experimentar /rpt_family="MER34" egion complement(1685117208) /evidence=not_experimental				<pre>/rpt_family="LIPA6" complement(15469, .15497) /norbe="xound exon prediction, score = 62% (0%)"</pre>	/evidence=not_experimental egion 1525515299 /evidence=not_experimental	/IPC_Idility" LIRA /A complement(14962. 115036) /note="MZEF, score = 93%"	egion complement(1431714614) /evidence=not_experimental	egion complement(1361313908) /evidence=not_experimental /rpt_familv="Alusx"	egion complement(1322613364) /evidence=not_experimental /rpt_family="LIMC2"	complement(1305713161) /note="MZEF, score = 76.18" /evidence=not_experimental		/evidence=not_experimental. /rpt_family="MLT1C" 1290213180	/note="MZEF, SCORe = /9.4%" /evidence=not_experimental egion complement(1234612827)	/evidence=nor_experimentar /rpt_family="Allog" complement(1152511777)	/rpt_family="LIMC/D" egion 1150311818	/ipt_dallity= Mulif egion 11318. 11417 /evidence=not experimental	egion 1066511028	egion 1024410664 /evidence=not_experimental /rpt_familv="MLTlE"	242	egion 9966. 10041	92909371 /note="GRAIL, score = 81.000%, comment = excellent shadow" /evidence=not experimental	<pre>complement(92739420) /note="GRAIL, score = 71.000%, comment = good" /evidence=not_experimental</pre>	egion complement(8738. 9232) /evidence=not_experimental /rpt_family="MLT1C"	80978119 Note="GRAIL, score = 45.000%, comment = marginal" /evidence=not experimental

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TATTTCCTGGGAGCTTGAGGTTCCCGTAAGCCATTCGAGTTACAATTCCTTTCTGGAGCC
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                                                                                                                                                                                                    GCAGCCCAGTGACTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGATC
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                                                                   CACTGAGGGTGAACCCTGTAATGTGACTTGCTATGCCGTGGGCTGGACCTCACTCCCGGA
                                                                                                  CGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACCCGGCTCCCGGA
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Sequence 9 from Patent W00200710
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TVVQPPPDS1GEEGPALPTWA1ILLAVAFSLLLI1YLLIIFCCCCASRREKEESTY
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SLPYQELNKHQPGPATHPRVSFDIASPQKVRNVTLV"
1 304 c 291 g 287 t
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                                                                                                                                                                                   Submitted (21-JAN-1999) Genome Analysis, Institute for Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 142742)
Taudien,S., Dagand,E., Hildmann,T., Nordsiek,G., Drescher,B., Schattevoy,R., Weber,J., Schilling,M., Menzel,U., Yaspo,M.L. and
                                                                                                                                                                                                                        Direct Submission
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Query Match 85.8%; Score 1064; DB 6; Length 1139; Best Local Similarity 97.2%; pred. No. 5.4e-242; Matches 1102; Conservative 0; Mismatches 10; Indels 22; Gaps 1; Qy 106 AGAAGCTGTAGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGT 165	CDS // CODON_Start=1 // COCON_START=1 // COCON_START=1 // COCON_START=1 // COCON_START=1 // CDD28219.1 // CDD38219.1 // CDD38219.	M Homo sapic Eukaryota, Mammalia; 1 1 S Welcher, A B7-like mc B7-like mc Patent: Wc Amgen, Inc	;D	Qy 1066 AACCGCTTCTCCCCAAATCCTGTGAATCCAGTGATCCTGAAACAAAGAAAG	Db 694 ATTATCAAGTTTACCGAGTTTTCATCGCCGACGTGTACTTTACAATACGCTGCTGGTG 885 Qy 826 ACTAGCAGGCACCATGCTTCTGACGCCGACGTGTACTTTACAATACGCTGCTGCTG 885
OY 1126 CHETGGCCCTCCTCACCAGGGCTGATCAACGTCCACCAGGCCAGGCCAGCCA	106 AACGCCTTCTCCCCAAATCCTGTGAATCCAGTGCTGCTGAACAAAGAAACAAAAGAAACAGTAG	627 AAATCTCACTGTGATTCCGTGTCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGT 766 ATTATCAAGTTTACCGAGGTTTAGGTTTTTCATTGCCTACTTGGGGCAAAGTTTGACTTGG [Qy 586 TCCGGAGCCCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAA 645	Qy 406 GCATGGATCTGCTTACCTTACCGTCCAAGTTATGGGAGAGCTGTTCATTCCCAGTGTTAA 465	Db 27 AGACCCACCGGTTCTGGGTCTGGTAATGAAGGCCCCCAAAATGCAAGAGT 86 Qy 166 CCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCAT 225

REFERENCE AUTHORS TITLE

JOURNAL

Welcher, A.A., Sarmiento, U.M., Schul B7-like molecules and uses thereof Patent: WO 0200710-A 3 03-JAN-2002;

Sarmiento, U.M., Schultz, H.J. and les and uses thereof

Chute, H.T.

Inc. (US)

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                                                                                                                            AATCTGGCCAGTCCTGAGAAGGTCAGTAATACAACTGTAGTATAG 1240
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Patent WO0200710.
Chordata;
Primates;
Craniata; Vo Catarrhini;
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                                                                    TGGGACTTTGACTTGCGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGT
                                                                                              CCACAATGTGGAGCCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCT 405
                              AAATCTCACTGTGATTCGGTGTCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGT
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                                                                                                 GACTAGCAGGCACCATGCTTCTGACGCCGACGTGTACTTTACAATACGCTGCTGCTGCT
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/clone_lib="PLACE6"
/note="cloning vector: pME188FL3"
463 c 474 g 534 t
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                                                                                                                          TCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTC
                                                                                                                                        TCCCAGGCTCGCTTCAACTGCACCGTCTCCCCAGGGCTGGAAGCTCATCATGTGGGCTCTC
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ACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATGTG
                                                             AGTGACATGGTGGTGCTAAGCGTCAGGCCCATGAGCCCATCATCACCAATGACCGCTTC
                                                                           AGTGACATGGTGGTGGTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1 from Patent W00200710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Welcher, A.A., Sarmiento, U.M., Schultz, H.J. and Chute, H.T. B7-like molecules and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                           /translation="MGLVIFLHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLI MWALSDMVVLSVRPMEPIITNDRFTSQRYDQGGNFTSEMIIHNDFSDSGNIRGSLQN SRLHGSAYLTVQVMGELFIPSVNLJVVAENEPCEVTCLPSHMTLHDISWELGLLVSHS SYYFYPEBSDLÖSAVSILALTPQSNGTLTCVATWKSLKARKSATVNLTYIRCPQDTGG GINIPGVLSSLPSLGESLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCCRCCCRRCFGRIGPGXLSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCCCCCRCFGRKRGFRIQFQKKSEKTNKETETESGNENSGYNSDEQKTTDTASLPPKSC ESSDPEGRNSSCGPPHQRADQRPPFASHPQASFNLASPEKVSNTTVV" 307 c 286 g 287 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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27. .1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAD28216.1"
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                                                                                                                                                                                                                                                                 Score 1123.4; DB 6; Pred. No. 4.3e-256;
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                                                                                                                                                                                                                   TCGGTGTCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGTATTATCAAGTTTACC
                                              CGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGAT
                                                                                                           CCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGACTTTGACTTG
                                                                                                                                                      CTGGGAGCTCGGTCTCGTCAGCCATTCAAGCTATTATTTTTGTTCCGGAGCCCAGCGA
                                                                                                                                                                       CTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGTTCCGGAGCCCAGCGA
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                             CGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGAT
                                                                                                                                                                                                                                                                                CCTTACCGTCCAAGTTATGGGAGAGCTGTTCATTCCCAGTGTTAATCTTGTAGTCGCTGA
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                                                                                            CCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGACTTTGACTTG
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PKSCESSDPEQRNSSCGPPHQRADQRPPRPASHPQASFNLASPEKVSNTTVV"

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80. .1240
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Pred. No. 8.7e-284;
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                                                                             CCAGCGGGCTGATCAACGTCCACCCAGGCCAGCAAGTCATCCACCAGGCTTCTTTAATCT 1200
                                                                                                                           TCCCAAATCCTGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCTCCTCA 1140
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GGCCAGTCCTGAGAAGGTCAGTAATACAACTGTAGTATAG 1240
                                                               CCAGCGGGCTGATCAACGTCCACCCAGGCCAGGCAAGTCATCCACAGGCTTCTTTTAATCT 1200
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RESULT 2 AK092516 SOURCE KEYWORDS VERSION ACCESSION DEFINITION ORGANISM Homo sap Homo sapiens oligo capping; fis (full insert sequence).
Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE6 AK092516.1 AK092516 Eukaryota; Metazoa; Mammalia; Eutheria; clone:PLACE6017788. AK092516 2016 2051 bp sapiens cDNA FLJ35197 fis, GI:21751130 Chordata; Primates; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. clone mRNA linear one PLACE6017788, PRI 15-JUL-2002 highly similar

REFERENCE

AUTHORS

Isono,Y.,

REFERENCE AUTHORS JOURNAL TITLE TITLE JOURNAL Kawakami,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai Direct Submission Unpublished sogai, T. and Yamamoto, J. (bases 1 to 2051) Isogai,T human cDNA sequencing project

Submitted (04-UL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and annotation: HRI and RAB.

COMMENT

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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2: gb_htg:*
3: gb_in:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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em_htgo_hum:*
em_htgo_mus:*
em_htgo_other:*
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                                                                       em_htg_pln:*
em_htg_rod:*
em_htg_mam:*
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em_ph:*
em_pl:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

+	
X380400	
OCUS	AX380400 1240 bp DNA linear PAT 18-MAR-2002
EFINITION	Sequence 5 from Patent WO0200710.
CCESSION	AX380400
ERSION	AX380400.1 GI:19575330
EYWORDS	•
OURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
EFERENCE	
AUTHORS	Welcher, A.A., Sarmiento, U.M., Schultz, H.J. and Chute, H.T.
TITLE	B7-like molecules and uses thereof
JOURNAL	Patent: WO 0200710-A 5 03-JAN-2002;

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STATE: New York
COUNTRY: U.S.A.
ZIP: 1036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/OBS/MS-DS
FILING DATE: 21-JAN-1994
CLASSIFICATION NUMBER: US/OB/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 7326-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 790-9090
TELEPX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LERGIST STATES
LERGIST STATES
LERGIST COMPANIES
LERGIST COMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: unknown; MOLECULE TYPE: cDNA US-08-185-432-23
Search completed: April 29, 2003, 10:51:03 Job time: 125.912 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.3%; Score 41; DB 1; Length 3771; Best Local Similarity 66.3%; Pred. No. 0.1; Matches 59; Conservative 0; Mismatches 30; Indels
                                                                                                                                                                                                1957 GCTGTTGCTGCGCGGATGCAGTGGTAAT 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DE
TITLE OF INVENTION: AN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            1897 GCTGCTGCTGCTGCTGCTGCTGCTGCACCTGTTGCTGCTGCTTGTTGCTGCT 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1155 AV
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                       933 GCTGTAGAAGAAAAAGAGGATTTCGTATT 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  873 GCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTGTTTCT 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3771 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELTEX PROTEINS, NUCLEIC ACIDS, AND ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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